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5	1449	100.0	1449	6	BD017452 C3a recep
6	1449	100.0	1449	9	AY268431 Homo sapi
7	1449	100.0	1449	9	HS32AAREC
8	1449	100.0	1449	6	AX646469 Sequence
9	1449	100.0	1849	9	AB065870 Homo sapi
10	1449	100.0	1985	9	BC020742 Homo sapi
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LOCUS BD017452 1449 bp DNA linear PAT 27-AUG-2002
DEFINITION C3a receptor and screening method using C3a.
ACCESSION BD017452.1 GI:22558628
VERSION JP 2001228137-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1449)
AUTHORS Jr,R.S.A., Bergsma,D.J., Foley,J.J., Kumar,C. and Saro,H.M.
TITLE C3a receptor and screening method using C3a
JOURNAL Patent: JP 2001228137-A 1 24-AUG-2001;
SMITHKLINE BEECHAM CORP
COMMENT OS Homo sapiens (human)
PN JP 2001228137-A/1
PD 24-AUG-2001
PP 11-JAN-2001 JP 2001003701
PR 17-JUN-1996 US 60/019627
PI ROBERT S AMES JR, DERK JOHN BERGSMAN, JAMES J FOLEY, CHANDLICA PI
KUMAR,
PI HENRY M SARO
PC GOIN33/15, C12Q1/02, C13Q1/68, G01N33/50//C07K14/47, C12N15/09, PC
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CC C3a receptor and screening method using C3a
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FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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 LOCUS
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1449)
 Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.
 Isolation of complete coding sequence for complement component 3a receptor 1 (C3AR1)
 Unpublished
 2 (bases 1 to 1449)
 Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.
 Direct Submission
 Submitted (01-APR-2003) Guthrie cDNA Resource Center, Guthrie Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
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ORIGIN

Query Match 100.0%; Score 1449; DB 9; Length 1449;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Locus		H.sapiens mRNA for C3a anaphylatoxin receptor.		
DEFINITION		C3a anaphylatoxin receptor.		
ACCESSION		Z73157.1 GI:2826756		
VERSION		C3a anaphylatoxin receptor.		
KEYWORDS		Homo sapiens (human)		
SOURCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
ORGANISM		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 1449)		
AUTHORS		Crass,T., Raffetseder,U., Martin,U., Grove,M., Klos,A., Kohl,J. and Bautsch,W.		
TITLE		Expression cloning of the human C3a anaphylatoxin receptor (C3AR) from differentiated U-937 cells		
JOURNAL		Eur. J. Immunol. 26 (8), 1944-1950 (1996)		
MEDLINE		96350520		
FUBMED		8765043		
REFERENCE		2		
AUTHORS		Bautsch,W.		
TITLE		Direct Submission		
JOURNAL		Submitted (07-JUN-1996) Crass T., Hannover Medical School, Institute of Medical Microbiology, Carl-Neuberg-Str. 1, Hannover,		
REMARK		Germany, 30625 Revised by [3]		
REFERENCE		3 (bases 1 to 1449)		
AUTHORS		Bautsch,W.		
TITLE		Direct Submission		
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RESULT 8
 LOCUS AX646469 1849 bp DNA linear PAT 04-MAR-2003
 DEFINITION Sequence 661 from Patent EP1270724.
 ACCESSION AX646469
 VERSION AX646469.1 GI:28798850
 KEYWORDS

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H. Guanosine triphosphate-binding protein coupled receptors Patent: EP 1270724-A 661 02-JAN-2003; National Institute of Advanced Industrial Science and Technology (JP); Center for Advanced Science and Technology Incubation, Ltd. (JP)
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ACCESSION AB065870
VERSION   AB065870.1 GI:21929004
KEYWORDS  .
SOURCE    Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsumoto, S., Teutsuni, S., Aburatani, H., Asai, K. and Akiyama, Y.
JOURNAL   Genome-wide discovery and analysis of human seven transmembrane helix receptor genes
REFERENCE 2 (bases 1 to 1849)
AUTHORS   Suwa, M.
TITLE     Direct Submission
JOURNAL   Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail: m-suwa@aist.go.jp, URL: http://www.cbrc.jp/, Tel: 81-3-3599-8080, Fax: 81-3-3599-8081)
COMMENT   This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.
          And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].
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REFERENCE 1 (bases 1 to 1985)
AUTHORS Strausberg, R., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE 2 (bases 1 to 1985)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URI: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 36 Row: 1 Column: 10
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VERSION AY455929.1 GI:38201494
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12053)
AUTHORS Rieder,M.J., Daniels,R.L., da Ponte,S.H., Hastings,N.C.,
Ahearn,M.O., Rajkumar,N., Yi,Q. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-2003) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: SeattleSNPs. NHLBI HL66682 Program
for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
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 Db 9622 ACTGTGTGA 9630

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 ACCESSION AC006511
 VERSION AC006511.5 GI:4713940
 KEYWORDS HTG
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 186321)
 Muzny D., Aronson A.D., Bouck J., Bunac C., Chen Z., Ding Y., Dugan S., Durbin J., Forcum J., Garcia C., Gorrell J.H., Gorrell L.L., Hernandez J., Issar A., Jackson L., Kneitz S., Kondrjewski N., Lau S., Leal B., Lee E., Lichtarge O., Liu W., Logan O., Lu J., Marondel I., Martinez C., Merscher S., Miller A., Montgomery K., Oswal G., Pampell L.R., Parish B.J., Perez L., Rashid N.D., Rives C., Scherer S.E., Shen H., Shim C., Simon M., Vo Q., Williamson A., Worley K.C., Xiang A.M., Yang R., Yu W., Zhou X., Kucherlapati R., Nelson D. and Gibbs R.A.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (29-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 4 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 5 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 6 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 7 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 8 (bases 1 to 186321)
 AUTHOR Worley K.C.
 TITLE Direct Submission
 JOURNAL Submitted (31-DEC-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT
 On Apr 29, 1999 this sequence version replaced gi:4309839.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email

gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
 STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

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repeat_region	1600..1722 /rpt_family="L2"
repeat_region	1723..2010 /rpt_family="AluSg"
repeat_region	2011..2891 /rpt_family="L2"
repeat_region	2910..3423 /rpt_family="MLT1H"
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LOCUS AX335504 1956 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 6013 from Patent WO0194629.
ACCESSION AX335504
VERSION AX335504.1 GI:18126223
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6013 13-DEC-2001;
Avalon Pharmaceuticals (US)
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DEFINITION Human putative G protein-coupled receptor (AZ3B) mRNA, linear PRI 21-FEB-1996
cds.
ACCESSION U28488
VERSION   U28488.1 GI:1199577
KEYWORDS Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1956)
AUTHORS Roglic,A., Prossnitz,E.R., Cavanagh,S.L., Pan,Z., Zou,A. and
Ye,R.D.
TITLE cDNA cloning of a novel G protein-coupled receptor with a large
extracellular loop structure
JOURNAL Biochim. Biophys. Acta 1305 (1-2), 39-43 (1996)
MEDLINE 96180983
PUBMED 8605247
REFERENCE 2 (bases 1 to 1956)
AUTHORS Ye,R.D.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-1995) Richard D. Ye, Immunology, IMM-25, Scripps
Research Institute, 10666 N. Torrey Pines Road, La Jolla, CA 92037,
USA

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121 AATGGGCTGGTGTGTGGGTGGCTGGCTGAAGATGCGAGCGAGTGAACACAAATTTGG 180
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181 TTCTCCACCTCAGCTTGGGGGACCTCTCTGCTGCTGCTCTCTCTGCTGCTCTCTCGTGGCT 240
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742 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAAGACCTTCTGCAGAT 801

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901 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGGTTTCCAGGATTTATTAACAATTTA 960
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QY 1441 ACTGTGTGA 1449
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DEFINITION Sequence 1 from patent US 6521418.
ACCESSION AR281967
VERSION AR281967.1 GI:29717946
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Ye,R.D.
TITLE G protein-coupled receptor with an enlarged extracellular domain
JOURNAL Patent: US 6521418-A 1 18-FEB-2003;
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Best Local Similarity 99.9%; Pred. No. 0;
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QY 1 ATGGCGCTTTCTCTGCTGAGACCAATTCACCTACTCTCTCAGCCATGGAATGAG 60
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QY 61 CCCCAGTAATTTCTCCATGCTCATCTCAGCCCTTACTTTTACTTGGGATGCCAGGC 120
Db 142 CCCCAGTAATTTCTCCATGCTCATCTCAGCCCTTACTTTTACTTGGGATGCCAGGC 201
QY 121 AATGGCTGGTGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 180
Db 202 AATGGCTGGTGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 261
QY 181 TTCTTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTTGGCCCTTCTGCTGGCT 240
Db 262 TTCTTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTTGGCCCTTCTGCTGGCT 321
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCC 300
Db 322 CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCC 381
QY 301 ATCAATCTCTCACATGTTTGGCAGTGTCTTCTGCTTACTGCGCAATTAGCCTGATGCG 360
Db 382 ATCAATCTCTCACATGTTTGGCAGTGTCTTCTGCTTACTGCGCAATTAGCCTGATGCG 441
QY 361 TGTCTTGTGTATTCAGGCCAATCTGGTGTGAGAAATCATCGCAATGTAGGGATGGCTGC 420
Db 442 TGTCTTGTGTATTCAGGCCAATCTGGTGTGAGAAATCATCGCAATGTAGGGATGGCTGC 501
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QY 421 TCTATCTGTGATGTATCTGGGTGTGGCTTTTGTGATGTGCATCTCTGTGTCTGTGTAC 480
Db 502 TCTATCTGTGATGTATCTGGGTGTGGCTTTTGTGATGTGCATCTCTGTGTCTGTGTAC 561
QY 481 CGGGAATCTTCTACCTACAGACAAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 562 CGGGAATCTTCTACCTACAGACAAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
QY 541 TCATTAGATTTATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAAT 600
Db 622 TCATTAGATTTATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAAT 681
QY 601 GTTCAGCGCTGAGGAAATGAATGATAGGTAGATCTCTCTCTTTCACAAACAAATGAT 660
Db 682 GTTCAGCGCTGAGGAAATGAATGATAGGTAGATCTCTCTCTTTCACAAACAAATGAT 741
QY 661 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTTCAAGACCTTCTGCGAGAT 720
Db 742 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTTCAAGACCTTCTGCGAGAT 801
QY 721 TCACTCCCTAGGGGTTCTGCTAGGTAAACAACTCAAACTCTGATTTCTAATGATTTAAA 780
Db 802 TCACTCCCTAGGGGTTCTGCTAGGTAAACAACTCAAACTCTGATTTCTAATGATTTAAA 861
QY 781 CCTGCTGATGTGCTCTACCTAAATCCCAAGTGGGTTTCTTATGAAGATCAAGAAC 840
Db 862 CCTGCTGATGTGCTCTACCTAAATCCCAAGTGGGTTTCTTATGAAGATCAAGAAC 921
QY 841 AGCCCACTGGATAACTCTGATGCTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
Db 922 AGCCCACTGGATAACTCTGATGCTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 981
QY 901 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 960
Db 982 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 1041
QY 961 GGCCAATTCACAGATGACGATCAAGTGCACCAACCCCTGCGCAATACGATCAGTAGG 1020
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QY 1021 CTAGTGGTGGTTCCTGCTGCGCTCTGTTATCATGATGACCTGTTTACAGCTTCATTGTC 1080
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QY 1081 TTCGGAATGCAAGGGGCGCTTGGCCAAAGTCTCAGAGCAAAACCTTTCAGTGGCGGTG 1140
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Db 1402 GATTTAGGAAGAAAGCAGGAGTCCATTCAGGAAATCTGGAGCAGCCTTCAGTGAG 1461
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Db 1462 GAGCTCACAGTTTCCACCCACTGTCCTCAAAATGTCATTTTCAGAAAGAAATAGTACA 1521
QY 1441 ACTGTGTGA 1449
Db 1522 ACTGTGTGA 1530
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Search completed: April 11, 2005, 05:27:40
Job time : 6439 secs

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OW nucleic - nucleic search, using sw model

Run on: April 11, 2005, 02:56:00 ; Search time 839 Seconds
(without alignments)
10223.725 Million cell updates/sec

Title: US-10-764-649-1
Perfect score: 1449
Sequence: 1 atggcgcttctctctgtga.....gaaatagtaactgtgtga 1449

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	1449	6	ABK86860 Human ana
2	1449	100.0	1449	8	ACA64730 Chemoattr
3	1449	100.0	1449	8	ABZ42643 Human com
4	1449	100.0	1449	10	ADF43377 Chemoattr
5	1449	100.0	1449	13	ADR05359 Human cDN
6	1449	100.0	1449	13	ADSO9203 Complemen
7	1449	100.0	1449	10	ADC86208 Human GPC
8	1449	100.0	2040	2	AAV03250 Homo sapi
9	1449	100.0	2096	12	ADQ23545 Human sof
10	1447.4	99.9	1449	12	ADO29820 Human GPC
11	1447.4	99.9	1956	6	ABL67676 Oesophagu
12	1447.4	99.9	1970	2	AAT64946 cDNA enco
13	1447.4	99.9	2040	2	AAT36375 Human G-p
14	1447.4	99.9	2040	9	ACD26620 cDNA enco
15	1447.4	99.9	2040	10	ADE84844 Farnesyl
16	1447.4	99.9	2040	12	ADL22831 Human C3a
17	1447.4	99.9	2040	12	ADQ19274 Human sof
18	1447	99.9	2040	3	AAF18195 Lung canc
19	1442.6	99.6	1449	5	ABI97972 Non-endog
20	1436.4	99.1	1446	2	AAT70001 C5a anaph

21	1436.4	99.1	1446	2	AAT45873	Aat45873 C5a-like
22	1155.6	79.8	1893	13	ACN42148	Acn42148 Human dia
23	988.2	68.2	7449	6	ABL32277	Abi32277 Human imm
24	876.2	60.5	7449	6	ABL32276	Abi32276 Human imm
25	788	54.4	1434	12	ADL22833	Adl22833 Murine C3
26	788	54.4	1434	12	ADO30111	Ado30111 Mouse GPC
27	788	54.4	2657	6	ABK13745	Abk13745 Mouse ana
28	788	54.4	2657	13	ADR05367	Adr05367 Mouse cDN
29	788	54.4	3329	5	AAD02458	Aad02458 Mouse C3a
30	330	22.8	453	9	ACH26794	Ach26794 Human adu
31	282	19.5	453	3	AAA52668	Aaa52668 Eosinophi
32	198	13.7	625	10	ADB85150	Ade85150 Farnesyl
33	174	12.0	611	10	ADB85151	Ade85151 Farnesyl
34	160.4	11.1	1053	5	ABI97973	Abi97973 Non-endog
35	160.4	11.1	1053	12	ADO29821	Ado29821 Human GPC
36	160.4	11.1	1078	6	ABN85452	Abn85452 Human C5a
37	160.4	11.1	1092	13	ADR05361	Adr05361 Human cDN
38	160.4	11.1	1696	6	AAS94842	Aag94842 Human DNA
39	160.4	11.1	1696	10	ADE53750	Ade53750 Human pro
40	160.4	11.1	2110	13	ACN42416	Acn42416 Human dia
41	160.4	11.1	2283	13	ADQ86921	Adq86921 Human tum
42	160.4	11.1	2328	8	ABZ42644	Abz42644 Human com
43	160.4	11.1	2328	10	ACA56590	Aca56590 Human sig
44	160.4	11.1	2328	11	ADI31692	Adi31692 Human cDN
45	160.4	11.1	2328	12	ADI56386	Adi56386 Human pol

ALIGNMENTS

RESULT 1
ABK86860
ID ABK86860 standard; cDNA; 1449 BP.

AC ABK86860;

DT 04-SEP-2002 (first entry)

XX Human anaphylotoxin C3a receptor cDNA.

Human; C3a; receptor; nootropic; neuroprotective; antiparkinsonian;
G protein-coupled receptor; GPCR; anaphylatoxin C3a receptor; AR;
Alzheimer's disease; Parkinson's disease; cell signalling; proliferation;
differentiation; leukocyte migration; gene transcription; vision; smell;
neurotransmission; hormonal response; ulcerative colitis; diabetes;
myocardial infarction; hypertension; asthma; bronchitis; pneumonia;
Crohn's disease; rheumatoid arthritis; Hodgkin's disease; glioblastoma;
neurodegenerative disorder; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 1. .1449
CDS /*tag= a
/product= "C3a receptor"

WO200244737-A2.

06-JUN-2002.

29-NOV-2001; 2001WO-US045220.

29-NOV-2000; 2000US-0250251P.

30-NOV-2000; 2000US-0250452P.

17-OCT-2001; 2001US-0330036P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

XX Brown JP, Burmer GC, Roush CL, Morningstar DA;

WPI; 2002-508526/54.

DR P-PSDB; RAU99102.

XX

tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.

Unidentified.

US2002177551-A1.

28-NOV-2002.

30-MAY-2001; 2001US-00870759.

31-MAY-2000; 2000US-0208128P.

(TERM/) TERMAN D S.

Terman DS;

WPI; 2003-361759/34.

P-PSDB; ABU79122.

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Example 2; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal APC activated immunocytes to the host), producing (M3) a tumouricidal APC population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipid to contact T cells, in which adaptor proteins which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence encodes an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from the US patent
CC office website at "seqdata.uspto.gov/sequence.html?DocID=2002077551"
XX
SQ Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;
Query Match 100.0%; Score 1449; DB 8; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGCTTTTCTCTGCTGAGACCAATTCAACCTACTCTCAGCCGATGAATGAG 60
Db 1 ATGCGCTTTTCTCTGCTGAGACCAATTCAACCTACTCTCAGCCGATGAATGAG 60
Qy 61 CCCCCAGTAATCTCTCCATGCTTCTCAGCCTTACTTTTCTTCTGCGATGCCAGGC 120
Db 61 CCCCCAGTAATCTCTCCATGCTTCTCAGCCTTACTTTTCTTCTGCGATGCCAGGC 120
Qy 121 AATGGGCTGCTGCTGCTGGCTGGCTGAGATGAGGAGGACAGTGACACAAATTTGG 180
Db 121 AATGGGCTGCTGCTGCTGGCTGGCTGAGATGAGGAGGACAGTGACACAAATTTGG 180
Qy 181 TTCTCCACCTCACTTTGGCGGACCTCTCTGCTGCTCTCTCTGCTTCTCGTGGCT 240
Db 181 TTCTCCACCTCACTTTGGCGGACCTCTCTGCTGCTCTCTCTGCTTCTCGTGGCT 240
Qy 241 CACTTGGCTCTCAGGAGACAGTGCGCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 300
Db 241 CACTTGGCTCTCAGGAGACAGTGCGCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 300
Qy 301 ATCATTTCTCTCAACATGTTTGGCAGTGCTTCTCTGCTTACTGCGCATTTAGGCTCGATCGC 360
Db 301 ATCATTTCTCTCAACATGTTTGGCAGTGCTTCTCTGCTTACTGCGCATTTAGGCTCGATCGC 360
Qy 361 TGTCTTGTGTTATTCAGGCAATCTGCTGTCAGAAATCATCGCAATGTAGGATGGCTGTC 420
Db 361 TGTCTTGTGTTATTCAGGCAATCTGCTGTCAGAAATCATCGCAATGTAGGATGGCTGTC 420
Qy 421 TCTATCTGTGATGATCTGCTGGTGGCTTTTGTGATGTCATCTCTGTTTCTGTGTAC 480
Db 421 TCTATCTGTGATGATCTGCTGGTGGCTTTTGTGATGTCATCTCTGTTTCTGTGTAC 480
Qy 481 CGGGAATCTTCACTACAGACAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 481 CGGGAATCTTCACTACAGACAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Qy 541 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAAACAGGCTCTCTTGAACAACT 600
Db 541 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAAACAGGCTCTCTTGAACAACT 600
Qy 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTTCTCTCTTCCAAACAAATGAT 660
Db 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTTCTCTCTTCCAAACAAATGAT 660
Qy 661 CATCTTGGACAGTCCCACTGCTCTTCAACCTCAAAACATTTCAAGACCTTCTGCGAT 720
Db 661 CATCTTGGACAGTCCCACTGCTCTTCAACCTCAAAACATTTCAAGACCTTCTGCGAT 720
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Db 721 TCATCTCCTAGGGTCTCTGCTAGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 780
Qy 781 CCTGCTGATGCTCTACCTAAATCCAGTGGGTTCTTCTATTTGAGATCAGCAAC 840
Db 781 CCTGCTGATGCTCTACCTAAATCCAGTGGGTTCTTCTATTTGAGATCAGCAAC 840
Qy 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 900
Db 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 900
Qy 901 TCTAGCAATTCCTTCTACGAGTCTGAGTACCACAGGTTTCCAGGATTTATTAATTTA 960
Db 901 TCTAGCAATTCCTTCTACGAGTCTGAGTACCACAGGTTTCCAGGATTTATTAATTTA 960

QY 961 GCCCAATTCACAGATGACGATCAAGTGCACACACCCCTCTGTCGGCAATACGATCACTAGG 1020
 Db 961 GCCCAATTCACAGATGACGATCAAGTGCACACACCCCTCTGTCGGCAATACGATCACTAGG 1020
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 Db 1021 CTAGTGGTGGTCTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
 QY 1081 TTCCCAATGCAAGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTCGAGTGGCCGTG 1140
 Db 1081 TTCCCAATGCAAGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTCGAGTGGCCGTG 1140
 QY 1141 GTGGTGGTGGTCTTCTTCTGCTGCTGCTGCTTCCATCACCACATTTTGGAGTCTCTGCA 1200
 Db 1141 GTGGTGGTGGTCTTCTTCTGCTGCTGCTGCTTCCATCACCACATTTTGGAGTCTCTGCA 1200
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 Db 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGAAACTCTGATGTCCTGGGATCATGTATGC 1260
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 Db 1261 ATTGCTCTAGCATCTGCCAATAGTTCCTTAACTCCCTTCTTATGCTTATGCTTGGGAAA 1320
 QY 1321 GATTTAGGAAGAAAGCAAGGAGTCCATTTCAGGGAATTCAGGAGGAGCTTCAGTGAG 1380
 Db 1321 GATTTAGGAAGAAAGCAAGGAGTCCATTTCAGGGAATTCAGGAGGAGCTTCAGTGAG 1380
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 Db 1381 GAGCTCACAGTTCACCCACTGCTCCCTCAACAAATGTCATTTCAGAAAGAAATAGTACA 1440
 QY 1441 ACTGTGTCA 1449
 Db 1441 ACTGTGTCA 1449

RESULT 3

ID ABZ42643
 ID ABZ42643 standard; DNA; 1449 BP.

AC ABZ42643;

DT 04-MAR-2003 (first entry)

DE Human complement component 3a receptor 1 nucleotide SEQ ID NO:77.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.

OS Homo sapiens.

PN WO200261087-A2.

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

PP (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burner GC, Roush CL, Brown JP;

XX

WPI; 2003-046718/04.
 P-PSDB; ABP81797.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;

Query Match 100.0%; Score 1449; DB 8; Length 1449;

Best Local Similarity 100.0%; Pred. NO. 0;

Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTCTCTCAGCCATGGAATGAG	60
Db	1	ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTCTCTCAGCCATGGAATGAG	60
QY	61	CCCCAGTAATTCCTCCATGCTGTCATTCAGCCTTACTTTTCTGCGATGCGAGGC	120
Db	61	CCCCAGTAATTCCTCCATGCTGTCATTCAGCCTTACTTTTCTGCGATGCGAGGC	120
QY	121	AATGGGCTGCTGCTGCTGGGCTGGCTGCAAGATGCGAGCGACAGTGAACACAAATTGG	180
Db	121	AATGGGCTGCTGCTGCTGGGCTGGCTGCAAGATGCGAGCGACAGTGAACACAAATTGG	180
QY	181	TTCTCCACCTCACTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT	240
Db	181	TTCTCCACCTCACTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT	240
QY	241	CAGTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCC	300
Db	241	CAGTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCCTATGCAAGCTCATCCCTCC	300
QY	301	ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTAGCTAGCTGATCGC	360
Db	301	ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTAGCTAGCTGATCGC	360
QY	361	TGCTTTGTGTAATTCAGCAATCTGGTGTGTCAGAAATCATCGCAATGTAGGATGGCTGC	420
Db	361	TGCTTTGTGTAATTCAGCAATCTGGTGTGTCAGAAATCATCGCAATGTAGGATGGCTGC	420
QY	421	TCTATCTGTGGATGATCTGGGTTGGGCTTTTGTGATGTGCTTCTGTTGTTGTTGATC	480
Db	421	TCTATCTGTGGATGATCTGGGTTGGGCTTTTGTGATGTGCTTCTGTTGTTGTTGATC	480

```
QY 481 CGGGAATCTTCACTACAGACCAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
DB 481 CGGGAATCTTCACTACAGACCAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGAGTCTCTTGAACAAATT 600
DB 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGAGTCTCTTGAACAAATT 600
QY 601 GTTCAGCGCTGGAGAAATGAATAGATTAGTCTCTCTCTTCCAAACAAATGAT 660
DB 601 GTTCAGCGCTGGAGAAATGAATAGATTAGTCTCTCTCTTCCAAACAAATGAT 660
QY 661 CATCTTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
DB 661 CATCTTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
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QY 961 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCATTAG 1020
DB 961 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCATTAG 1020
QY 1021 CTAGTGTGGGTTTCTGCTGCTCTCTTTATCATGATAGCTGTTACAGCTTCAATGTC 1080
DB 1021 CTAGTGTGGGTTTCTGCTGCTCTCTTTATCATGATAGCTGTTACAGCTTCAATGTC 1080
QY 1081 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
DB 1081 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
QY 1141 GTGTGTGGGCTGTCTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1200
DB 1141 GTGTGTGGGCTGTCTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1200
QY 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAACCTCTGATGTCCTGGGATCATGTATGC 1260
DB 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAACCTCTGATGTCCTGGGATCATGTATGC 1260
QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTCTTGGGAAA 1320
DB 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTCTTGGGAAA 1320
QY 1321 GATTTAGGAAGAAAGCAAGCAGTCCATTGAGGAATTTGAGGAGCCCTTCAAGTGAG 1380
DB 1321 GATTTAGGAAGAAAGCAAGCAGTCCATTGAGGAATTTGAGGAGCCCTTCAAGTGAG 1380
QY 1381 GAGCTCACAGTTTCCACCCTCTCCCTCAACCAATGTCTTTCGAAAGAAATAGTACA 1440
DB 1381 GAGCTCACAGTTTCCACCCTCTCCCTCAACCAATGTCTTTCGAAAGAAATAGTACA 1440
QY 1441 ACTGTGTA 1449
DB 1441 ACTGTGTA 1449
```

RESULT 4
ADF43377
ID ADF43377 standard; DNA; 1449 BP.

```
XX ADF43377;
AC 12-FEB-2004 (first entry)
DT Chemoattractant polynucleotide seq id 97.
XX receptor; lipid-based tumour associated antigen; cytostatic;
XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
XX infectious disease; chemoattractant; ds.
OS Unidentified.
XX US2003157113-A1.
XX 21-AUG-2003.
XX 28-DEC-2000; 2000US-00751708.
XX 28-DEC-1999; 99US-0173371P.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2003-787326/74.
XX P-PSDB; ADF43378.
XX New receptor in a mammalian cell that inhibits regular activation by
XX receptors specific for lipid-based tumor associated antigens, useful for
XX treating a neoplastic disease or tumor, and infectious diseases.
XX Example 3; SEQ ID NO 97; 151pp; English.
XX The invention describes a receptor in a mammalian cell that inhibits
XX regular activation by receptors specific for lipid-based tumour
XX associated antigen. The receptor has cytostatic and antimicrobial
XX properties and is suitable for use in gene therapy. The receptors,
XX methods and compositions are useful for treating a neoplastic disease or
XX tumour (cancer), and infectious diseases. This sequence represents a
XX chemoattractant polynucleotide, a cell surface moiety, the DNA of which
XX can be transfected into a cell with superantigen DNA to generate
XX antitumour immunity.
XX Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;
QY Query Match 100.0%; Score 1449; DB 10; Length 1449;
DB Best Local Similarity 100.0%; Pred. No. 0;
QY Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 ATGGCGTCTTCTCTGTGAGACCAATTCAACTGACCTACTCTCAGCCCATGGAATGAG 60
QY 61 CCCCAGTAAATCTCTCATGTCTTCTCAGCCTTACTTTTACTCGGATTGCGAGC 120
DB 61 CCCCAGTAAATCTCTCATGTCTTCTCAGCCTTACTTTTACTCGGATTGCGAGC 120
QY 121 AATGGGCTGTGTGTGTGGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
DB 121 AATGGGCTGTGTGTGTGGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
QY 181 TTCTCTCACTCTCAGCTTGGCGGACCTCTCTGTGCTCTCTCTGCTTCTCGTGGCT 240
DB 181 TTCTCTCACTCTCAGCTTGGCGGACCTCTCTGTGCTCTCTCTGCTTCTCGTGGCT 240
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGAGGTTTCTATGCAAGCTCATCCCTCC 300
DB 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGAGGTTTCTATGCAAGCTCATCCCTCC 300
QY 301 ATCATTTGTCTCAACATGTTTGGCCAGTGTCTTCTCTGCTTACTTGCCTTAGCTGGATCGC 360
DB 301 ATCATTTGTCTCAACATGTTTGGCCAGTGTCTTCTCTGCTTACTTGCCTTAGCTGGATCGC 360
```


QY 361 TGTCTTGTGGTATTCAAGCCAAATCTGGTGTGAGATCATCGAATGTAGGATGCGCTGC 420
 Db 361 TGTCTTGTGGTATTCAAGCCAAATCTGGTGTGAGATCATCGAATGTAGGATGCGCTGC 420
 QY 421 TCTATCTGTGGATGTATCTGGGTGTGCTTTTGTGATGTGCATTCCTGTGTCTGTGTAC 480
 Db 421 TCTATCTGTGGATGTATCTGGGTGTGCTTTTGTGATGTGCATTCCTGTGTCTGTGTAC 480
 QY 481 CGGGAATCTTCACTACAGACAAACATTAATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 540
 Db 481 CGGGAATCTTCACTACAGACAAACATTAATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTGAACAATT 600
 Db 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTGAACAATT 600
 QY 601 GTTCAGCGCTCGAGAAATGAATGATAGTTAGATCCTCTCTTTCCAAACAAATGAT 660
 Db 601 GTTCAGCGCTCGAGAAATGAATGATAGTTAGATCCTCTCTTTCCAAACAAATGAT 660
 QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 Db 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 QY 721 TCACTCCCTAGGGTCTGTAGTTTAAAGTCAAAATCTGATTTCTTAATGATTTTAAA 780
 Db 721 TCACTCCCTAGGGTCTGTAGTTTAAAGTCAAAATCTGATTTCTTAATGATTTTAAA 780
 QY 781 CCTCTGATGGTCTCACTTAAATCCCAAGTGGTTTCTTATGAAGATCAAGAAACC 840
 Db 781 CCTCTGATGGTCTCACTTAAATCCCAAGTGGTTTCTTATGAAGATCAAGAAACC 840
 QY 841 AGCCCACTGGATTAATCTGATGCTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 Db 841 AGCCCACTGGATTAATCTGATGCTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 QY 901 TCTAGCAATTCCTTCTAGAGTCTGAGTCAACAGGTTTCCAGGATTTATCAATTTA 960
 Db 901 TCTAGCAATTCCTTCTAGAGTCTGAGTCAACAGGTTTCCAGGATTTATCAATTTA 960
 QY 961 GGCAATTCAGATGAGATCAAGTGCACACACCCCTCGTGGCAATAACGATCACTAGG 1020
 Db 961 GGCAATTCAGATGAGATCAAGTGCACACACCCCTCGTGGCAATAACGATCACTAGG 1020
 QY 1021 CTAGTGTGGTTCCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCATTTGTC 1080
 Db 1021 CTAGTGTGGTTCCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCATTTGTC 1080
 QY 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
 Db 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
 QY 1141 GTGTGTGGTGTCTTCTTGTCTGTGAGTCCATACACATTTTGGAGTCTCTGCA 1200
 Db 1141 GTGTGTGGTGTCTTCTTGTCTGTGAGTCCATACACATTTTGGAGTCTCTGCA 1200
 QY 1201 TTGCTTACTGACCCAGAAACTCCCTCGGGAAACTCTGATGCTCGGATCATGTATGC 1260
 Db 1201 TTGCTTACTGACCCAGAAACTCCCTCGGGAAACTCTGATGCTCGGATCATGTATGC 1260
 QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
 Db 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
 QY 1321 GATTTTAGGAAGAAGCAAGCAGTCTCATTCAGGAAATCTGGAGGAGCCTTCAGTGAG 1380
 Db 1321 GATTTTAGGAAGAAGCAAGCAGTCTCATTCAGGAAATCTGGAGGAGCCTTCAGTGAG 1380
 QY 1381 GAGCTCACAGTTCACCCACTGTCCTCAAAATGTCTTTCAGAAAGAAATAGTACA 1440
 Db 1381 GAGCTCACAGTTCACCCACTGTCCTCAAAATGTCTTTCAGAAAGAAATAGTACA 1440

QY 1441 ACTGTGTGA 1449
 Db 1441 ACTGTGTGA 1449
 RESULT 5
 ADR05359
 ID ADR05359 standard; cDNA; 1449 BP.
 XX AC ADR05359;
 DT 04-NOV-2004 (first entry)
 XX Human cDNA encoding anaphylatoxin receptor C3aR.
 DE Human; ss; gene; anaphylatoxin receptor; C3aR; white adipose tissue;
 KW non-insulin dependent diabetes mellitus; obesity; metabolic disorder;
 KW diabetes; endocrine abnormality; triglyceride storage disease;
 KW Bardet-Biedl syndrome; Lawrence-Moon syndrome;
 KW Prader-Willi syndrome; lipid metabolism disorder; OPN; HAP;
 KW MCP-1; osteopontin; haptoglobin; monocyte chemoattractant protein-1;
 KW C3aR.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 1..1449
 FT /*tag= a
 FT /product= "Anaphylatoxin receptor C3aR"
 XX US2004157253-A1.
 XX 12-AUG-2004.
 XX 26-JAN-2004; 2004US-00764649.
 XX 07-FEB-2003; 2003US-0446041P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Xu H, Chen H, Barnes G;
 XX WPI; 2004-614754/59.
 XX P-PSDB; ADR05360.
 XX Identifying a nucleic acid molecule/polypeptide associated with a
 XX metabolic disorder for use in treating obesity, comprises contacting a
 XX sample with a compound that binds to anaphylatoxin receptor.
 XX Claim 1; SEQ ID NO 1; 59pp; English.
 XX The invention relates to identifying (M1) a nucleic acid molecule or
 XX polypeptide associated with a metabolic disorder, comprises contacting a
 XX sample with a compound which binds to the nucleic acids or their encoded
 XX proteins representing human anaphylatoxin receptors C3aR and C5aR,
 XX osteopontin (OPN), haptoglobin (HAP) or monocyte chemoattractant protein
 XX (MCP-1) and detecting the presence of a nucleic acid molecule or protein
 XX in the sample that binds to the compound. OPN, HAP and MCP-1 are all
 XX modulated by C3aR and C5aR (both expressed in the white adipose tissue).
 XX Also included are identifying (M2) a subject having a metabolic
 XX disorder/at risk for developing a metabolic disorder (involving
 XX contacting a sample obtained from the subject comprising nucleic acid
 XX molecules or polypeptides with the above identified compound, and
 XX detecting the presence of a nucleic acid molecule or polypeptide in the
 XX sample that binds to the compound, where detection of a nucleic acid
 XX molecule or polypeptide chosen from anaphylatoxin receptors C3aR, C5aR,
 XX HAP, OPN or MCP-1, identifying (M3) a compound capable of treating a
 XX metabolic disorder (involving assaying the ability of a compound to
 XX modulate anaphylatoxin receptor C3aR or C5aR nucleic acid expression or
 XX anaphylatoxin receptor C3aR or C5aR polypeptide activity, and identifying
 XX the compound), identifying (M4) a compound capable of modulating an
 XX anaphylatoxin receptor mediated metabolic activity (involving contacting
 XX a composition comprising anaphylatoxin receptor with a test compound, and

assaying the ability of the test compound to modulate the expression of a anaphylatoxin receptor nucleic acid or the activity of a anaphylatoxin receptor polypeptide, thus identifying a compound capable of modulating anaphylatoxin receptor mediated metabolic activity, where the anaphylatoxin receptor comprises C3aR or C5aR) and modulating (M5) an anaphylatoxin receptor mediated metabolic activity (involving contacting a cell or a tissue expressing the anaphylatoxin receptor with a anaphylatoxin receptor modulator, thus modulating the anaphylatoxin receptor mediated metabolic activity, where the anaphylatoxin receptor is C3aR or C5aR). (M1) is useful for identifying a nucleic acid molecule or polypeptide associated with a metabolic disorder. (M2) is useful for identifying subject having metabolic disorder, for detecting mRNA and genomic DNA in the sample. (M3) is useful for identifying a compound capable of treating a metabolic disorder such as obesity, diabetes (especially non-insulin dependent), or insulin resistance. The metabolic disorders treated by the compound include endocrine abnormalities, triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon syndrome, Prader-Labhart-Willi syndrome and disorders of lipid metabolism. The present sequence encodes human C3aR.

SQ	Sequence	1449 BP;	331 A;	380 C;	310 G;	428 T;	0 U;	0 Other;
Query Match	100.0%;	Score	1449;	DB	13;	Length	1449;	
Best Local Similarity	100.0%;	Pred. No.	0;	Mismatches	0;	Indels	0;	Gaps
Matches	1449;	Conservative	0;					
Qy	1	ATGCGCTCTTTCTCTGTGTGAGACCAAAATTCAA	CTGACTTCTCTCAGCCCATGGGAATGAG	60				
Dd	1	ATGCGGCTTTTCTCTGTGTGAGACCAAAATTCAA	CTGACTTCTCTCAGCCCATGGGAATGAG	60				
Qy	61	CCCCAGTAATTCCTCATCGTGTCATTCCTCAGCCCTTA	CTTTTTTATCTGGGATGCGCAGGC	120				
Dd	61	CCCCCAGTAATTCCTCATCGTGTCATTCCTCAGCCCTTA	CTTTTTTATCTGGGATGCGCAGGC	120				
Qy	121	AATGGGCTGGTCTGTGTGGGTGGCTGGCCCTGAAGATG	CAGCGGACAGTGAACAATTTGG	180				
Dd	121	AATGGGCTGGTCTGTGTGGGTGGCTGGCCCTGAAGATG	CAGCGGACAGTGAACAATTTGG	180				
Qy	181	TTCCTCTCACACCTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTCTGCCCTTTC	TCGCTGGCT	240				
Dd	181	TTCCTCTCACACCTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTCTGCCCTTTC	TCGCTGGCT	240				
Qy	241	CAC TTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCTCATGCAAGCTCATCCCTCC	300					
Dd	241	CAC TTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCTCATGCAAGCTCATCCCTCC	300					
Qy	301	ATCATTTGTCTCAACATGTTTGCCAGTGTCTTCTGTCTTACTGTCGCAATTAGCTGGATCGC	360					
Dd	301	ATCATTTGTCTCAACATGTTTGCCAGTGTCTTCTGTCTTACTGTCGCAATTAGCTGGATCGC	360					
Qy	361	TGCTCTGTGGTATTCAAGCCAAATCTGGTGTGCAGAATCATCGCAATGTAGGAGTGGCTGC	420					
Dd	361	TGCTCTGTGGTATTCAAGCCAAATCTGGTGTGCAGAATCATCGCAATGTAGGAGTGGCTGC	420					
Qy	421	TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCTGTGTAC	480					
Dd	421	TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCTGTGTAC	480					
Qy	481	CGGGAAATCTTTCACCTACAGACAAACCATAATAGATGGTGCCTACAAATTTGGTCTCTCCAGC	540					
Dd	481	CGGGAAATCTTTCACCTACAGACAAACCATAATAGATGGTGCCTACAAATTTGGTCTCTCCAGC	540					
Qy	541	TCATTAGATTATCCAGACTTTTATGAGAGATCCACTAGAAAAACAGGTCTCTTGAAAACATT	600					
Dd	541	TCATTAGATTATCCAGACTTTTATGAGAGATCCACTAGAAAAACAGGTCTCTTGAAAACATT	600					
Qy	601	GTTTCAGCCGCTGGAGAAATGAATGATGGTTAGATCCTTCTCTTTTCCAAACAAATGAT	660					
Dd	601	GTTTCAGCCGCTGGAGAAATGAATGATGGTTAGATCCTTCTCTTTCCAAACAAATGAT	660					
Qy	661	CATCTTTGGACAGTCCCACCTGTCTTCCAACTCCTCAAAACATTTCAAAGACCTTCTGCAGAT	720					
Dd	661	CATCTTTGGACAGTCCCACCTGTCTTCCAACTCCTCAAAACATTTCAAAGACCTTCTGCAGAT	720					

RESULT 7
 ID ADC86208 standard; DNA; 1849 BP.
 AC ADC86208;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human GPCR gene SEQ ID NO:661.
 XX
 KW ds; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 DR WPI: 2003-315783/31.
 DR P-PSDB; ADC86209.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 1; SEQ ID NO 661; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.
 SQ Sequence 1849 BP; 462 A; 451 C; 395 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1449; DB 10; Length 1849;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGGGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGATGAG 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 201 ATGGGGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGATGAG 260
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 CCCCCAGTAATCTCTCATGCTGATCTCTCAGCCTTACTTTTACTGGGATTCGCGGC 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 261 CCCCCAGTAATCTCTCATGCTGATCTCTCAGCCTTACTTTTACTGGGATTCGCGGC 320
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 AATGGGCTGGTCTGTGGGTGGCTGGCTGAGATGACGGGACAGTGAACAAATTTGG 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 321 AATGGGCTGGTCTGTGGGTGGCTGGCTGAGATGACGGGACAGTGAACAAATTTGG 380
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 TTCCTCCACCTCAGCTTGGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 381 TTCCTCCACCTCAGCTTGGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCT 440
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 CACTTTGGCTCTCCAGGACAGTGGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCC 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 441 CACTTTGGCTCTCCAGGACAGTGGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCC 500

QY 301 ATCAATGCTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCCATAGCCTGCGATCGC 360
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 501 ATCAATGCTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCCATAGCCTGCGATCGC 560
 QY 361 TGTCTTGTGGTATTTCAGGCCAATCTGGGTGTCAGAAATCATCGCAATGTAGGGATGCGCTGC 420
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 561 TGTCTTGTGGTATTTCAGGCCAATCTGGGTGTCAGAAATCATCGCAATGTAGGGATGCGCTGC 620
 QY 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATTCCTTCTGTGTTCTGTGATC 480
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 621 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATTCCTTCTGTGTTCTGTGATC 680
 QY 481 CGGGAATCTTCACCTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 681 CGGGAATCTTCACCTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 740
 QY 541 TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTTGAAAAACATT 600
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 741 TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTTGAAAAACATT 800
 QY 601 GTTCAGCGCTGGAGAAATCAATGATAGTTAGATCCTTCTCTCTTTTCCAAACAAATGAT 660
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 801 GTTCAGCGCTGGAGAAATCAATGATAGTTAGATCCTTCTCTCTTTTCCAAACAAATGAT 860
 QY 661 CATCCTTGGACAGTCCCGCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAT 720
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 861 CATCCTTGGACAGTCCCGCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAT 920
 QY 721 TCACCTCCCTAGGGGTTCTGTAGTTTAAACAAGTCAAAATCTGTATTTCTAATGTTATTTAAA 780
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 921 TCACCTCCCTAGGGGTTCTGTAGTTTAAACAAGTCAAAATCTGTATTTCTAATGTTATTTAAA 980
 QY 781 CCTCTGATGGTCTCACCTAAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 840
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 981 CCTCTGATGGTCTCACCTAAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 1040
 QY 841 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1041 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 1100
 QY 901 TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAACAAGGTTTCCAGGATTTATTAACAATTTA 960
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1101 TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAACAAGGTTTCCAGGATTTATTAACAATTTA 1160
 QY 961 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCACTAGG 1020
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1161 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCACTAGG 1220
 QY 1021 CTAGTGGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTTACAGCTTCAATGTC 1080
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1221 CTAGTGGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTTACAGCTTCAATGTC 1280
 QY 1081 TTCCGAATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCCAGTGGCCGCTG 1140
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1281 TTCCGAATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCCAGTGGCCGCTG 1340
 QY 1141 GTGGTGGTGGTGTCTTTTCTTGTCTGTGAGTCCATACCAATTTTGGAGTCTCTGTCA 1200
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1341 GTGGTGGTGGTGTCTTTTCTTGTCTGTGAGTCCATACCAATTTTGGAGTCTCTGTCA 1400
 QY 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGGAATACTCTGATGCTCTGGGATCATGTATGC 1260
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1401 TTGCTTACTGACCCAGAAACTCCCTTGGGGAATACTCTGATGCTCTGGGATCATGTATGC 1460
 QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCCCTCTTGGGGAAA 1320
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1461 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCCCTCTTGGGGAAA 1520
 QY 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTGAGGAATTTCTGGAGGAGCCCTTCAAGTGAG 1380
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1521 GATTTTAGAAGAAAGCAAGGAGTCCATTGAGGAATTTCTGGAGGAGCCCTTCAAGTGAG 1580

Qy 1381 GAGCTCACACGTTCCACCCACTGTCCTCAACAAATGTCATTTCAGAAAGAAATAGTACA 1440
 Db |||||
 Qy 1581 GAGCTCACACGTTCCACCCACTGTCCTCAACAAATGTCATTTCAGAAAGAAATAGTACA 1640
 Db |||||
 Qy 1441 ACTGTGTGA 1449
 Db |||||
 Qy 1641 ACTGTGTGA 1649

RESULT 8
 AAV03250
 ID AAV03250 standard; cDNA; 2040 BP.
 AC AAV03250;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Homo sapiens cDNA encoding C3a receptor.
 XX
 KW C3a receptor; treatment; diagnosis; atherosclerosis; chronic;
 KW polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's;
 KW disease; acute inflammatory disease; Crohn's disease; food; allergies;
 KW non-bronchial allergies; osteoarthritis; osteoporosis; thyroid disease;
 KW coronary heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 153..1601
 FT /*tag= a
 FT /product= "C3a receptor"
 XX
 XX EP814158-A2.
 PN
 XX
 PD 29-DEC-1997.
 XX
 PF 17-JUN-1997; 97EP-00304250.
 XX
 PR 17-JUN-1996; 96US-0019627P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Ames RS, Bergsma DJ, Foley JJ, Kumar C, Sarau HM;
 XX
 DR WPI; 1998-044336/05.
 DR P-FSDB; AAW42376.
 XX

C3a receptor agonists, antibodies and antagonists - useful for diagnosis of disease related to expression of C3a receptor, e.g. acute inflammatory disease, atherosclerosis, chronic polyarthritis, etc.
 Disclosure; Fig 1; 43pp; English.
 The sequence is that encoding the C3a receptor. It can be used in a process for diagnosing a disease or susceptibility to a disease related to expression of the C3a receptor. This process involves determining the presence of a mutation in the nucleic acid sequence encoding the polypeptide, the disease being selected from acute inflammatory disease, atherosclerosis, chronic polyarthritis, systemic vasculitis, multiple sclerosis, Alzheimer's Disease, CNS inflammatory disease, Crohn's Disease, food allergies, non-bronchial allergies, osteoarthritis, osteoporosis, thyroid disease, coronary heart disease, Systemic Lupus Erythematosus SLE-associated nephritis, membranoproliferative GN, membranous nephritis, rheumatoid arthritis, Behcet's syndrome, juvenile rheumatoid arthritis, Sjogren's syndrome, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome, pemphigus/pemphigoid, phototoxic reactions, vasculitis, post-bypass syndrome, catheter reactions, sepsis, ARDS, anaphylaxis, transplant rejection, pre-eclampsia, atheroma, bowel inflammation, thyroiditis, infertility, susceptibility to pyogenic infections, glomerulonephritis, susceptibility to neisserial infections, recurrent subcutaneous swelling and mucosal oedema, and recurrent episodes of thrombosis/haemolysis. C3a receptor agonists, antagonists and antibodies can be used in the treatment of patients having need to

CC inhibit or activate a C3a receptor
 XX Sequence 2040 BP; 530 A; 493 C; 432 G; 585 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 1449; DB 2; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACAGCCATGAATGAG 60
 Db |||||
 Qy 153 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACAGCCATGAATGAG 212
 Db |||||
 Qy 61 CCCCCAGTAATTCTCTCATGCTCAATCTAGCCTTACTTTTTTACTGGGATGCGAGGC 120
 Db |||||
 Qy 213 CCCCCAGTAATTCTCTCATGCTCAATCTAGCCTTACTTTTTTACTGGGATGCGAGGC 272
 Db |||||
 Qy 121 AATGGGCTGTGTGTGGGTGGCTGAAGATGACGGACAGTGAAACACAAATTTGG 180
 Db |||||
 Qy 273 AATGGGCTGTGTGTGGGTGGCTGAAGATGACGGACAGTGAAACACAAATTTGG 332
 Db |||||
 Qy 181 TTCTTCCACCTCACTTGGGGGACCTCTCTGCTGCTCTCTCTGCTTCCCTTCTCGTGGCT 240
 Db |||||
 Qy 333 TTCTTCCACCTCACTTGGGGGACCTCTCTGCTGCTCTCTCTGCTTCCCTTCTCGTGGCT 392
 Db |||||
 Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGGTTCCCTATGCAAGCTCATGCCCTCC 300
 Db |||||
 Qy 393 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGGTTCCCTATGCAAGCTCATGCCCTCC 452
 Db |||||
 Qy 301 ATCAATGTCCTCAACATGTTTGGCCAGTGCTTCTCTGCTTACTGTCATTGAGCTGGATCGC 360
 Db |||||
 Qy 453 ATCAATGTCCTCAACATGTTTGGCCAGTGCTTCTCTGCTTACTGTCATTAGCTGGATCGC 512
 Db |||||
 Qy 361 TGTCTTGTGTATTCAGCCCAATCTGGTGTCAGAAATCATCGCAATGAGGATGSCCTGC 420
 Db |||||
 Qy 513 TGTCTTGTGTATTCAGCCCAATCTGGTGTCAGAAATCATCGCAATGAGGATGSCCTGC 572
 Db |||||
 Qy 421 TCTATCTGTGATGATATCTGGGTGGTCTTTTGTGATGTCAATTCCTGTGTCTGTGTAC 480
 Db |||||
 Qy 573 TCTATCTGTGATGATATCTGGGTGGTCTTTTGTGATGTCAATTCCTGTGTCTGTGTAC 632
 Db |||||
 Qy 481 CGGAAATCTTCTACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 Db |||||
 Qy 633 CGGAAATCTTCTACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 692
 Db |||||
 Qy 541 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT 600
 Db |||||
 Qy 693 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT 752
 Db |||||
 Qy 601 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCCTTCTCTTTTCCAAACAAATGAT 660
 Db |||||
 Qy 753 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCCTTCTCTTTTCCAAACAAATGAT 812
 Db |||||
 Qy 661 CATCTTGGACAGTCCCCACATGTCTTCAACCTCAACATTTCAAAGACCTTCTGCAGAT 720
 Db |||||
 Qy 813 CATCTTGGACAGTCCCCACATGTCTTCAACCTCAACATTTCAAAGACCTTCTGCAGAT 872
 Db |||||
 Qy 721 TCATCTCCCTAGGGTCTCTGCTAGGTAAACAAATCTGTAATCTTAATGTAATTTAAA 780
 Db |||||
 Qy 873 TCATCTCCCTAGGGTCTCTGCTAGGTAAACAAATCTGTAATCTTAATGTAATTTAAA 932
 Db |||||
 Qy 781 CCTGCTGATGTGGTCTCACTCTAAATCCCAAGTGGGTTTCTTATGGAAGATCACGAAACC 840
 Db |||||
 Qy 933 CCTGCTGATGTGGTCTCACTCTAAATCCCAAGTGGGTTTCTTATGGAAGATCACGAAACC 992
 Db |||||
 Qy 841 AGCCCATGGATATACTGTAGTCTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 Db |||||
 Qy 993 AGCCCATGGATATACTGTAGTCTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 1052
 Db |||||
 Qy 901 TCTAGCAATTCCTTCTACAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACAATTTA 960
 Db |||||
 Qy 1053 TCTAGCAATTCCTTCTACAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACAATTTA 1112
 Db |||||
 Qy 961 GGCCCAATTCACAGATGACGATCAAGTGCCACACCCCTCGTGGCAATTAACGATCACTAGG 1020
 Db |||||

Db 1113 GGCCTATTCACAGATGACATCAGTGCACACCCCTCGTGGCAATACGATCACTAGG 1172
 Qy 1021 CTAGTGGTGGTTCCTGCTGCTCTCTGTATCATGATAGCTGTTACAGCTTCAATGTC 1080
 Db 1173 CTAGTGGTGGTTCCTGCTGCTCTCTGTATCATGATAGCTGTTACAGCTTCAATGTC 1232
 Qy 1081 TTCCGAATGCAAGGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCCGTG 1140
 Db 1233 TTCCGAATGCAAGGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCCGTG 1292
 Qy 1141 GTGGTGGTGGTCTCTTCTGCTGCTGAGTCCATACCAATTTTGGAGTCTCTGCA 1200
 Db 1293 GTGGTGGTGGTCTCTTCTGCTGCTGAGTCCATACCAATTTTGGAGTCTCTGCA 1352
 Qy 1201 TTGCTTACTGACCCAGAAACTCCCTTTGGGAAAACTCTGATGCTCTGGGATCAATATGC 1260
 Db 1353 TTGCTTACTGACCCAGAAACTCCCTTTGGGAAAACTCTGATGCTCTGGGATCAATATGC 1412
 Qy 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCTCTTGGGAAA 1320
 Db 1413 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCTCTTGGGAAA 1472
 Qy 1321 GATTTTAGGAAGAAAGCAAGCAGTCCATTCAGGGAATTCAGGCGCAGCCCTTCAGTGAG 1380
 Db 1473 GATTTTAGGAAGAAAGCAGCAGTCCATTCAGGGAATTCAGGCGCAGCCCTTCAGTGAG 1532
 Qy 1381 GAGCTCACAGTTCACCCACCTGTCCTCTCAACAAATGTCATTTTCAGAAAGAAATAGTACA 1440
 Db 1533 GAGCTCACAGTTCACCCACCTGTCCTCTCAACAAATGTCATTTTCAGAAAGAAATAGTACA 1592
 Qy 1441 ACTGTGTGA 1449
 Db 1593 ACTGTGTGA 1601

RESULT 9
 ID ADQ23545
 AC ADQ23545;
 DT 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 6365.
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.
 XX Homo sapiens.
 OS WO2004048938-A2.
 PN 10-JUN-2004.
 PD 26-NOV-2003; 2003WO-US038193.
 PP 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 DR Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX Example 2; SEQ ID NO 6365; 210pp; English.
 PS The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC DNA of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 Qy Sequence 2096 BP; 559 A; 498 C; 439 G; 600 T; 0 U; 0 Other;
 Db
 Qy Query Match 100.0%; Score 1449; DB 12; Length 2096;
 Db Best Local Similarity 100.0%; Pred. No. 0;
 Qy Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db
 Qy 1 ATGGGGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGATGAG 60
 Db 156 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGATGAG 215
 Qy 61 CCCCAGTAATTTCTCTCATGCTCATTTCTCAGCCCTACTTTTTTACTGGGATTCGACGC 120
 Db 216 CCCCAGTAATTTCTCTCATGCTCATTTCTCAGCCCTACTTTTTTACTGGGATTCGACGC 275
 Qy 121 AATGGCTGTGTCTGTGGGTGGCTGGCTGAAGATGACAGCGACAGTGAACACAAATTTGG 180
 Db 276 AATGGCTGTGTCTGTGGGTGGCTGGCTGAAGATGACAGCGACAGTGAACACAAATTTGG 335
 Qy 181 TTCTCTCAGCTCAGCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
 Db 336 TTCTCTCAGCTCAGCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 395
 Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTACCGGAGTTCCTATGCAAGCTCATCCCTCC 300
 Db 396 CACTTGGCTCTCCAGGACAGTGGCCCTACCGGAGTTCCTATGCAAGCTCATCCCTCC 455
 Qy 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGCATTTAGCTGATGCG 360
 Db 456 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGCATTTAGCTGATGCG 515
 Qy 361 TGTCTTGGTATTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGAGTGGCTGCG 420
 Db 516 TGTCTTGGTATTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGAGTGGCTGCG 575
 Qy 421 TCTATCTGTGATGTATCTGGGTGGTGGTGTGATGTGATGTGATGTGATGTGATGTGAT 480
 Db 576 TCTATCTGTGATGTATCTGGGTGGTGGTGTGATGTGATGTGATGTGATGTGATGTGAT 635
 Qy 481 CGGAAATCTTCTACACAGCAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 Db 636 CGGAAATCTTCTACACAGCAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 695
 Qy 541 TCATTAGATTCAGACTTTTATGGAGATCCACTAGBAACAGCTCTCTTGAACATTT 600
 Db 696 TCATTAGATTCAGACTTTTATGGAGATCCACTAGBAACAGCTCTCTTGAACATTT 755
 Qy 601 GTTCAGCGCTGGAGAAATGAATAGATGTAGATCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 Db 756 GTTCAGCGCTGGAGAAATGAATAGATGTAGATCTCTCTCTCTCTCTCTCTCTCTCTCT 815
 Qy 661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTTCAAGACCTTCTCGAGAT 720
 Db 816 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTTCAAGACCTTCTCGAGAT 875
 Qy 721 TCATCTCCCTAGGGTTCGTAGTAACTCAAGTCAAAATCTGTATCTTAATGATTTTAAA 780
 Db 876 TCATCTCCCTAGGGTTCGTAGTAACTCAAGTCAAAATCTGTATCTTAATGATTTTAAA 935
 Qy 781 CCTGCTGATGTGCTCTCACCTAAATCCAGTGGGTTTCTTATGGAAGATCAGCAACACC 840

Db 936 CCTGCTGATGTGGTCTCACCTAAATCCCAAGTGGGTTCTTATTGAAGATCAAGAAACC 995
 QY 841 AGCCCACTGGATAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTTCCTAGCGCT 900
 Db 996 AGCCCACTGGATAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTTCCTAGCGCT 1055
 QY 901 TCTAGCAATTCCTTCTAGAGTCTCAGAGTACCAAGGTTTCCAGGATTTATTACAAATTGA 960
 Db 1056 TCTAGCAATTCCTTCTAGAGTCTCAGAGTACCAAGGTTTCCAGGATTTATTACAAATTGA 1115
 QY 961 GGCCTAATTCAGATGATCAAGTGCACACCCCTCGTGGCAATAACGATCACTAGG 1020
 Db 1116 GGCCTAATTCAGATGATCAAGTGCACACCCCTCGTGGCAATAACGATCACTAGG 1175
 QY 1021 CTAGTGGTGGTTCCTGCTGCTCTCTCTATCATGATAGCTGTTCAGCTTCAATGTC 1080
 Db 1176 CTAGTGGTGGTTCCTGCTGCTCTCTCTATCATGATAGCTGTTCAGCTTCAATGTC 1235
 QY 1081 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCGGTG 1140
 Db 1236 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCGGTG 1295
 QY 1141 GTGTGGTGGTCTCTCTCTGCTGCTGCTCATACCAATTTTGGAGTCTCTGTCA 1200
 Db 1296 GTGTGGTGGTCTCTCTCTGCTGCTGCTCATACCAATTTTGGAGTCTCTGTCA 1355
 QY 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAACCTCTGATGCTCTGGATCATGTATGC 1260
 Db 1356 TTGCTTACTGACCCAGAACTCCCTTGGGGAACCTCTGATGCTCTGGATCATGTATGC 1415
 QY 1261 ATTGCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCCCTTATGCTCTTGGGAAA 1320
 Db 1416 ATTGCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCCCTTATGCTCTTGGGAAA 1475
 QY 1321 GATTTAGAGAAAGCAAGCAGTCCATTAGGGAATCTGGAGGAGCCTTCAGTGAG 1380
 Db 1476 GATTTAGAGAAAGCAAGCAGTCCATTAGGGAATCTGGAGGAGCCTTCAGTGAG 1535
 QY 1381 GAGCTCACAGCTTCCACCCTGCTCCCTCAACCAATGTCATTTCAGAAAGAAATAGTACA 1440
 Db 1536 GAGCTCACAGCTTCCACCCTGCTCCCTCAACCAATGTCATTTCAGAAAGAAATAGTACA 1595
 QY 1441 ACTGTGTGA 1449
 Db 1596 ACTGTGTGA 1604

RESULT 10

ID ADO29820

AC ADO29820 standard; cDNA; 1449 BP.

XX ADO29820;

XX 29-JUL-2004 (first entry)

XX Human GPCR C3AR1 polynucleotide, SEQ ID NO:922.

DE G protein-coupled receptor; GPCR; drug screening; diagnosis;

XX transgenic mouse; neurological disorder; adrenal gland disorder;

XX colon disorder; intestinal disorder; cardiovascular disorder;

XX muscular disorder; blood disorder; immune disorder; bone disorder;

XX joint disorder; metabolic disorder; nutritive disorder; cancer;

XX kidney disorder; liver disorder; lung disorder; breast disorder;

XX ovary disorder; uterus disorder; prostate disorder; testis disorder;

XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;

XX thymus disorder; thyroid disorder; antiparkinsonian; antianemic;

XX cytosolic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;

XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

XX virucide; hepatotoxic; antibacterial; antianemic; antiseborrhoeic;

XX dermatological; antitumor; antithyroid; antiallergic; anorectic;

XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;

XX gene; ss.

OS Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX P-PSDB; ADO29203.

XX Novel mammalian G protein coupled receptors, useful for identifying

XX compounds that modulates diagnosing and treating disease condition

XX associated with GPCR dysfunction e.g. autoimmune diseases, angina

XX pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 922; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors

XX (GPCRs) and nucleic acids encoding them. The invention also relates to

XX sequences at least 90% identical to the GPCR proteins and nucleic acids

XX of the invention; methods of treating, preventing or diagnosing diseases

XX associated with GPCRs of the invention; methods of screening for

XX compounds useful in the treatment of GPCR-related diseases; a transgenic

XX mouse comprising a GPCR gene of the invention; a mouse comprising a

XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived

XX from the transgenic mice; kits comprising several mice, each of which has

XX a mutation in a different GPCR gene of the invention; and kits comprising

XX probes which hybridize to GPCR polynucleotides of the invention. The

XX invention further discloses variants of the GPCR polypeptides and vectors

XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may

XX be used in the diagnosis, treatment or prevention of a wide variety of

XX diseases including neurological disorders (e.g., Alzheimer's disease,

XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);

XX disorders of the adrenal gland; disorders of the colon or intestine

XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel

XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or

XX myocardial infarction); muscular disorders; blood disorders (e.g.,

XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or

XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid

XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,

XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related

XX diseases); and disorders of the kidney, liver, lung, breast, ovary,

XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and

XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding

XX nucleic acid of the invention. Note: The full sequence data for this

XX patent did not form part of the printed specification; those sequences

XX not shown were obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1449 BP; 331 A; 379 C; 311 G; 428 T; 0 U; 0 Other;

XX Query Match 99.9%; Score 1447.4; DB 12; Length 1449;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 1449; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 ATGGCGTCTTCTCTGTCGAGCAATTCACCTACTCTCAGACCATGATGAG 60

XX Db 1 ATGGCGTCTTCTCTGTCGAGCAATTCACCTACTCTCAGACCATGATGAG 60

XX QY 61 CCCCCAGTAAATCTCTCCATGGTCATTCTCAGCCTTACTTTTTTACTGGGATGCCAGGC 120

XX Db 61 CCCCCAGTAAATCTCTCCATGGTCATTCTCAGCCTTACTTTTTTACTGGGATGCCAGGC 120

XX QY 121 AATGGCGTGTGCTGTGGTGGCTGGCTGAGATGACGGGACAGTGAACACAAATTGG 180

PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX (AVAL-) AVALON PHARM.
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 PS Claim 1; SEQ ID NO 6013; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
 CC tumour
 XX
 SQ Sequence 1956 BP; 488 A; 479 C; 418 G; 571 T; 0 U; 0 Other;
 Query Match 99.9%; Score 1447.4; DB 6; Length 1956;
 Best Local Similarity 99.9%; Pred No. 0;
 Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGAATGAG 141
 DB 82 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGAATGAG 141
 QY 61 CCCCAGTAAATCTCCATGGTCAATCTGAGCCTTACTTTTCTGAGGATGCCAGGC 120
 DB 142 CCCCAGTAAATCTCCATGGTCAATCTGAGCCTTACTTTTCTGAGGATGCCAGGC 201
 QY 121 AATGGCTGGTGTCTGTTGGTGGCTGGCTGAAGATGACGGACGAGTGAACACAAATTTGG 180
 DB 202 AATGGCTGGTGTCTGTTGGTGGCTGGCTGAAGATGACGGACGAGTGAACACAAATTTGG 261
 QY 181 TTCTCCACCTCAGCTTGGGGAGCCTGCTCTGCTGCTCTCTCTGCTGCTCTGCTGCTGCT 240
 DB 262 TTCTCCACCTCAGCTTGGGGAGCCTGCTCTGCTGCTCTCTCTGCTGCTCTGCTGCTGCT 321
 QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTTCTTATGCAAGCTCATCCCTCC 300
 DB 322 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTTCTTATGCAAGCTCATCCCTCC 381
 QY 301 ATCAATGCTCACAATGTTTGGCAGTGTCTCTGCTTACTGCTTACTGCTTACTGCTGCTGCT 360
 DB 382 ATCAATGCTCACAATGTTTGGCAGTGTCTCTGCTTACTGCTTACTGCTTACTGCTGCTGCT 441

QY 361 TGTCTTGTGGTATTTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGSCCTGC 420
 DB 442 TGTCTTGTGGTATTTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGSCCTGC 501
 QY 421 TCTATCTGTGATGATCTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 480
 DB 502 TCTATCTGTGATGATCTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 561
 QY 481 CGGAAATCTTCACTCAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 DB 562 CGGAAATCTTCACTCAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
 QY 541 TCATTAGATTTCCAGACTTTTATGGAGATCCCACTAGAAAACAGGTCTCTTGAACAAAT 600
 DB 622 TCATTAGATTTCCAGACTTTTATGGAGATCCCACTAGAAAACAGGTCTCTTGAACAAAT 681
 QY 601 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCTCTCTCTCTCTCTCTCTCTCTCT 660
 DB 682 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCTCTCTCTCTCTCTCTCTCTCTCT 741
 QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAAGACCTTCTGAGAT 720
 DB 742 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAAGACCTTCTGAGAT 801
 QY 721 TCACCTCCCTAGGGTCTCTGCTAGGTAAACAGTCAAAATCTGTATTCTTAATGATTTAAA 780
 DB 802 TCACCTCCCTAGGGTCTCTGCTAGGTAAACAGTCAAAATCTGTATTCTTAATGATTTAAA 861
 QY 781 CCTGCTGATGTGTCTCACTCACTAAATCCCAAGTGGTGTCTCTATTTGAAGATCAACAAAC 840
 DB 862 CCTGCTGATGTGTCTCACTCACTAAATCCCAAGTGGTGTCTCTATTTGAAGATCAACAAAC 921
 QY 841 AGCCCACTGATGATCTGATGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
 DB 922 AGCCCACTGATGATCTGATGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 981
 QY 901 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
 DB 982 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1041
 QY 961 GGCAATTCAGATGATGATCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020
 DB 1042 GGCAATTCAGATGATGATCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1101
 QY 1021 CTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1080
 DB 1102 CTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1161
 QY 1081 TTCGAATGCAAGGGGCGCTTTCGCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCGGTG 1140
 DB 1162 TTCGAATGCAAGGGGCGCTTTCGCCAAGTCTCAGAGCAAAACCTTTCGAGTGGCGGTG 1221
 QY 1141 GTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200
 DB 1222 GTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1281
 QY 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGGGAAACTCTGATGCTCTGGGATCATGTATGC 1260
 DB 1282 TTGCTTACTGACCCAGAAACTCCCTTGGGGGAAACTCTGATGCTCTGGGATCATGTATGC 1341
 QY 1261 ATTGCTCTAGCATCTGCAATAGTGTCTTAAATCCCTTCTCTCTCTCTCTCTCTCTCTCT 1320
 DB 1342 ATTGCTCTAGCATCTGCAATAGTGTCTTAAATCCCTTCTCTCTCTCTCTCTCTCTCTCT 1401
 QY 1321 GATTTTAGGAAGAAAGCAAGGAGTCCATTCAGGGAATCTGAGGAGCAGCTTCAGTGAG 1380
 DB 1402 GATTTTAGGAAGAAAGCAAGGAGTCCATTCAGGGAATCTGAGGAGCAGCTTCAGTGAG 1461
 QY 1381 GAGCTCACAGTTCACCCCACTGCTCCCTCAAAATGCTCATTTTCAGAAAGAAATAGTACA 1440
 DB 1462 GAGCTCACAGTTCACCCCACTGCTCCCTCAAAATGCTCATTTTCAGAAAGAAATAGTACA 1521
 QY 1441 ACTGTGTGA 1449

QY 901 TCTAGCAATTCCTTCTACGAGCTGAGCTACCAACAGGTTTCCAGGATTATTAACAATTTA 960
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 DB 1593 ACTGTGTGA 1601

RESULT 14

ACD26620
 ID ACD26620 standard; cDNA; 2040 BP.

XX AC ACD26620;

XX DT 11-SEP-2003 (first entry)

XX cDNA encoding putative mature human G protein coupled receptor.

XX G protein coupled receptor; GPCR; human; infection;
 XX immunodeficiency disease; asthma; bronchial allergy;
 KW chronic inflammation; systemic lupus erythematosus; gout;
 KW transplant rejection; hypertension; abnormal cell growth;
 KW neurological disease; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 153..1601
 XX /*tag= a
 XX /product= "GPCR"
 XX /note= "G protein coupled receptor"

XX US2003022310-A1.

XX 30-JAN-2003.

XX 30-SEP-2002; 2002US-00259521.

XX 17-FEB-1995; 95WO-US001992.

PR 05-JUN-1995; 95US-00462314.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Li Y, Rosen CA;
 XX WPI; 2003-531445/50.
 DR P-PSDB; ABU62861.
 XX

XX New G-protein coupled receptor polypeptides and polynucleotide, useful
 for screening receptor agonists and/or antagonists and/or receptor
 ligands, in chromosome identification, and in for producing antibodies.

PS Disclosure; Fig 1A-D; 26pp; English.

XX The invention describes an isolated polynucleotide (1) comprising a
 sequence which: (a) encodes a polypeptide having a sequence of 482 amino
 acids (11) given in the specification; (b) encodes a mature polypeptide
 encoded or expressed by the DNA contained in ATCC deposit number 75982;
 (c) is capable of hybridizing to and which is at least 70% identical to
 (a) or (b); or (d) a fragment of (a), (b) or (c). The G-protein coupled
 receptors (GPCR) are useful for screening receptor agonists and/or
 antagonists and/or receptor ligands. GPCR agonists are useful for
 stimulating GPCR for the treatment of conditions related to the under-
 expression of GPCR, e.g. bacterial or viral infection, immunodeficiency
 diseases and severe infections. GPCR antagonists are useful for
 inhibiting the action of GPCR for treating conditions associated with
 over-expression of the GPCR, e.g. asthma, bronchial allergy, chronic
 inflammation, systemic lupus erythematosus, gout, transplant rejection,
 hypertension, abnormal cell growth, and neurological diseases. The GPCR
 genes are also useful in diagnostic assays for detecting diseases or
 susceptibility to diseases related to the presence of mutations in the
 GPCR genes. These may also be used in chromosome identification. The
 polypeptides are useful as immunogens for producing antibodies. This
 sequence encodes a putative mature human G protein coupled receptor

SQ Sequence 2040 BP; 530 A; 493 C; 433 G; 584 T; 0 U; 0 Other;

Query Match 99.9%; Score 1447.4; DB 9; Length 2040;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 273 AATGGCGTGTGCTGTGGTGGCTGGCTGAGATGCGGCGACAGTGAACACAAATTTGG 332
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Job time : 847 secs

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OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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40 80.4 5.5 1083 4 US-09-170-496D-27 Sequence 179, App
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44 79.4 5.5 1796 1 US-08-417-103-11 Sequence 11, Appli
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ALIGNMENTS

RESULT 1
US-08-876-874-1
; Sequence 1, Application US/08876874
; Patent No. 5942405
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert
; APPLICANT: Bergsma, Derk
; APPLICANT: Foley, James
; APPLICANT: Kumar, Chandrika
; APPLICANT: Sarau, Henry
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
; TITLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAINIER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: /US/08/876,874
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,627
FILING DATE: 16-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1449 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-876-874-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 1, Application US/09117440
; Patent No. 6521418
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; FILE REFERENCE: SCR20418
; CURRENT APPLICATION NUMBER: US/09/117,440
; EARLIER FILING DATE: 1998-07-28
; EARLIER FILING DATE: 1997-01-30
; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1970
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82) .. (1527)
US-09-117-440-1

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Query Match 99.9%; Score 1447.4; DB 4; Length 1970;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 202 AATGGGCTGCTGCTGGTGGCTGCTGAGATGCGGAGCAGTGAACAAATTTGG 261

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 Qy 961 GGCCAAATTCAGATGAGATCAAGTGCACACCCCTCGTGGCAATAACGATCACTAGG 1020
 Db |||||
 Qy 1021 CTAGTGTGGGTTTCTGCTGCTCTGTTATCATGATAGCTGTTCAGCTTCAATTTGTC 1080
 Db |||||
 Qy 1021 CTAGTGTGGGTTTCTGCTGCTCTGTTATCATGATAGCTGTTCAGCTTCAATTTGTC 1080
 Db |||||
 Qy 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 Db |||||
 Qy 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 Db |||||
 Qy 1141 GTGTGTGGTGTCTTCTTGTCTGTGAGTCCATACACATTTTGGAGTCTCTGTCA 1200
 Db |||||
 Qy 1141 GTGTGTGGTGTCTTCTTGTCTGTGAGTCCATACACATTTTGGAGTCTCTGTCA 1200
 Db |||||
 Qy 1201 TTGCTTACTGACCCAGAACTCCCTTGGGAAACTCTGATGCTCGGATCATGTATGC 1260
 Db |||||
 Qy 1201 TTGCTTACTGACCCAGAACTCCCTTGGGAAACTCTGATGCTCGGATCATGTATGC 1260
 Db |||||
 Qy 1261 ATTGCTCTAGCATCTGCCAATPAGTTGCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
 Db |||||
 Qy 1261 ATTGCTCTAGCATCTGCCAATPAGTTGCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
 Db |||||
 Qy 1321 GATTTTAGGAGAAAGCAAGGAGTCCATTCAGGGAATCTGGAGGAGCCCTTCAGTGAG 1380
 Db |||||
 Qy 1321 GATTTTAGGAGAAAGCAAGGAGTCCATTCAGGGAATCTGGAGGAGCCCTTCAGTGAG 1380
 Db |||||
 Qy 1381 GAGCTCACAGTTCACCCACTGTCCCTCAAACTGTCTTTCAGAAAGAAATAGTACA 1440
 Db |||||
 Qy 1381 GAGCTCACAGTTCACCCACTGTCCCTCAAACTGTCTTTCAGAAAGAAATAGTACA 1440
 Db |||||
 Qy 1441 ACTGTGTGA 1449
 Db |||||
 Qy 1441 ACTGTGTGA 1449
 Db |||||

RESULT 4

US-09-826-509-466
 ; Sequence 466, Application US/09826509
 ; Patent No. 6806054
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
 ; FILE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 466
 ; LENGTH: 1053
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-826-509-466

Query Match 11.1%; Score 160.4; DB 4; Length 1053;

Best Local Similarity 61.0%; Pred. No. 6.5e-39;
 Matches 260; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy 64 CCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTACTGGGATTCAGGCAAT 123
 Db |||||
 Qy 106 CCAGACATCTGGCTTTGGTCACTTTTGCAGTCTCTTCTGTGGGAGTCTGGCAAT 165
 Db |||||
 Qy 124 GGGCTGTGTGTGGTGGCTGGCTGAAGATGAGGAGCAAGTGAACACAAATTTGGTTC 183
 Db |||||
 Qy 166 GCCCTGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTTC 225
 Db |||||
 Qy 184 CTCACCTCACTTGGGGAGCTCTCTGTGCTGCTCTCTTGGCTTCTTGGCTGGTCTCAC 243
 Db |||||
 Qy 226 CTCACCTTGGGGTAGCGGACTTCTCTCTGCTGGGCTGGCCATCTTGTTCACGTCC 285
 Db |||||
 Qy 244 TTGGCTCTCCAGGAGAGTGGCCCTACGGAGGTTCTATGCAAGCTCATCCCTCCATC 303
 Db |||||
 Qy 286 ATTGTACAGCATCACCCTGGCCCTTTGGGGGGCCGCTGACGATCTTCCCTCCCTC 345
 Db |||||
 Qy 304 ATTGTCTCAACATGTTTGGCAGTCTTCTGCTTACTGCTTACTGCTAGCTGATCGCTGT 363
 Db |||||
 Qy 346 ATCTGCTCAACATGATGAGCCAGCATCTGCTCTGGCCACCATCAGCGCGACCGCTTT 405
 Db |||||
 Qy 364 CTTGTGTATTCAAGCCAAATCTGGTGTGAGAAATCATCGCAATGATGAGGATGGCTGTCT 423
 Db |||||
 Qy 406 CTGCTGTGTTTAAACCAATCTGGTGCAGAACTTCCGAGGGCCGCTTGGCTGGATC 465
 Db |||||
 Qy 424 ATCTGTGATGATCTGGTGGTGGCTTTTGTGATGCAATCTCTGTGTGTGTACCGG 483
 Db |||||
 Qy 466 GCCTGTGCTGGCTTGGGGTTAGCCCTGTGTGTGACCATACCCCTCTCTGTACCGG 525
 Db |||||
 Qy 484 GAAATC 489
 Db |||||
 Qy 526 GTGGTC 531
 Db |||||

RESULT 5

US-09-672-071-1
 ; Sequence 1, Application US/09672071
 ; Patent No. 6723743
 ; GENERAL INFORMATION:
 ; APPLICANT: THURKAUF, ANDREW
 ; APPLICANT: MAYNARD, GEORGE
 ; APPLICANT: HE, XIAO-SHU
 ; APPLICANT: ZHAO, HE
 ; APPLICANT: PETERSON, JOHN
 ; APPLICANT: ZHANG, XIAOYAN


```

; Patent No. 6773895
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082 00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-944-807-1

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Query Match	9.8%;	Score 142.2;	DB 4;	Length 1910;
Best Local Similarity	58.3%;	Pred. No. 4.1e-33;		
Matches 249;	Conservative 0;	Mismatches 178;	Indels 0;	Gaps 0;

QY	70	ATTCCTCTCATGGTCATTCCTCAGCCTTACCTTTTACTGGGATTCGACGGCAATGGGCTG	129
Db	113	ATCCTCCCATGGTGGTGCTTGGGGTCACCTTTGTCTCGGGGTCTCGGGCAATGGGCTT	172
QY	130	GTGCTGTGGGTGGCTGGCGCTGAAGATCAGCGGACAGTGAACAACAATTTGGTTCCTCCAC	188
Db	173	GTGATCTCGGTGGGTGGATTCCGGATGACACGCACAGTCACCACCATCTGTTACCTGAAC	232
QY	190	CTCAGCTTGGCGGACCTCCTCTGTGCTCTCTCTCGCTTCCTCGCTTCTCGCTGGCTCACTTGCT	249
Db	233	CTGGCCCTGGCTGACTTTCTTTTCAGGCCACATTACCACTCTCATTTGTCTCCATGGCC	292
QY	250	CTCCAGGACAGTGGCCCTACGGCAGTTCCTATGCAAGCTCATCCCTCCATCATTTGTC	309
Db	293	ATGGGAGAAAAATGGCCCTTTTGGCTGGTCTCTGTGAAGTTAATTCACATCGTGGTGAC	352
QY	310	CTCAACATGTTTGGCAGTGCTTCCCTGCTTACTGCCATTAGCTGGATCGCTGCTTGTC	369
Db	353	ATCAACCTCTTTGGAAGTGCTTCTTGATTGGTTTCATTGGCACTGGACCGCTGCATTTGT	412
QY	370	GTATTCAAGCCAATCTGGTGTCAGAAATCATCGCAATGTAGGGATGGCTGCTCATCTGT	429
Db	413	GTCTCTGATCCAGTCTGGGCCCAAGAACCCAGCACTGTGAGTCTGGCCAATGAAGTGATC	472
QY	430	GGATGTATCTGGGTGGGTGCTTTTGTGATGTGATCTGCTGCTTCTGCTACGGGAATC	489
Db	473	GTCCGACCTTGGATCTTTGCTCTAGTCCCTTACCTTGGCAGTTTCCCTCTTTTGGACTACA	532
QY	490	TTGACTA	496
Db	533	GTA	539

RESULT 12
US-09-023--655-1083
; Sequence 1083, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA

ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1083:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2631 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g182741
 US-09-023-655-1083

Query Match	9.8%; Score 142.2; DB 4; Length 2631;
Best Local Similarity	58.3%; Pred. No. 5e-33;
Matches	249; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
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Db	
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QY	130 GTGCTGTGGGTGCTGGCCTGAAGATGCACGCGACAGTGAACAAATTTGGTTCTCTCCAC 189
Db	
Db	911 GTGATCTGGGTGCTGGATTCGCGATGACACGCACACAGTCAACCACTCTGTTACCTGAAC 970
QY	190 CTCACCTTGGCGACCTCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
Db	
Db	971 CTGGCCCTGGCTGACCTTCTCTTTCACGGCCACATTAACCATCTCTCATTTGTCCTCATGGCC 1030
QY	250 CTCACGGACAGTGGGCCCTAAGCAGGTCCTATGCAAGCTCATCCCTCCATCATTTGTC 309
Db	
Db	1031 ATGGGAGAAAAATGGCCTTTTGGCTGGTCTCTGTGTAAGTTAATTCACATCGTGGTGGAC 1090
QY	310 CTCAAACATGTTTGGCCAGTGTCTTCCGTCTACTGCGCATAGCTGATCGCTGCTCTGTG 369
Db	
Db	1091 ATCAACTCTTTTGGAAAGTGTCTTCTGATGGTTTCATTGCACTGGACCGCTGCATTTGT 1150
QY	370 GTATTCAAGCCAAATCTGGTGTGAGAAATCATCGCAATGTAGGATGGCCCTGCTCTATCTGT 429
Db	
Db	1151 GTCCTGCATCCAGTCTGGGCCCAGAACCCGACCTGTGAGTCTGGCCCATGAAGGTGATC 1210
QY	430 GGATGTATCTGGGTGTGTGCTTTTGTGATGTGCATCTCCTGTGTCTGTGTACCGGGAATC 489
Db	
Db	1211 GTGCGACCTTGGATCTTGCTCTAGTCTTACCTTGCCAGTCTTTCTCTTTTGTACTACA 1270
QY	490 TTCACTA 496
Db	
Db	1271 GTAACCTA 1277

RESULT 13
US-09-023-655-1082
; Sequence 1082, Application US/09023655
; Patent No. 6607879

Query Match	9.7%; Score 140.4; DB 4; Length 994;
Best Local Similarity	60.5%; Pred. No. 9.8e-33;
Matches 231; Conservative	0; Mismatches 151; Indels 0; Gaps 0;
QY	95 TTACTTTTTTACTGGGATTCGACGGCAATGGGCTGGTGCTGTGGTGGCTCGGCTGAAGA 154
DB	104 TCACCTTGTGCTCGGGGCTTCGGCAACGGGCTTGTGATCTGGTGGCTGGATTCCGGA 167
QY	155 TGCAGGGGACAGTGAACACAATTTGGTTCCTCCACCTTCACTCTTGGCGGACCTCTCTGTCT 214
DB	164 TGACACACAGTCACACCACTCATGTTACCTGAACCTGGCGTGGCTGACATTCGTGTTTCA 223
QY	215 GCCTCTCTTGGCCCTTCTCGCTGCTCACAATTGGCTCTCCAGGGACAGTGGCCCTACGGCA 274
DB	224 CCTCCAATTTGGCCATTCTTCATGTCAGGAAGGCCATGGGAGGACATTTGGCTTTTGGCT 283
QY	275 GGTTCCTATGCAAGCTCATCCCTCCCAATCATGTGCTCTCAACATGTTTGCACGTGCTCTCC 334
DB	284 GGTTCCTGTGCAAAATTCGTCTTTACCATAGTGGACATCAACTGTTTCGGAAGTGCTCTTCC 343
QY	335 TGCTTACTGCGCAATTAGCGCTGGATCGCTGTCTTTGGTGATTCAAGCCCAATCTGGTGTGAGA 394
DB	344 TGAATGGCCCTATTGCTCTGGAACGCTGTGTTTGGGTCCTGCATCCAGTCTGGACCCAGA 403
QY	395 ATCATGCAATATGAGGATGGCCCTGCTCTATCTGTGGATGATCTGGGTGGTGGCTTTTG 454
DB	404 ACCACCGCACCGTGAGCTCGGCCAAGAAGGTGATCAATGGGCCCTGGGTGATGCTCTGC 463

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016,434
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0002 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1205:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1866 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: g182662
;; US-09-016-434-1205

Query Match 9.7%; Score 140.4; DB 4; Length 1866;
Best Local Similarity 60.5%; Pred. No. 1.5e-32;
Matches 231; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
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149 TCACCTTGTCTCGGGTCTCGGGACAGGGCTTGTGATCTGGTGGCTGGATCCGA 208
QY 155 TGCAGCGGACAGTGAACAAATTTGGTTCTCCACCTCACTTGGCGGACCTCTCTGCT 214
Db |||||
209 TGACACACACAGTCAACACCATCAGTTACCTGAACCTGGCGGTGGCTGACTTCTGTTCA 268
QY 215 GCCTCTCTTGGCTTCTCGGTGGCTCACTTGGCTCTCCAGGGACAGTGGCCCTACGGCA 274
Db |||||
269 CTTCCACTTTGCCATCTCTCATGTTGAGGAGGCCATGGGAGGACATTTGGCTTTGGCT 328
QY 275 GGTTCCTATGAAGTCATCCCTCCATCATTTGTCTCAACATGTTTGCCAGTGTCTTCC 334
Db |||||
329 GGTTCCTGTGAATCTCTTTACCATAGTGGACATCACTTGTTCGAGTGTCTTCC 388
QY 335 TGCTTACTGCCATAGCTGAGTCGTCTTGTGGTATTCAGCCAAATCTGGTGTGAGA 394
Db |||||
389 TGATCGCCCTCATTTGCTCTGGACCGCTGTGTTTGGCTCTGCATCCAGTCTGGACCCAGA 448
QY 395 ATCATCGCAATGAGGATGGCTCTCTATCTGGATGATCTTGGGTGGCTTTTG 454
Db |||||
449 ACCACCGCAGCTGAGCTTGCCCAAGAGGTGATCATTTGGGCGCTGGGCTGTGCTGCG 508
QY 455 TGATGTGCAATCTCTGTGTTCTG 476
Db |||||
509 TCCTCACATTGCCAGTTATCAT 530

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Job time : 270 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 05:41:50 ; Search time 5245 Seconds

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Title: US-10-764-649-1

Perfect score: 1449

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Minimum DB seq length: 0

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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1449	100.0	1449	15	US-10-225-567A-77
4	1449	100.0	1449	16	US-10-206-395B-1
5	1449	100.0	1449	18	US-10-764-649-1
6	1449	100.0	1449	18	US-10-428-817A-93
7	1449	100.0	1449	15	US-10-017-161-759
8	1449	100.0	1449	17	US-10-292-798-661
9	1449	100.0	2096	18	US-10-723-860-6365
10	1447.4	99.9	1956	9	US-09-962-832-127
11	1447.4	99.9	1956	19	US-10-843-641A-6013

12	1447.4	99.9	1970	16	US-10-367-035-1	Sequence 1, Appli
13	1447.4	99.9	2040	8	US-08-482-314-1	Sequence 1, Appli
14	1447.4	99.9	2040	14	US-10-259-521-1	Sequence 1, Appli
15	1447.4	99.9	2040	18	US-10-283-975A-63	Sequence 63, Appl
16	1447.4	99.9	2040	18	US-10-723-860-2093	Sequence 2093, Ap
17	1447	99.9	2040	9	US-09-925-302-214	Sequence 214, App
18	1447	99.9	2040	10	US-09-925-302-214	Sequence 214, App
19	1442.6	99.6	1449	10	US-09-826-509-464	Sequence 464, App
20	1442.6	99.6	1449	19	US-10-925-095-464	Sequence 464, App
c 21	988.2	68.2	7449	15	US-10-311-455-250	Sequence 250, App
22	876.2	60.5	7449	15	US-10-311-455-249	Sequence 249, App
23	788	54.4	2657	9	US-09-892-206-1	Sequence 1, Appli
24	788	54.4	2657	18	US-10-764-649-9	Sequence 9, Appli
25	330	22.8	453	10	US-09-918-995-14006	Sequence 14006, A
26	314.4	21.7	468	17	US-10-242-535A-27645	Sequence 27645, A
27	314.4	21.7	468	17	US-10-085-783A-27645	Sequence 27645, A
28	282	19.5	453	17	US-10-350-923B-68	Sequence 68, Appl
c 29	198	13.7	625	18	US-10-283-975A-367	Sequence 367, App
30	189.8	13.1	295	9	US-09-892-206-7	Sequence 7, Appli
c 31	174	12.0	611	18	US-10-283-975A-368	Sequence 368, App
32	160.4	11.1	1053	10	US-09-826-509-466	Sequence 466, App
33	160.4	11.1	1053	19	US-10-925-095-466	Sequence 466, App
34	160.4	11.1	1092	18	US-10-764-649-3	Sequence 3, Appli
35	160.4	11.1	1696	16	US-10-240-965-97	Sequence 97, Appl
36	160.4	11.1	1696	16	US-10-252-157-97	Sequence 97, Appl
37	160.4	11.1	2328	15	US-10-225-567A-79	Sequence 79, Appl
38	160.4	11.1	2328	17	US-10-305-720-1188	Sequence 1188, Ap
39	160.4	11.1	2328	17	US-10-641-643-1018	Sequence 1018, Ap
40	160.4	11.1	2328	18	US-10-723-860-2338	Sequence 2338, Ap
41	160.4	11.1	2381	18	US-10-723-860-6535	Sequence 6535, Ap
42	149.2	10.3	1116	10	US-09-905-253A-3	Sequence 3, Appli
43	149.2	10.3	1116	15	US-10-201-187-3	Sequence 3, Appli
44	149.2	10.3	1116	17	US-10-603-566-3	Sequence 3, Appli
45	147.6	10.2	1892	9	US-09-900-699A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-870-759-97
; Sequence 97, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION: David S
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1449)
; OTHER INFORMATION:
US-09-870-759-97

Query Match	100.0%	Score 1449;	DB 9;	Length 1449;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1449;	Conservative	0;	Mismatches	0;
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Db	1	ATGCGCTTCTTCTGCTGAGACCAATCACTGACCTACTCTCACAGCCATGGAATGAG	60	
Qy	61	CCCCAGTAATTCCTCATGCTTACTTCTGAGCTTACTTTTCTTCTGAGGATTCGACGC	120	

QY 361 TGTCTTGTGGTATTCAGCCAAATCTGGTGTGAGATCATCGCAATGTAGGAGATGCGCTGC 420
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 Db 421 TCTATCTGTGGATGTATCTGGGTGTGGCTTTTGTGATGTGCATTCCTGTGTTCGTGTAC 480
 QY 481 CGGGAAATCTTCACTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 Db 481 CGGGAAATCTTCACTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTATCCAGACTTTTATGGAGTCCACTAGAAAACAGGTCTCTTGAACAATTT 600
 Db 541 TCATTAGATTATCCAGACTTTTATGGAGTCCACTAGAAAACAGGTCTCTTGAACAATTT 600
 QY 601 GTTCAGCGCCCTGGAGAAATGATAGTGTAGATCTTCTCTCTCTTTCACAAACAATGAT 660
 Db 601 GTTCAGCGCCCTGGAGAAATGATAGTGTAGATCTTCTCTCTCTTTCACAAACAATGAT 660
 QY 661 CATCTTGGACAGTCCCCACTGTCTTCCAACTCAAAATTTCAAAGACCTTCTCAGAT 720
 Db 661 CATCTTGGACAGTCCCCACTGTCTTCCAACTCAAAATTTCAAAGACCTTCTCAGAT 720
 QY 721 TCACCTCCCTAGGGTCTCTAGGTATTAACAAGTCAAAATCTGTATTTCTAAATTTTAAA 780
 Db 721 TCACCTCCCTAGGGTCTCTAGGTATTAACAAGTCAAAATCTGTATTTCTAAATTTTAAA 780
 QY 781 CCTGCTGATGTCTCACTTAAATCCCAGTGGTTCCTTATTAAGATCAAGAAACC 840
 Db 781 CCTGCTGATGTCTCACTTAAATCCCAGTGGTTCCTTATTAAGATCAAGAAACC 840
 QY 841 AGCCCACTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCTAGCGCT 900
 Db 841 AGCCCACTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCTAGCGCT 900
 QY 901 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 960
 Db 901 TCTAGCAATTCCTTCTAGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 960
 QY 961 GSCCAATTCACAGATGAGTCAAGTCCCAACACCCCTCGTGGCAATTAACGATCACTAGG 1020
 Db 961 GSCCAATTCACAGATGAGTCAAGTCCCAACACCCCTCGTGGCAATTAACGATCACTAGG 1020
 QY 1021 CTAGTGTGGTCTTCTGCTGCCCTCTGTATCATGATAGCTGTTCAGAGCTTCAATGTC 1080
 Db 1021 CTAGTGTGGTCTTCTGCTGCCCTCTGTATCATGATAGCTGTTCAGAGCTTCAATGTC 1080
 QY 1081 TTCCGAATGCAAGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 Db 1081 TTCCGAATGCAAGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 QY 1141 GTGTGTGGTCTTCTTCTGCTGCTGAGTCCATACCAATTTTGGAGTCCCTGTCA 1200
 Db 1141 GTGTGTGGTCTTCTTCTGCTGCTGAGTCCATACCAATTTTGGAGTCCCTGTCA 1200
 QY 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAAAACCTCTGATGCTCGGGATCATGTATGC 1260
 Db 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAAAACCTCTGATGCTCGGGATCATGTATGC 1260
 QY 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTTTCCTTTATGCCCCTCTTGGGGAAA 1320
 Db 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTTTCCTTTATGCCCCTCTTGGGGAAA 1320
 QY 1321 GATTTTAGGAAGAAAGCAGGAGTCCATTTCAGGGAATTTCTGGAGGAGCCTTTCAGTGAG 1380
 Db 1321 GATTTTAGGAAGAAAGCAGGAGTCCATTTCAGGGAATTTCTGGAGGAGCCTTTCAGTGAG 1380
 QY 1381 GAGCTCACACGTTTCCACCCACTGTCCCTCAACAATGTCTTTTCAAGAAAGAAATAGTACA 1440
 Db 1381 GAGCTCACACGTTTCCACCCACTGTCCCTCAACAATGTCTTTTCAAGAAAGAAATAGTACA 1440

QY 1441 ACTGTGTGA 1449
 Db 1441 ACTGTGTGA 1449
 RESULT 3
 US-10-225-567A-77
 ; Sequence 77, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenna C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 77
 ; LENGTH: 1449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-225-567A-77
 Query Match 100.0%; Score 1449; DB 15; Length 1449;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGTCTTCTCTGTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
 Db 1 ATGGCGTCTTCTCTGTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
 QY 61 CCCCCAGTAATCTCTCCATGCTCAATCTCAGCCCTACTTTTACTGGGATGCGAGC 120
 Db 61 CCCCCAGTAATCTCTCCATGCTCAATCTCAGCCCTACTTTTACTGGGATGCGAGC 120
 QY 121 AATGGCTGTGTGTGGTGGCTGGCTGAAGATGACGCGACAGTCAACAAATTTGG 180
 Db 121 AATGGCTGTGTGTGGTGGCTGGCTGAAGATGACGCGACAGTCAACAAATTTGG 180
 QY 181 TTCTCCACCTCACTTGGCGGACCTCTCTGTGCTCTCTCTGCTGCTCTCTGCTGCT 240
 Db 181 TTCTCCACCTCACTTGGCGGACCTCTCTGTGCTCTCTCTGCTGCTCTCTGCTGCT 240
 QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCCCTATGCAAGCTCATCCCTCC 300
 Db 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCCCTATGCAAGCTCATCCCTCC 300
 QY 301 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTTGCCTATGAGCTGATGCG 360
 Db 301 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTTGCCTATGAGCTGATGCG 360
 QY 361 TGTCTTGTGGTATTCAGCCAAATCTGTGTGAGATCATCGCAATGTAGGAGATGCGCTGC 420
 Db 361 TGTCTTGTGGTATTCAGCCAAATCTGTGTGAGATCATCGCAATGTAGGAGATGCGCTGC 420
 QY 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCGTGTAC 480
 Db 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCGTGTAC 480
 QY 481 CGGGAATCTTTCACCTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 Db 481 CGGGAATCTTTCACCTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAATTT 600
 Db 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAATTT 600
 QY 601 GTTCAGCGCCCTGGAGAAATGATAGTGTAGTATGCTTCTCTCTTTCACAAACAATGAT 660

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601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTTCTCTTCCAAACAAATGAT 660
661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGCAGAT 720
661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGCAGAT 720
721 TCACCTCCCTAGGGTTCGTAGGTAAACAAGTCAAAATCTGTATCTAAATGATTTAAA 780
721 TCACCTCCCTAGGGTTCGTAGGTAAACAAGTCAAAATCTGTATCTAAATGATTTAAA 780
781 CCTGCTGATGTGCTCACTCACTAAATCCCAAGTGGTTCCTATTTGAAGATCAAGAAACC 840
781 CCTGCTGATGTGCTCACTCACTAAATCCCAAGTGGTTCCTATTTGAAGATCAAGAAACC 840
841 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
841 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
901 TCTAGCAATCTCTTACAGTCTGAGCTACCAAGGTTTCCAGGATTTATCAATTTA 960
901 TCTAGCAATCTCTTACAGTCTGAGCTACCAAGGTTTCCAGGATTTATCAATTTA 960
961 GGCCAAATTCACAGATGACGATCAAGTCCAAACACCCCTCTGTGGCAATAACGATCAGTAGG 1020
961 GGCCAAATTCACAGATGACGATCAAGTCCAAACACCCCTCTGTGGCAATAACGATCAGTAGG 1020
1021 CTAGTGGTGGTTCCTGCTGCTCTCTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
1021 CTAGTGGTGGTTCCTGCTGCTCTCTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCCGAGTGGCCGTG 1140
1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCCGAGTGGCCGTG 1140
1141 GTGTGGTGGTGTCTTCTTGTCTGTGGTCTCCATACCAACATTTTGGAGTCTGTGCA 1200
1141 GTGTGGTGGTGTCTTCTTGTCTGTGGTCTCCATACCAACATTTTGGAGTCTGTGCA 1200
1201 TTGCTTACTGACCCAGCAACTCCCTTGGGAAACTCTGATGCTCTGGATCATGTATGC 1260
1201 TTGCTTACTGACCCAGCAACTCCCTTGGGAAACTCTGATGCTCTGGATCATGTATGC 1260
1261 ATTGCTTAGCATCTGCCAATAGTGTCTTAACTCCCTTATGCTCTTGGGAAA 1320
1261 ATTGCTTAGCATCTGCCAATAGTGTCTTAACTCCCTTATGCTCTTGGGAAA 1320
1321 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCAGGAGGAGCCCTTCAGTGAG 1380
1321 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCAGGAGGAGCCCTTCAGTGAG 1380
1381 GAGCTCACAGTTCACCCACTGTCCTTCAACATGTCATTTCAAGAAAGAAATAGTACA 1440
1381 GAGCTCACAGTTCACCCACTGTCCTTCAACATGTCATTTCAAGAAAGAAATAGTACA 1440
1441 ACTGTGTGA 1449
1441 ACTGTGTGA 1449
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RESULT 4
US-10-206-395B-1
; Sequence 1, Application US/10206395B
; Publication No. US20030157570A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Morningstar, Douglas A.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO G
; TITLE OF INVENTION: COUPLED RECEPTOR (GPCR) ANAPHYLATOXIN C3a RECEPTOR
; FILE REFERENCE: 1920-1-6

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; CURRENT APPLICATION NUMBER: US/10/206.395B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/330,036
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-395B-1

Query Match      100.0%; Score 1449; DB 16; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGCGCTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
Db      1 ATGCGCTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
Qy      61 CCCCAGTAATTCCTCCATGTCATTCAGCCTTACTTTTACTGGGATTCGCCAGC 120
Db      61 CCCCAGTAATTCCTCCATGTCATTCAGCCTTACTTTTACTGGGATTCGCCAGC 120
Qy      121 AATGGCTGTGCTGTGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
Db      121 AATGGCTGTGCTGTGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
Qy      181 TTCTCCACCTCACCCTTGGGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 240
Db      181 TTCTCCACCTCACCCTTGGGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 240
Qy      241 CACTTGGCTCTCCAGGGACAGTGGCCCTACGGAGGTTCTCTATGCAAGCTCATCCCTCC 300
Db      241 CACTTGGCTCTCCAGGGACAGTGGCCCTACGGAGGTTCTCTATGCAAGCTCATCCCTCC 300
Qy      301 ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATTTAGCTGATGCG 360
Db      301 ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATTTAGCTGATGCG 360
Qy      361 TGTCTGTGTGTTTCAAGCCAAATCTGCTGTCAGAAATCATGCAATGTAGGATGGCTTCG 420
Db      361 TGTCTGTGTGTTTCAAGCCAAATCTGCTGTCAGAAATCATGCAATGTAGGATGGCTTCG 420
Qy      421 TCTATCTGTGAGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTTCTGTGATC 480
Db      421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTTCTGTGATC 480
Qy      481 CGGGAATCTTCACTACAGAACCAATTAATAGATGGCTACAAATTTGGTCTCTCCAGC 540
Db      481 CGGGAATCTTCACTACAGAACCAATTAATAGATGGCTACAAATTTGGTCTCTCCAGC 540
Qy      541 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAACT 600
Db      541 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAACT 600
Qy      601 GTTCAGCGCTGGAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      601 GTTCAGCGCTGGAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy      661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAAACTTCAAGACCTTCTGCAGAT 720
Db      661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAAACTTCAAGACCTTCTGCAGAT 720
Qy      721 TCACCTCCCTAGGGTTCGTAGGTAAACAAGTCAAAATCTGTATCTAAATGATTTAAA 780
Db      721 TCACCTCCCTAGGGTTCGTAGGTAAACAAGTCAAAATCTGTATCTAAATGATTTAAA 780
Qy      781 CCTGCTGATGTGCTCACCTCACTAAATCCCAAGTGGTTCCTATTTGAAGATCAAGAAACC 840
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QY 1021 CTAGTGGTGGGTTTCTGCTGCCCTCTGTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
 Db 1021 CTAGTGGTGGGTTTCTGCTGCCCTCTGTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
 QY 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
 Db 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
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 Db 1141 GTGGTGGTGGTCTTCTTCTGCTGGAGTCTCATACCAATTTTGGAGTCTCTGCA 1200
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 QY 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTTTAACTCCCTTCTTTATGCCCTCTTGGGAAA 1320
 Db 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTTTAACTCCCTTCTTTATGCCCTCTTGGGAAA 1320
 QY 1321 GATTTAGGAAGAAGCAGTCCATTCAGGGAATTCGGAGGAGCCCTTCAGTGAG 1380
 Db 1321 GATTTAGGAAGAAGCAGTCCATTCAGGGAATTCGGAGGAGCCCTTCAGTGAG 1380
 QY 1381 GAGCTCACACGTTCCACCCACTGTCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1440
 Db 1381 GAGCTCACACGTTCCACCCACTGTCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1440
 QY 1441 ACTGTGTGA 1449
 Db 1441 ACTGTGTGA 1449

RESULT 6

US-10-428-817A-93
 ; Sequence 93, Application US/10428817A
 ; Publication No. US20040214783A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 38373-189118
 ; CURRENT APPLICATION NUMBER: US/10/428,817A
 ; CURRENT FILING DATE: 2003-05-05
 ; PRIOR APPLICATION NUMBER: US 60/378,988
 ; PRIOR FILING DATE: 2002-05-08
 ; PRIOR APPLICATION NUMBER: US 60/389,366
 ; PRIOR FILING DATE: 2002-06-15
 ; PRIOR APPLICATION NUMBER: US 60/406,697
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: US 60/406,750
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/415,310
 ; PRIOR FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: US 60/415,400
 ; PRIOR FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: US 60/438,686
 ; PRIOR FILING DATE: 2003-01-09
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 93
 ; LENGTH: 1449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1449)
 US-10-428-817A-93

Query Match 100.0%; Score 1449; DB 18; Length 1449;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCTTTTCTCTGCTGAGACCAATTAACCTACTCTCAGACCATGAATGAG 60
 Db 1 ATGGCGCTTTTCTCTGCTGAGACCAATTAACCTACTCTCAGACCATGAATGAG 60
 QY 61 CCCCAGTAATCTCTCCATGGTCAATCTCAGCCTTACTTTTTTACTGGGATGCCAGGC 120
 Db 61 CCCCAGTAATCTCTCCATGGTCAATCTCAGCCTTACTTTTTTACTGGGATGCCAGGC 120
 QY 121 AATGGGCTGTGTGTGGGTGGCTTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 180
 Db 121 AATGGGCTGTGTGTGGGTGGCTTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 180
 QY 181 TTCTTCCACCTCACTTTGGCGGACCTCTCTGTGCTCTCTCTTGGCCTTCTGCTGGCT 240
 Db 181 TTCTTCCACCTCACTTTGGCGGACCTCTCTGTGCTCTCTCTTGGCCTTCTGCTGGCT 240
 QY 241 CACTTGGCTCTCAGGAGACAGTGGCCCTAGCGAGGTTCCTATGCAAGCTCATCCCCCTCC 300
 Db 241 CACTTGGCTCTCAGGAGACAGTGGCCCTAGCGAGGTTCCTATGCAAGCTCATCCCCCTCC 300
 QY 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTTGCATTTAGCCTGGATCGC 360
 Db 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTTGCATTTAGCCTGGATCGC 360
 QY 361 TGTCTTGTGTATTCAGGCAATCTGTGTGAGAAATCATCGCAATGAGGATGGCCTGC 420
 Db 361 TGTCTTGTGTATTCAGGCAATCTGTGTGAGAAATCATCGCAATGAGGATGGCCTGC 420
 QY 421 TCTATCTGTGATGTATCTGGTGGTGGCTTTTGTGATGTGCTTCTGCTGCTGCTAC 480
 Db 421 TCTATCTGTGATGTATCTGGTGGTGGCTTTTGTGATGTGCTTCTGCTGCTGCTAC 480
 QY 481 CGGGAATCTTCACTCAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 Db 481 CGGGAATCTTCACTCAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAACT 600
 Db 541 TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAACT 600
 QY 601 GTTCAGGCGCTTGAGAAATGAATGATAGTGTAGATCTCTCTCTTCCAAACAAATGAT 660
 Db 601 GTTCAGGCGCTTGAGAAATGAATGATAGTGTAGATCTCTCTCTTCCAAACAAATGAT 660
 QY 661 CATCTTTGGACAGTCCCACTGTCTTCCAACTCAAAACATTTCAAAGACCTTCTGCGAGAT 720
 Db 661 CATCTTTGGACAGTCCCACTGTCTTCCAACTCAAAACATTTCAAAGACCTTCTGCGAGAT 720
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 Db 721 TCATCTCCTAGGGGTTCTGTAGGTTAAAGTCAAAATCTGTATTTAATGTTTAA 780
 QY 781 CCTGCTGATGGTCTCACCTTAAATCCAGTGGGTTTCTTATGAGATCAGAAACC 840
 Db 781 CCTGCTGATGGTCTCACCTTAAATCCAGTGGGTTTCTTATGAGATCAGAAACC 840
 QY 841 AGCCCACTGGAATACTCTGTATGCTTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 Db 841 AGCCCACTGGAATACTCTGTATGCTTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
 QY 901 TCTAGCAATTCCTTCTACGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 960
 Db 901 TCTAGCAATTCCTTCTACGAGTCTGAGTACCAAGGTTTCCAGGATTTATCAATTTA 960
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 Db 961 GGCCAATTCAGATGACGATCAAGTCCACACCCCTCGTGGCAATAACCATCAGTAGG 1020
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 Db 1021 CTAGTGGTGGGTTTCTGCTGCCCTCTGTTATCATGATAGCTGTTACAGCTTCATTGTC 1080
 QY 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140

Db 1081 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
Qy 1141 GTGGTGGTGGTGTCTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTGTGCA 1200
Db 1141 GTGGTGGTGGTGTCTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTGTGCA 1200
Qy 1201 TTGCTTACTGACCCAGAACCTCCCTTGGGGAACCTCTGATGCTCTGGATCATGTATGC 1260
Db 1201 TTGCTTACTGACCCAGAACCTCCCTTGGGGAACCTCTGATGCTCTGGATCATGTATGC 1260
Qy 1261 ATTGCTTAGCATCTGCCAATAGTGTCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
Db 1261 ATTGCTTAGCATCTGCCAATAGTGTCTTTAATCCCTTCTTTATGCCCCTCTTGGGAAA 1320
Qy 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCCTGGAGGAGCCCTTCAGTGAG 1380
Db 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCCTGGAGGAGCCCTTCAGTGAG 1380
Qy 1381 GAGCTCACACGTTCCACCCACTGTCCCTCAACCAATGTCAATTCAGAAAGAAATAGTACA 1440
Db 1381 GAGCTCACACGTTCCACCCACTGTCCCTCAACCAATGTCAATTCAGAAAGAAATAGTACA 1440
Qy 1441 ACTGTGTCA 1449
Db 1441 ACTGTGTCA 1449

RESULT 7

US-10-017-161-759
; Sequence 759, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIORITY FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 759
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: source
; LOCATION: (1)..(1849)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(829)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1106)..(1649)
US-10-017-161-759

Query Match 100.0%; Score 1449; DB 15; Length 1849;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGTCTTTCTGTGAGACCAATTCACCTGACCTACTCTACAGCCATGGAATGAG 60
Db 201 ATGGCGTCTTTCTGTGAGACCAATTCACCTGACCTACTCTACAGCCATGGAATGAG 260
Qy 61 CCCCCAGTAATTCCTCCATGCTCAATTCCTCAGCCCTACTTTTTTACTGGGATTCAGGC 120
Db 261 CCCCCAGTAATTCCTCCATGCTCAATTCCTCAGCCCTACTTTTTTACTGGGATTCAGGC 320
Qy 121 AATGGGCTGTGCTGTGGGTGGCTGGCTGAAGATGCAGCGGACAGTGAACAAATTTGG 180

Db 321 AATGGGCTGTGCTGTGGGTGGCTGGCTGAAGATGCAGCGGACAGTGAACAAATTTGG 380
Qy 181 TTCTCCACCTCACCTTTGGGGACCTCTCTGTGCTCTCTCTTGTGCCCTTCTCGCTGGCT 240
Db 381 TTCTCCACCTCACCTTTGGGGACCTCTCTGTGCTCTCTCTTGTGCCCTTCTCGCTGGCT 440
Qy 241 CACTTGGCTCTCCAGGAGCAGTGGGCGCTTACGGCAGGTTCTTATGCAAGCTCATCCCCCTCC 300
Db 441 CACTTGGCTCTCCAGGAGCAGTGGGCGCTTACGGCAGGTTCTTATGCAAGCTCATCCCCCTCC 500
Qy 301 ATCAATGTCTCAACATGTTTGGCCAGTGTCTTCTGTGCTTACTTGCCATTTAGGATGCG 360
Db 501 ATCAATGTCTCAACATGTTTGGCCAGTGTCTTCTGTGCTTACTTGCCATTTAGGATGCG 560
Qy 361 TGTCTTGTGTAATTCAGGCCAATCTGTGTGTCAGAAATCAATCGCAATGTAGGAGTGCCTGC 420
Db 561 TGTCTTGTGTAATTCAGGCCAATCTGTGTGTCAGAAATCAATCGCAATGTAGGAGTGCCTGC 620
Qy 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTGTGTGTAC 480
Db 621 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTGTGTGTAC 680
Qy 481 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 681 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 740
Qy 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAAAT 600
Db 741 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAAAT 800
Qy 601 GTTCAGCGGCTGGAGAAATGAATGATAGTGTAGTCTCTCTCTTCCAAACAAATGAT 660
Db 801 GTTCAGCGGCTGGAGAAATGAATGATAGTGTAGTCTCTCTCTTCCAAACAAATGAT 860
Qy 661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTTGCAGAT 720
Db 861 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTTGCAGAT 920
Qy 721 TCACCTCCCTAGGGGTTCTGTAGTGTAAACAGTCAAAATCTGTAATTAATGATTTAAA 780
Db 921 TCACCTCCCTAGGGGTTCTGTAGTGTAAACAGTCAAAATCTGTAATTAATGATTTAAA 980
Qy 781 CCGTCTGATGTGTCTCACCTAAAATCCCAAGTGGGTTTCTTATGAAGATCAGAAACC 840
Db 981 CCGTCTGATGTGTCTCACCTAAAATCCCAAGTGGGTTTCTTATGAAGATCAGAAACC 1040
Qy 841 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTACTTAAAGCTGTCTCCCTAGCGCT 900
Db 1041 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTACTTAAAGCTGTCTCCCTAGCGCT 1100
Qy 901 TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTA 960
Db 1101 TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTA 1160
Qy 961 GGGCAATTCAGATGAGATCAAGTGCCAAACCCCTCGTGGCAATTAACATCACTAGG 1020
Db 1161 GGGCAATTCAGATGAGATCAAGTGCCAAACCCCTCGTGGCAATTAACATCACTAGG 1220
Qy 1021 CTAGTGTGGGTTTCTGTGCTGCCCTCTGTTATCATGATGAGCTGTTCAGCTTCAATGTC 1080
Db 1221 CTAGTGTGGGTTTCTGTGCTGCCCTCTGTTATCATGATGAGCTGTTCAGCTTCAATGTC 1280
Qy 1081 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1140
Db 1281 TTCCGAATGCAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGTG 1340
Qy 1141 GTGGTGGTGTCTTTCTTGTGTGTGTGAGTCTCCATACCAATTTTGGAGTCTCTGCA 1200
Db 1341 GTGGTGGTGTCTTTCTTGTGTGTGTGAGTCTCCATACCAATTTTGGAGTCTCTGCA 1400
Qy 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGGAACCTCTGATGCTCTGGATCATGTATGC 1260

1401	TTGCTTACTGACCCAGAAACTCCCTTTGGGGAAAACCTCTGATGTCCTGGGATCATGTATGC	1460
1261	ATTGCTCTAGCATCTGCAATAGTTGCTTTAAATCCCTTCCTTTATGSCCTCTTTGGGGAAA	1320
1461	ATTGCTCTAGCATCTGCCAATAGTTGCTTTAAATCCCTTCCTTTATGSCCTCTTTGGGGAAA	1520
1321	GAATTTAGGAAGAAAGCAAGGCAGTCCATTCAGGGAAATTCGTGAGGAGCGCTTCAGTGAG	1380
1521	GAATTTAGGAAGAAAGCAAGGCAGTCCATTCAGGGAAATTCGTGAGGAGCGCTTCAGTGAG	1580
1381	GAGCTCACAGTTCACCCACTGTCCTCAAAACAATGTCATTTTCAGAAAAAATAGTACA	1440
1581	GAGCTCACAGTTCACCCACTGTCCTCAAAACAATGTCATTTTCAGAAAAAATAGTACA	1640
1441	ACTGTGTGA	1449
1641	ACTGTGTGA	1649

RESULT 8

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US-10-292-798-661
; Sequence 661, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 661
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1849)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1649)
US-10-292-798-661

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Query Match	100.0%;	Score 1449;	DB 17;	Length 1849;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1449;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGCGCTTTCTCTGCTGAGACCAATTCAACTGACTACTCTCACAGCCATGGATGAG	60	
Db	201	ATGCGCTTTCTCTGCTGAGACCAATTCAACTGACTACTCTCACAGCCATGGATGAG	260	
Qy	61	CCCCAGTAATCTCTCCATGGTCATTCTCAGCGCTTACTTTTTTACTGGGATTGCCAGGC	120	
Db	261	CCCCAGTAATCTCTCCATGGTCATTCTCAGCGCTTACTTTTTTACTGGGATTGCCAGGC	320	
Qy	121	AATGGCGTGTGCTGTGGGTGGCTGGCGCTGAAGATGACGGCGACAGTGAACAAATTTGG	180	
Db	321	AATGGCGTGTGCTGTGGGTGGCTGGCGCTGAAGATGACGGCGACAGTGAACAAATTTGG	380	
Qy	181	TTCTCTCACACTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTCGCTGGCT	240	
Db	381	TTCTCTCACACTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTCGCTGGCT	440	
Qy	241	CACCTTGCTCTTCCAGGACAGTGCCCTTACGGCAGGTTCTCTATGCAAGCTCATCCCTCC	300	

Db	441	C	A	C	T	T	G	C	T	C	T	C	A	G	G	G	A	C	A	G	T	G	G	C	C	T	A	G	G	C	A	G	G	T	T	C	T	A	T	A	G	C	A	A	G	T	C	A	T	C	C	C	T	C		500
Qy	301	A	T	C	A	T	T	G	T	C	T	C	A	A	C	A	T	G	T	T	T	G	C	C	A	G	T	C	T	T	C	C	T	C	T	T	A	C	T	G	C	A	T	A	G	C	C	T	T	A	G	C	T		360	
Db	501	A	T	C	A	T	T	G	T	C	T	C	A	A	C	A	T	G	T	T	T	T	G	C	C	A	G	T	C	T	T	C	C	T	T	A	C	T	A	T	A	G	C	C	T	T	A	G	C	T		560				
Qy	361	T	G	T	T	T	G	T	A	T	T	C	A	A	G	C	A	A	T	C	T	G	G	T	C	A	A	T	C	A	T	C	A	T	G	C	A	A	T	C	A	T	G	C	A	A	T	T	G	C	T		420			
Db	561	T	G	T	T	T	G	T	A	T	T	C	A	A	G	C	A	A	T	C	T	G	G	T	C	A	A	T	C	A	T	C	A	T	G	C	A	A	T	C	A	T	G	C	A	A	T	T	G	C	T		620			
Qy	421	T	C	T	A	T	C	T	G	T	G	G	A	T	C	T	G	G	T	G	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		480						
Db	621	T	C	T	A	T	C	T	G	T	G	G	A	T	C	T	G	G	T	G	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		680							
Qy	481	C	G	G	A	A	T	C	T	T	C	A	T	C	A	G	A	C	A	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T		540					
Db	681	C	G	G	A	A	T	C	T	T	C	A	T	C	A	G	A	C	A	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T	A	T		740					
Qy	541	T	C	A	T	T	A	G	A	T	T	C	C	A	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		600							
Db	741	T	C	A	T	T	A	G	A	T	T	C	C	A	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		800							
Qy	601	G	T	T	C	A	G	C	C	G	C	T	G	A	G	A	A	T	G	A	T	A	G	T	T	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		660						
Db	801	G	T	T	C	A	G	C	C	G	C	T	G	A	G	A	A	T	G	A	T	A	G	T	T	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		860							
Qy	661	C	A	T	C	T	T	G	G	A	C	T	C	C	C	A	C	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		720							
Db	861	C	A	T	C	T	T	G	G	A	C	T	C	C	C	A	C	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		920							
Qy	721	T	C	A	T																																																			

QY 1381 GAGCTCACAGTTCACCCAGTGTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA 1440
DB 1581 GAGCTCACAGTTCACCCAGTGTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA 1640
QY 1441 ACTGTGTGA 1449
DB 1641 ACTGTGTGA 1649

RESULT 9

US-10-723-860-6365
; Sequence 6365, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent version 3.2
; SEQ ID NO 6365
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-6365

Query Match 100.0%; Score 1449; DB 18; Length 2096;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAAATGAG 60
DB 156 ATGGGCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAAATGAG 215
QY 61 CCCGAGTAATCTCTCCATGTCATCTCAGCCCTACTCTTTTACTGGGATTCAGGC 120
DB 216 CCCGAGTAATCTCTCCATGTCATCTCAGCCCTACTCTTTTACTGGGATTCAGGC 275
QY 121 AATGGCTGTGTGTGGGTGGCTGGCTGAAGATGACGGACAGTGAACACAAATTTGG 180
DB 276 AATGGCTGTGTGTGGGTGGCTGGCTGAAGATGACGGACAGTGAACACAAATTTGG 335
QY 181 TTCTTCGACCTCACCTTGGGGAGCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCT 240
DB 336 TTCTTCGACCTCACCTTGGGGAGCTCTCTGTGGCTCTCTGTGGCTCTCTGTGGCT 395
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGTTCTATGCAAGCTCATCCCTCC 300
DB 396 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGTTCTATGCAAGCTCATCCCTCC 455
QY 301 ATCAATGTCTCAACATGTTGGCCAGTGTCTCTGTGTTACTTGCCATTAGCTGTGATGCG 360
DB 456 ATCAATGTCTCAACATGTTGGCCAGTGTCTCTGTGTTACTTGCCATTAGCTGTGATGCG 515
QY 361 TGCTTTGGTATTCAGCCCAATCTGGGTGTGAGATCATGCAATGTAGGATGGCTTGC 420
DB 516 TGCTTTGGTATTCAGCCCAATCTGGGTGTGAGATCATGCAATGTAGGATGGCTTGC 575
QY 421 TCTATCTGTGATGTATCTGGGTGTGCTTTTGTGATGTCAATCTCTGTCTCTGTGATC 480
DB 576 TCTATCTGTGATGTATCTGGGTGTGCTTTTGTGATGTCAATCTCTGTCTCTGTGATC 635
QY 481 CGGAAATCTTCACTACAGACACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
DB 636 CGGAAATCTTCACTACAGACACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 695

QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAAACATT 600
DB 696 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAAACATT 755
QY 601 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCCTTCTCTTTTCAAAACAAATGAT 660
DB 756 GTTCAGCGCGCTGGAGAAATGAATGATAGGTAGATCCTTCTCTTTTCAAAACAAATGAT 815
QY 661 CATCTTTGGACAGTCCCGACCTGCTTCCAACTCAAACTCAAACTTCAAAACCTTCTGAGAT 720
DB 816 CATCTTTGGACAGTCCCGACCTGCTTCCAACTCAAACTCAAACTTCAAAACCTTCTGAGAT 875
QY 721 TCACCTCCCTAGGGGTTCTGCTAGGTAAACAACTCAAACTCAAACTTCAAACTTCAAA 780
DB 876 TCACCTCCCTAGGGGTTCTGCTAGGTAAACAACTCAAACTCAAACTTCAAACTTCAAA 935
QY 781 CCTGCTGATGTGGTCTCACCTTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 840
DB 936 CCTGCTGATGTGGTCTCACCTTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 995
QY 841 AGCCCACTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 900
DB 996 AGCCCACTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 1055
QY 901 TCTAGCAATTCCTTCTAGGCTCTGAGCTACCAAGGTTTCCAGGATTTATACAAATTTA 960
DB 1056 TCTAGCAATTCCTTCTAGGCTCTGAGCTACCAAGGTTTCCAGGATTTATACAAATTTA 1115
QY 961 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCACTAGG 1020
DB 1116 GGCCAAATTCAGATGACGATCAAGTGCCAAACACCCCTCGTGGCAATTAACGATCACTAGG 1175
QY 1021 CTAGTGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCAATGTC 1080
DB 1176 CTAGTGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCAATGTC 1235
QY 1081 TTCCGAATGCAAAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
DB 1236 TTCCGAATGCAAAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1295
QY 1141 GTGCTGTGGGCTGTCTTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1200
DB 1296 GTGCTGTGGGCTGTCTTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1355
QY 1201 TTGCTTACTACCCAGCAAACTCCCTTGGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1260
DB 1356 TTGCTTACTACCCAGCAAACTCCCTTGGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1415
QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCTCTTGGGGAAA 1320
DB 1416 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCCCTCTTGGGGAAA 1475
QY 1321 GATTTTAGGAAGAAAGCAAGCAGTCCATTTCAGGGAATTTTCGAGGAGCCCTTCAGTGAG 1380
DB 1476 GATTTTAGGAAGAAAGCAAGCAGTCCATTTCAGGGAATTTTCGAGGAGCCCTTCAGTGAG 1535
QY 1381 GAGCTCACGCTTCCACCCACTGCTCCCTCAAACTCAAACTCAAACTTCAAAAGAAATAGTACA 1440
DB 1536 GAGCTCACGCTTCCACCCACTGCTCCCTCAAACTCAAACTCAAACTTCAAAAGAAATAGTACA 1595
QY 1441 ACTGTGTGA 1449
DB 1596 ACTGTGTGA 1604

RESULT 10

US-09-962-832-127
; Sequence 127, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets

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; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-127

Query Match      99.9%; Score 1447.4; DB 9; Length 1956;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1  ATGGCGTCTTCTCTGCTGAGACCAATTCACACTGACCTACTCTCAGACCCATGGAATGAG 60
Db 82  ATGGCGTCTTCTCTGCTGAGACCAATTCACACTGACCTACTCTCAGACCCATGGAATGAG 141

Qy 61  CCCCAGTAATCTCTCCATGCTCACTCTCAGCCCTACTTTTCTAGTGGGATTCGACGGC 120
Db 142  CCCCAGTAATCTCTCCATGCTCACTCTCAGCCCTACTTTTCTAGTGGGATTCGACGGC 201

Qy 121  AATGGCGTGGTCTGTGGGCTGGCTGGCTGAAGATGAGCGGACGACAGTGAACAAATTTGG 180
Db 202  AATGGCGTGGTCTGTGGGCTGGCTGGCTGAAGATGAGCGGACGACAGTGAACAAATTTGG 261

Qy 181  TTCCTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db 262  TTCCTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 321

Qy 241  CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTATGCAAGCTCATCCCCCTCC 300
Db 322  CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTATGCAAGCTCATCCCCCTCC 381

Qy 301  ATCAATGTCCTCAACATGTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTG 360
Db 382  ATCAATGTCCTCAACATGTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTG 441

Qy 361  TGTCTGTGGTATTCAGCCCAATCTGCTGTGTCAGAAATCATCGCAATGTAGGATGGCTGC 420
Db 442  TGTCTGTGGTATTCAGCCCAATCTGCTGTGTCAGAAATCATCGCAATGTAGGATGGCTGC 501

Qy 421  TCTATCTGTGATGATCTGCGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCTGTGTAC 480
Db 502  TCTATCTGTGATGATCTGCGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCTGTGTAC 561

Qy 481  CGGAAATCTTTCACCTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 562  CGGAAATCTTTCACCTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621

Qy 541  TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTTGAAAACATT 600
Db 622  TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTTGAAAACATT 681

Qy 601  GTTCAGCGGCTGAGAAATGAATGATAGTTAGATCTCTTCTCTTTCCAAACAAATGAT 660
Db 682  GTTCAGCGGCTGAGAAATGAATGATAGTTAGATCTCTTCTCTTTCCAAACAAATGAT 741

Qy 661  CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGCGAGAT 720
Db 742  CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGCGAGAT 801

Qy 721  TCATCCCTAGGGTCTGTAGGTAAACAAAGTCAAAATCTGTATTTCTAATGTATTTAAA 780
Db 802  TCATCCCTAGGGTCTGTAGGTAAACAAAGTCAAAATCTGTATTTCTAATGTATTTAAA 861

Qy 781  CCTGCTGATGGTCTCACCTAAATCCCAAGTGGGTTCTTATTTGAGATCAGCAACC 840

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Db 862  CTGCTGATGGTCTCACCTAAATCCCAAGTGGGTTTCTTATTTGAAGATCAGCAACC 921
Qy 841  AGCCCACTGGATAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTTTCCCTAGCGCT 900
Db 922  AGCCCACTGGATAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTTTCCCTAGCGCT 981
Qy 901  TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATACAAATTTA 960
Db 982  TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATACAAATTTA 1041
Qy 961  GGCCAAATTCACAGATGACGATCAAGTGCACACCCCTCTGTGGCAATAACGATCACTAGG 1020
Db 1042  GGCCAAATTCACAGATGACGATCAAGTGCACACCCCTCTGTGGCAATAACGATCACTAGG 1101
Qy 1021  CTAGTGGTGGGTTTCTGCTGCTCTCTGTTATCATGATAGCTCTTACAGCTTCAATGTC 1080
Db 1102  CTAGTGGTGGGTTTCTGCTGCTCTCTGTTATCATGATAGCTCTTACAGCTTCAATGTC 1161
Qy 1081  TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAAAACCTTTCCGAGTGGCCGTG 1140
Db 1162  TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAAAACCTTTCCGAGTGGCCGTG 1221
Qy 1141  GTGCTGGTGGCTGTCTTTTCTGCTGCTGGAATCCATACCAATTTTGGAGTCTCTGTCA 1200
Db 1222  GTGCTGGTGGCTGTCTTTTCTGCTGGAATCCATACCAATTTTGGAGTCTCTGTCA 1281
Qy 1201  TTGCTTACTGACCCAGAACTCCCTTGGGNAAACTCTGATGCTCTGGGATCATGTATGC 1260
Db 1282  TTGCTTACTGACCCAGAACTCCCTTGGGNAAACTCTGATGCTCTGGGATCATGTATGC 1341
Qy 1261  ATTCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCTTATGCTCTTGGGAAA 1320
Db 1342  ATTCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCTTATGCTCTTGGGAAA 1401
Qy 1321  GATTTTGGAGAAAGCAAGGAGTCCATTGAGGAAATCTGAGGAGCAGCTTCCAGTGAG 1380
Db 1402  GATTTTGGAGAAAGCAAGGAGTCCATTGAGGAAATCTGAGGAGCAGCTTCCAGTGAG 1461
Qy 1381  GAGCTCACAGTCCACCCACTGCTCCCTCAACCAATGTCTTTTCCAGAAAGAAATAGTACA 1440
Db 1462  GAGCTCACAGTCCACCCACTGCTCCCTCAACCAATGTCTTTTCCAGAAAGAAATAGTACA 1521
Qy 1441  ACTGTGTGA 1449
Db 1522  ACTGTGTGA 1530

RESULT 11
US-10-843-641A-6013
; Sequence 6013, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007

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; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6013
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-6013

Query Match      99.9%; Score 1447.4; DB 19; Length 1956;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGAATGAG 60
Db      1  ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGAATGAG 141
Qy      61  CCCCAGTAATTCCTCCATGCTCATTCTCAGCCTTACTTTTACTGGGATTCGCCAGGC 120
Db      142  CCCCAGTAATTCCTCCATGCTCATTCTCAGCCTTACTTTTACTGGGATTCGCCAGGC 201
Qy      121  AATGGCTGGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 180
Db      202  AATGGCTGGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 261
Qy      181  TTCTTCCACCTCAGCTTGGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTGCTGCT 240
Db      262  TTCTTCCACCTCAGCTTGGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTGCTGCT 321
Qy      241  CACTTGGCTCTCCAGGACAGTGGCCCTTACCGCAGGTTCTTATGCAAGCTCATCCCTCC 300
Db      322  CACTTGGCTCTCCAGGACAGTGGCCCTTACCGCAGGTTCTTATGCAAGCTCATCCCTCC 381
Qy      301  ATCAATGCTCCTCAATGTTTGGCAGTGTCTTCTGCTTACTGCTGCTGCTGCTGCTGCT 360
Db      382  ATCAATGCTCCTCAATGTTTGGCAGTGTCTTCTGCTTACTGCTGCTGCTGCTGCTGCT 441
Qy      361  TGCTTGTGTTATTCAGCCCAATCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db      442  TGCTTGTGTTATTCAGCCCAATCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
Qy      421  TCTATCTGTGATGTATCTGGGTGGTGGTCTTGTGATGTGCTTCTGCTGCTGCTGCTGCT 480
Db      502  TCTATCTGTGATGTATCTGGGTGGTGGTCTTGTGATGTGCTTCTGCTGCTGCTGCTGCT 561
Qy      481  CGGAAATCTTCTACACAGCAACCATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db      562  CGGAAATCTTCTACACAGCAACCATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
Qy      541  TCATTAGATTCAGACTTTTATGGAGATCCACTAGAAACAGTCTCTTGAACAACTT 600
Db      622  TCATTAGATTCAGACTTTTATGGAGATCCACTAGAAACAGTCTCTTGAACAACTT 681
Qy      601  GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTCTCTCTTCTTCCAAACAAATGAT 660
Db      682  GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTCTCTCTTCTTCCAAACAAATGAT 741
Qy      661  CATCTTTGGACAGTCCCACTGTCTTCCAACTCAAACTTCAAGACCTTCTGCGAGAT 720
Db      742  CATCTTTGGACAGTCCCACTGTCTTCCAACTCAAACTTCAAGACCTTCTGCGAGAT 801
Qy      721  TCACCTCCCTAGGGTCTGCTAGGTATTAACAGTCAAACTGATTTCTAATGATTTAAA 780
Db      802  TCACCTCCCTAGGGTCTGCTAGGTATTAACAGTCAAACTGATTTCTAATGATTTAAA 861
Qy      781  CCTGCTGATGTTCTCACTCACTAAATCCCACTGGTCTTCTTATTTGAAGTACAGAAACC 840
Db      862  CCTGCTGATGTTCTCACTCACTAAATCCCACTGGTCTTCTTATTTGAAGTACAGAAACC 921

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Qy      841  AGCCCACTGGATAAATCTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
Db      922  AGCCCACTGGATAAATCTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 981
Qy      901  TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATCAAAATTTA 960
Db      982  TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATCAAAATTTA 1041
Qy      961  GGCCAAATTCACAGATGACGATCAAGTCCCAACCCCTCTGCGCAATAACGATCACTAGG 1020
Db      1042  GGCCAAATTCACAGATGACGATCAAGTCCCAACCCCTCTGCGCAATAACGATCACTAGG 1101
Qy      1021  CTAGTGTGGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db      1102  CTAGTGTGGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
Qy      1081  TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGCTG 1140
Db      1162  TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGCTG 1221
Qy      1141  GTGCTGTGCTGTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db      1222  GTGCTGTGCTGTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1281
Qy      1201  TTGCTTACTACCCAGCAAACTCCCTTGGGGAACCTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db      1282  TTGCTTACTACCCAGCAAACTCCCTTGGGGAACCTCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1341
Qy      1261  ATTGCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCTTATGCTTCTTCTGCTGCTGCT 1320
Db      1342  ATTGCTCTAGCATCTGCAATAGTTGCTTTTAACTCCCTTCTTATGCTTCTTCTGCTGCTGCT 1401
Qy      1321  GATTTTAGGAAGCAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
Db      1402  GATTTTAGGAAGCAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461
Qy      1381  GAGCTCACAGTTCACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db      1462  GAGCTCACAGTTCACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
Qy      1441  ACTGTGTGA 1449
Db      1522  ACTGTGTGA 1530

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RESULT 12
US-10-367-035-1
; Sequence 1, Application US/10367035
; Publication No. US20030187244A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; TITLE OF INVENTION: EXTRACELLULAR DOMAIN
; FILE REFERENCE: TSRI 511.1D1
; CURRENT APPLICATION NUMBER: US/10/367,035
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/117,440
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: PCT/US97/01736
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 60/010,808
; PRIOR FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1970
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(1527)
US-10-367-035-1

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Query Match 99.9%; Score 1447.4; DB 16; Length 1970;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGTCTTCTGCTGAGACCAATCAAGTACCTACTCTACAGCCATGGAATGAG 60
Db ATGGCGTCTTCTGCTGAGACCAATCAAGTACCTACTCTACAGCCATGGAATGAG 141

Qy 61 CCCCCAGTAATCTCCATGCTCAATCTCAGCCTACTTTTACTGGATGCGAGGC 120
Db CCCCCAGTAATCTCCATGCTCAATCTCAGCCTACTTTTACTGGATGCGAGGC 201

Qy 121 AATGGCTGGTCTGCTGGGTGGCTGGCTGAAGATGCGAGCGACAGTGAACACAAATTTGG 180
Db AATGGCTGGTCTGCTGGGTGGCTGGCTGAAGATGCGAGCGACAGTGAACACAAATTTGG 261

Qy 181 TTCTTCACCTCACCTTGGGGAACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db TTCTTCACCTCACCTTGGGGAACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 321

Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTACCGCAGTTCCTATGCAAGCTCATCCCTCC 300
Db CACTTGGCTCTCCAGGACAGTGGCCCTACCGCAGTTCCTATGCAAGCTCATCCCTCC 381

Qy 301 ATCATTTGCTCAACATGTTTCCAGTGTCTTCTGCTTACTGCAATTAGCTCGATCGC 360
Db ATCATTTGCTCAACATGTTTCCAGTGTCTTCTGCTTACTGCAATTAGCTCGATCGC 441

Qy 361 TGTCTTGGTATTCAAGCCAACTGCGTGCAGAAATCATGCAATGATGAGGATGCGCTGC 420
Db TGTCTTGGTATTCAAGCCAACTGCGTGCAGAAATCATGCAATGATGAGGATGCGCTGC 501

Qy 421 TCTATCTGATGATGATCTGCGTGGTCTTGTGATGTCATTCCTGCTGCTGCTGAC 480
Db TCTATCTGATGATGATCTGCGTGGTCTTGTGATGTCATTCCTGCTGCTGCTGAC 561

Qy 481 CGGAAATCTTCACTACAGACCAATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 540
Db CGGAAATCTTCACTACAGACCAATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 621

Qy 541 TCATTAGATATCCAGACTTTTATGGAGTCCACTAGAAACAGTCTCTTGAACAACT 600
Db TCATTAGATATCCAGACTTTTATGGAGTCCACTAGAAACAGTCTCTTGAACAACT 681

Qy 601 GTTCAGCGCTGAGAAATGAATGATAGTGTAGATCTTCTCTTCCAAACAAATGAT 660
Db GTTCAGCGCTGAGAAATGAATGATAGTGTAGATCTTCTCTTCCAAACAAATGAT 741

Qy 661 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTTCAAGACCTTCTGCAAGAT 720
Db CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTTCAAGACCTTCTGCAAGAT 801

Qy 721 TCATCTCCTAGGGTCTGCTAGGTAACTAGTCAAAATCTGATTTCTAATGATTTAAA 780
Db TCATCTCCTAGGGTCTGCTAGGTAACTAGTCAAAATCTGATTTCTAATGATTTAAA 861

Qy 781 CCTGCTGATGGTCTCACCTAAATCCAGTGGGTTTCTATTTGAAGATCAGAAACC 840
Db CCTGCTGATGGTCTCACCTAAATCCAGTGGGTTTCTATTTGAAGATCAGAAACC 921

Qy 841 AGCCCACTGATTAATCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
Db AGCCCACTGATTAATCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 981

Qy 901 TCTAGCAATCTCTTCTACGAGTCTGAGTCAACAGGTTTCCAGGATTTATCAATTTA 960
Db TCTAGCAATCTCTTCTACGAGTCTGAGTCAACAGGTTTCCAGGATTTATCAATTTA 1041

Qy 961 GGCCAAATTCAGATGAGTCAAGTCCCAACCCCTCGTGGCAATACGATCACTAGG 1020
Db GGCCAAATTCAGATGAGTCAAGTCCCAACCCCTCGTGGCAATACGATCACTAGG 1101

Qy 1021 CTAGTGTGGGTTTCCTGCTGCGCTCTGTTATCATGTAGCCTGTTACAGCTTCAATTGTC 1080
Db CTAGTGTGGGTTTCCTGCTGCGCTCTGTTATCATGTAGCCTGTTACAGCTTCAATTGTC 1161

Qy 1081 TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
Db TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1221

Qy 1141 GTGTGGTGGTGTCTTCTTCTGCTGCTGAGTCCATACCAATTTTTCGAGTGGTCTGTC 1200
Db GTGTGGTGGTGTCTTCTTCTGCTGCTGAGTCCATACCAATTTTTCGAGTGGTCTGTC 1281

Qy 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGAAACTCTGATGCTGCGATCATGTATGC 1260
Db TTGCTTACTGACCCAGAAACTCCCTTGGGAAACTCTGATGCTGCGATCATGTATGC 1341

Qy 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTCTTGGGAAA 1320
Db ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTCTTGGGAAA 1401

Qy 1321 GATTTTAGGAGAAAGCAAGGCACTCCATTAGGGAATCTGGAGGAGCCCTTCAGTGAG 1380
Db GATTTTAGGAGAAAGCAAGGCACTCCATTAGGGAATCTGGAGGAGCCCTTCAGTGAG 1461

Qy 1381 GAGCTCACAGTTCACCCACTGTCCTCAAACTCAATGTCAATTCAGAAAGAAATAGTACA 1440
Db GAGCTCACAGTTCACCCACTGTCCTCAAACTCAATGTCAATTCAGAAAGAAATAGTACA 1521

Qy 1441 ACTGTGTGA 1449
Db 1522 ACTGTGTGA 1530

RESULT 13
US-08-462-314-1
; Sequence 1, Application US/08462314
; Publication No. US20030027245A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human G-protein coupled Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,314
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01992
; FILING DATE: 17 FEB 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-382
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2040 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-462-314-1

Query Match 99.9%; Score 1447.4; DB 8; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCAGCCGATGGAATGAG	60
Db	153	ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCAGCCGATGGAATGAG	212
QY	61	CCCCAGTAATTCCTCCATGTCATCTCAGCCTTACTTTTACTGGAATGCGAGGC	120
Db	213	CCCCAGTAATTCCTCCATGTCATCTCAGCCTTACTTTTACTGGAATGCGAGGC	272
QY	121	AATGGGCTGGTCTGCTGGGTGGCTGGCTGAGAGTGCAGCGGACAGTGAACACAAATTTGG	180
Db	273	AATGGGCTGGTCTGCTGGGTGGCTGGCTGAGAGTGCAGCGGACAGTGAACACAAATTTGG	332
QY	181	TTCTTCCACTCACCCTTGGGAGCCTCTCTGTGCTGCTCTCTGCTGCTCTCTGCTGCT	240
Db	333	TTCTTCCACTCACCCTTGGGAGCCTCTCTGTGCTGCTCTCTGCTGCTCTCTGCTGCT	392
QY	241	CACCTTGGCTCTCCAGGGACAGTGGCCCTACGCGAGTTCCTATGCAAGCTCATCCCTCC	300
Db	393	CACCTTGGCTCTCCAGGGACAGTGGCCCTACGCGAGTTCCTATGCAAGCTCATCCCTCC	452
QY	301	ATCATTTGCTCAACATGTTGGCCAGTGTCTTCTGCTTACTTGCCTATGAGCTGGATCGC	360
Db	453	ATCATTTGCTCAACATGTTGGCCAGTGTCTTCTGCTTACTTGCCTATGAGCTGGATCGC	512
QY	361	TGCTTTGGTATTCAGCCCAATCTGGTGTGTCAGAAATCATGCAATGTAGGAGTGGCTGC	420
Db	513	TGCTTTGGTATTCAGCCCAATCTGGTGTGTCAGAAATCATGCAATGTAGGAGTGGCTGC	572
QY	421	TCTATCTGCTGATGATCTGGGTGGTGGCTTTTGTGATGTCATCTCTGTTGTGTGAC	480
Db	573	TCTATCTGCTGATGATCTGGGTGGTGGCTTTTGTGATGTCATCTCTGTTGTGTGAC	632
QY	481	CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540
Db	633	CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	592
QY	541	TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAAAT	600
Db	693	TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAAAT	752
QY	601	GTTACAGCGCTGGAGAAATGAATGATAGGTAGATCTTCTCTCTTCCAAACAAATGAT	660
Db	753	GTTACAGCGCTGGAGAAATGAATGATAGGTAGATCTTCTCTCTTCCAAACAAATGAT	812
QY	661	CATCTCTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTCAGAT	720
Db	813	CATCTCTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTCAGAT	872
QY	721	TCATCTCTAGGGTCTGCTAGGTAAACAGTCAAAATCTGATATCTAATGATTTATAA	780
Db	873	TCATCTCTAGGGTCTGCTAGGTAAACAGTCAAAATCTGATATCTAATGATTTATAA	932
QY	781	CCTGCTGATGCTCTACCTTAATATCCCACTGGGTCTCTTATGAAGATCAGCAACC	840
Db	933	CCTGCTGATGCTCTACCTTAATATCCCACTGGGTCTCTTATGAAGATCAGCAACC	992
QY	841	AGCCCACTGGATACTCTGATGCTTTTCTCTCTACTCTATTTAAAGCTGTCTCCAGCGT	900
Db	993	AGCCCACTGGATACTCTGATGCTTTTCTCTCTACTCTATTTAAAGCTGTCTCCAGCGT	1052
QY	901	TTAGCAATTCCTTCTACAGGCTGAGTACCAAGGTTTCCAGGATTTATPACAATTTA	960
Db	1053	TTAGCAATTCCTTCTACAGGCTGAGTACCAAGGTTTCCAGGATTTATPACAATTTA	1112
QY	961	GGCCAAATTCAGATGACGATCAAGTGCCCAACCCCTCGTGGCAATTAACGATCACTAGG	1020

RESULT 14

US-10-259-521-1
; Sequence 1, Application US/10259521
; Publication No. US20030022310A1
; GENERAL INFORMATION:

APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/259.521
FILING DATE: 30-Sep-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/462,314
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US95/01992
FILING DATE: 17 FEB 1995

ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-382 (PF159)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-259-521-1

Query Match 99.9%; Score 1447.4; DB 14; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCCATGGATGAG 60
DB 153 ATGGCGCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCCATGGATGAG 212

QY 61 CCCCCAGTAATCTCTCCATGATGTCATTCTCAGCCTTACTTTTACTGGGATGGCAGGC 120
DB 213 CCCCCAGTAATCTCTCCATGATGTCATTCTCAGCCTTACTTTTACTGGGATGGCAGGC 272

QY 121 AATGGCTGCTGCTGGGTGGCTGGCTGCTGAAGATGACGCGACAGTGAACAATTTGG 180
DB 273 AATGGCTGCTGCTGGGTGGCTGGCTGCTGAAGATGACGCGACAGTGAACAATTTGG 332

QY 181 TTCTCTCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 240
DB 333 TTCTCTCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 392

QY 241 CACTTGGCTCTCAGGACAGTGGCGCTTACGGCAGGTTCTTANGCAAGCTCATCCCTCC 300
DB 393 CACTTGGCTCTCAGGACAGTGGCGCTTACGGCAGGTTCTTANGCAAGCTCATCCCTCC 452

QY 301 ATCAATGCTCTCAACATGTTTCCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTGCT 360
DB 453 ATCAATGCTCTCAACATGTTTCCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTGCT 512

QY 361 TGTCTTGGTATTCAGCCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 513 TGTCTTGGTATTCAGCCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572

QY 421 TCTATCTGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 573 TCTATCTGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632

QY 481 CGGAAATCTTCACTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
DB 633 CGGAAATCTTCACTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 692

QY 541 TCATTAGATTATCCAGCTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAACT 600
DB 693 TCATTAGATTATCCAGCTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAACT 752

QY 601 GTTCAGCGCTGGAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 753 GTTCAGCGCTGGAGAAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812

QY 661 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAA 720
DB 813 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAA 872

QY 721 TCACTCTCTAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 873 TCACTCTCTAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932

QY 781 CCTGCTGATGGTCTCACTAAATCCCAAGTGGGTTTCTTATGAGATCAAGAAACC 840
DB 933 CCTGCTGATGGTCTCACTAAATCCCAAGTGGGTTTCTTATGAGATCAAGAAACC 992

QY 841 AGCCCACTGGATACTCTGATGCTTTTCTCTCTACTCAATTAAGCTGTTCCCTAGGCT 900
DB 993 AGCCCACTGGATACTCTGATGCTTTTCTCTCTACTCAATTAAGCTGTTCCCTAGGCT 1052

QY 901 TCTAGCAATTCCTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACAAATTA 960
DB 1053 TCTAGCAATTCCTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACAAATTA 1112

QY 961 GGCCAATTCACAGATGACGATCAAGTGCCAAACCCCTCGTGGCAATAACGATCACTAGG 1020
DB 1113 GGCCAATTCACAGATGACGATCAAGTGCCAAACCCCTCGTGGCAATAACGATCACTAGG 1172

QY 1021 CTAGTGGTGGGTTTCTGCTGCTCTCTTATCATGATAGCTGTTTACAGCTTCATTGTC 1080
DB 1173 CTAGTGGTGGGTTTCTGCTGCTCTCTTATCATGATAGCTGTTTACAGCTTCATTGTC 1232

QY 1081 TTCCGATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCCGAGTGGCCGTG 1140
DB 1233 TTCCGATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTCCGAGTGGCCGTG 1292

QY 1141 GTGGTGGGCTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1293 GTGGTGGGCTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352

QY 1201 TTGCTTACTACCCAGAAACTCCCTTGGGGAATACTCTGATGCTCTGGGATCATGTATGC 1260
DB 1353 TTGCTTACTACCCAGAAACTCCCTTGGGGAATACTCTGATGCTCTGGGATCATGTATGC 1412

QY 1261 ATTGCTCTAGCATCTGCAATAGTGTCTTTAATCCCTTCTTATGCCCTCTTGGGGAATA 1320
DB 1413 ATTGCTCTAGCATCTGCAATAGTGTCTTTAATCCCTTCTTATGCCCTCTTGGGGAATA 1472

QY 1321 GATTTTAGGAAGAAGCAAGCAGTCCATTCAGGGAATCTGGAGGAGCCTTCAGTGAG 1380
DB 1473 GATTTTAGGAAGAAGCAAGCAGTCCATTCAGGGAATCTGGAGGAGCCTTCAGTGAG 1532

QY 1381 GAGCTCACAGTTCACCCACTGTCCCTCAAACTCAATGTCATTTCAGAAAGAAATAGTACA 1440
DB 1533 GAGCTCACAGTTCACCCACTGTCCCTCAAACTCAATGTCATTTCAGAAAGAAATAGTACA 1592

QY 1441 ACTGTGTGA 1449
DB 1593 ACTGTGTGA 1601

RESULT 15
US-10-283-975A-63
; Sequence 63, Application US/10283975A
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Orcho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 PCT
; CURRENT APPLICATION NUMBER: US/10/283,975A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/340,938
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/338,997
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340,081
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/341,012
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-63

Query Match 99.9%; Score 1447.4; DB 18; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTTTCTCTGCTGAGACCAATTCACACTGACCTACTCTCAGCCATGGATGAG 60

Db 153 ATGGCGCTCTTCTCTGCTGAGACCAATTCACTGACCTACTCTCAGACCCATGGAATGAG 212
Qy 61 CCCCGAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTACTGGGATTCGACGGC 120
Db 213 CCCCGAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTACTGGGATTCGACGGC 272
Qy 121 AATGGGCTGGTCTGCTGGGCTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
Db 273 AATGGGCTGGTCTGCTGGGCTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 332
Qy 181 TTCTTCCACCTCACCCTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 240
Db 333 TTCTTCCACCTCACCCTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 392
Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCCCTCC 300
Db 393 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCCCTCC 452
Qy 301 ATCATTTGCTTCAACATGTTTCCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTTACTGCT 360
Db 453 ATCATTTGCTTCAACATGTTTCCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTTACTGCT 512
Qy 361 TGTCTTGTGGTATTCAAGCCAACTCTGGTGTGTCAGAAATCATGCAATGTAGGATGGCCCTGC 420
Db 513 TGTCTTGTGGTATTCAAGCCAACTCTGGTGTGTCAGAAATCATGCAATGTAGGATGGCCCTGC 572
Qy 421 TCTATCTGTGGATGATCTGGGCTGGTGGCTTTTGTGATGTGCTTCTCTGCTTCTGCTGTAC 480
Db 573 TCTATCTGTGGATGATCTGGGCTGGTGGCTTTTGTGATGTGCTTCTCTGCTTCTGCTGTAC 632
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Qy 601 GTTCAGCGCCTGGAGAAATGAATAGTGTAGTCTCTCTCTTCTTCCAAACAAATGAT 660
Db 753 GTTCAGCGCCTGGAGAAATGAATAGTGTAGTCTCTCTCTTCTTCCAAACAAATGAT 812
Qy 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAAGACCTTCTGCGAT 720
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Db 1413 ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCTCTTGGGAAA 1472
Qy 1321 GATTTTAGGAAGAAAGCAAGGAGTCCATTTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
Db 1473 GATTTTAGGAAGAAAGCAAGGAGTCCATTTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1532
Qy 1381 GAGCTCACACGTTCCACCCACTGTCCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1440
Db 1533 GAGCTCACACGTTCCACCCACTGTCCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1592
Qy 1441 ACTGTGTGA 1449
Db 1593 ACTGTGTGA 1601

Search completed: April 11, 2005, 10:38:18
Job time : 5247 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 02:57:50 ; Search time 5114 Seconds
(without alignments)
10785.124 Million cell updates/sec

Title: US-10-764-649-1

Perfect score: 1449
Sequence: 1 atggcgctttctctgtga.....gaaatagataactgtgtga 1449

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	1449	9 AY410247	Homo sapi
2	1449	100.0	1885	3 CR601349	full-leng
3	1449	100.0	1888	3 CR590169	full-leng
4	1449	100.0	1899	3 CR623914	full-leng
5	1449	100.0	1910	3 CR591233	full-leng
6	1449	100.0	1951	3 CR609272	full-leng
7	1415.8	97.7	1449	9 AY410248	Pan trogl
8	915	63.1	1122	5 BX395616	
9	911.4	62.9	1092	5 BX381444	
10	897	61.9	1137	5 BX396411	
11	856.6	59.1	1035	5 BX381109	
12	830.4	57.3	1112	4 BM562131	AGENCOURT
13	827.4	57.1	934	5 BX337391	AGENCOURT
14	815.8	56.3	976	5 BX381073	
15	809.4	55.9	1093	5 BM920604	AGENCOURT
16	789.6	54.5	859	5 BX355871	
17	788	54.4	1434	9 AY410249	Mus muscu
18	785	54.2	797	5 BX095575	
19	784.8	54.2	2931	3 AK054017	Mus muscu
20	761.4	52.5	969	4 BM804784	AGENCOURT
21	758.6	52.4	1067	5 BM919467	AGENCOURT
22	749.6	51.7	1093	1 AL513912	
23	744.6	51.4	1124	4 BM546347	AGENCOURT
24	711	49.1	887	4 B1769086	603057065

25	706.4	48.8	1067	5 BX378071	BX378071
26	660.2	45.6	799	7 CO957263	CO957263
27	641.4	44.3	729	6 CD102504	AGENCOURT
28	621.4	42.9	849	4 B1821479	B1821479
c	616.6	42.6	1173	5 BX378155	BX378155
c	613.4	42.3	716	6 CB054504	NISC gm04
30	606.6	41.9	1111	5 BX395615	BX395615
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32	594.4	41.0	704	5 BX482976	DRP2p688A
33	588.4	40.6	869	6 CD246185	AGENCOURT
34	588	40.6	816	6 CD520940	AGENCOURT
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c	576.4	39.8	803	7 CO957262	AGENCOURT
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37	572.4	39.5	630	2 AW581977	RC3-ST018
c	548.4	37.8	1089	5 BX381443	BX381443
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40	545.8	37.7	663	6 CD685945	EST2466 h
c	545.8	37.7	997	5 BX337390	BX337390
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c	537.2	37.1	978	5 BX378070	BX378070
44	533	36.8	728	1 AUI38812	AUI38812

ALIGNMENTS

RESULT 1
AY410247
LOCUS Homo sapiens C3AR1 gene, VIRTUAL TRANSCRIPT, partial sequence, 1449 bp DNA linear GSS 16-DEC-2003
DEFINITION Homo sapiens C3AR1 gene, VIRTUAL TRANSCRIPT, partial sequence, 1449 bp DNA linear GSS 16-DEC-2003
ACCESSION AY410247
VERSION AY410247.1 GI:39766215
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1449)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1449)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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source 1. 1449
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1449
/gene="C3AR1"
/locus_tag="HCN3827"

Query Match 100.0%; Score 1449; DB 9; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGCTTTCTCTGTCGACCAATTCACCTGACCTACTCTCTCAGCAGCATGGAATGAG 60
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61	CCCCAGTAATTCTCTCCATGGTCAATTCAGACCTTACTTTTTTACTGGGATGGCAGGC	120
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121	AATGGGCTGGTGTGTGGGTGGCTGAGATGCGCGGACAGTGAAACAAATTGG	180
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421	TCTATCTGTGGATGTAATCTGGGTGGTGGCTTCTGCTGATGTGCAATCCTGTGTTCGTGTAC	480
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601	GTT CAGCGGCTGGAGAAATGAATGATAGGTGTAGATCCTTCTCTTCCAAACAAATGAT	660
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661	CATCTTGGACAGTCCCACCTGTCTTCCAACTCAAACTTTCAAAGACCTTCTGCGAGAT	720
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781	CTGTCTGATGTGTCTCACTAAATCCCAGTGGGTTTCTATGTAAGATACGAAACC	840
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841	AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTAAAGCTGTTCCTTAGCGCT	900
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901	TCTAGCAATTCCTTCTACCGAGCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTA	960
961	GGCCAAATTCACAGATCAAGTCAAGTGCCAAACCCCTCGTGGCAATAACGATCACTAGG	1020
961	GGCCAAATTCACAGATCAAGTCAAGTGCCAAACCCCTCGTGGCAATAACGATCACTAGG	1020
1021	CTAGTGGTGGGTTTCTGTGCTGCCCTCTGTTATCATGATAGCTGTTCAGCTTCATGTGC	1080
1021	CTAGTGGTGGGTTTCTGTGCTGCCCTCTGTTATCATGATAGCTGTTCAGCTTCATGTGC	1080
1081	TTCCGNAATCGAAGGGCGCTTCGCGAAGTCTCAGAGCAAAACCTTTCAGTGGCGCGTG	1140
1081	TTCCGNAATCGAAGGGCGCTTCGCGAAGTCTCAGAGCAAAACCTTTCAGTGGCGCGTG	1140

Qy	1141	GTGGTGGTGGCTGTCTTTCTTGTCTGCTGGACTCCACATACATTTTGGAGTCTGTGCA	1200
Db	1141	GTGGTGGTGGCTGTCTTTCTTGTCTGCTGGAATCCATACACATTTTGGAGTCTGTGCA	1200
Qy	1201	TTGCTTTACTGACCCAGAAAACCTCCCTTTGGGGAAAACCTCTGATGTCCTGGGATCATGTATGC	1260
Db	1201	TTGCTTTACTGACCCAGAAAACCTCCCTTTGGGGAAAACCTCTGATGTCCTGGGATCATGTATGC	1260
Qy	1261	ATTGCTCTAGCATCTGCGCAATAGTTCCTTTTAATCCCTTCTTTATGCCCCCTCTTGGGGAAA	1320
Db	1261	ATTGCTCTAGCATCTGCCAATAGTTCCTTTTAATCCCTTCTTTATGCCCCCTCTTGGGGAAA	1320
Qy	1321	GATTTTATAGGAAGAAACAAAGGCAGTCCATTTCAGGGAAATTTCTGGAGGCAGCCCTTTCAGTGAAG	1380
Db	1321	GATTTTATAGGAAGAAACAAAGGCAGTCCATTTCAGGGAAATTTCTGGAGGCAGCCCTTTCAGTGAAG	1380
Qy	1381	GAGCTCACACGTTCCACCCACATGTCCCTCAACACATGTCTATTTTCAGAAAGAAATAGTACA	1440
Db	1381	GAGCTCACACGTTCCACCCACATGTCCCTCAACACATGTCTATTTTCAGAAAGAAATAGTACA	1440
Qy	1441	ACTGTGTGA	1449
Db	1441	ACTGTGTGA	1449

RESULT 2	
CR601349	
LOCUS	1885 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CS0DI065YH15 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR601349
VERSION	CR601349.1 GI:50482156
KEYWORDS	HTC; CNSLT_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

Query Match	100.0%	Score 1449;	DB 3;	Length 1885;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1449;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	79	ATFGCGGTCTTTCTCTGTGAGACCAATTCACCTTGA	CTTACTCTCAGCCCATGGAATGAG	138

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QY 121 AATGGCTGGTGTCTGTGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 180
Db 199 AATGGCTGGTGTCTGTGGTGGCTGGCTGAAGATGACGGGACAGTGAACACAAATTTGG 258
QY 181 TTCTCCACCTCACTTGGCGGACCTCTCTGTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db 259 TTCTCCACCTCACTTGGCGGACCTCTCTGTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 318
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGTTTCTATGCAAGCTCATCCCTCC 300
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QY 361 TGTCTTGGTATTCACGCCAATCTGGTGTGAGATCATGCAATCATGCAATGATGCAATGATG 420
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QY 421 TCTATCTGTGATGTATCTGGTGTGCTTGTGATGTCATCTCTGCTGCTGCTGCTGCTG 480
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QY 541 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGCTCTCTTGAACAACT 600
Db 619 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGCTCTCTTGAACAACT 678
QY 601 GTTCAGCCGCTTGGGAATGAATGATAGTTAGATCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 679 GTTCAGCCGCTTGGGAATGAATGATAGTTAGATCTCTCTCTCTCTCTCTCTCTCTCT 738
QY 661 CATCTCTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGT 720
Db 739 CATCTCTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGT 798
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Db 919 AGCCCACTGGATAACTCTGATGCTTTCTCTCTACTCAATTTAAAGCTGTTCCCTAGGCT 978
QY 901 TCTAGCAATCTCTTACAGTCTGAGTCAACCAAGTTCCTAGGATTTATCAATTTA 960
Db 979 TCTAGCAATCTCTTACAGTCTGAGTCAACCAAGTTCCTAGGATTTATCAATTTA 1038
QY 961 GGCCAAATTCAGATGACATCAAGTGCACACCCCTCGTGGCAATTAACATCACTAGG 1020
Db 1039 GGCCAAATTCAGATGACATCAAGTGCACACCCCTCGTGGCAATTAACATCACTAGG 1098
QY 1021 CTAGTGGTGGTTCCTCTGCTGCTCTGTTATCATGATGAGCTGTATCAGCTTCTATGTC 1080
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QY 1081 TTCGAATGCAAGGGGCGCTTCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
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Db 1339 ATTGCTCTAGCATCTGCAATGATGTTTAAATCCCTTCTTTATGCTCTTTGGGAAA 1398
QY 1321 GATTTTAGGAAGAAGCAAGCAGTCCATTTCAGGAAATTTCTGGAGGAGCTCTCAGTCAG 1380
Db 1399 GATTTTAGGAAGAAGCAAGCAGTCCATTTCAGGAAATTTCTGGAGGAGCTCTCAGTCAG 1458
QY 1381 GAGCTCACACCTTCCACCCACTGTCCCTCAAACTGCTTTCAGAAAGAAATAGTACA 1440
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QY 1441 ACTGTGTGA 1449
Db 1519 ACTGTGTGA 1527

RESULT 3
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LOCUS full-length cDNA clone CS0D1003YE01 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR590169
VERSION CR590169.1 GI:50470976
KEYWORDS HTC; CNSIT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1888)
AUTHORS Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1888)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dN) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1888
/organism="Homo sapiens"
/mol type="mRNA"
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/clone="CS0D1003YE01"
/tissue type="Placenta Cot 25-normalized"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 69 ATGCGCTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 128
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 189 AATGGCTGGTGTCTGTGGGTGGCTGGCTGAAGATGCGAGCAGTGAACACAAATTTGG 248
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 TTCTCCACCTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTGGTGGCT 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 249 TTCTCCACCTCACCTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTGGTGGCT 308
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 309 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGTTTCTATGCAAGCTCATCCCTCC 368
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QY 369 ATCATTTGCTCAACATGTTGCCAGTGTCTTCTGCTTACTTGCCTATAGCTTGCATGCG 428
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QY 429 TGTCTTGGTATTTCAAGCCATCTGGTGTGCTCAGATCATCGCATGTAGGATGCCCTGC 488
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QY 421 TCTATCTGTGATGATCTGGGTGTGCTTTTGTGATGTGCATTCCTGTGTTCTGTGTAC 480
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QY 609 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAACAGCTCTCTGAAACATT 668
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QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTTCCAAACAAATGAT 660
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QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGT 720
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QY 729 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGT 788
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 721 TCCTCTCCCTAGGGTCTGTAGTGTAAACAGTCAAAATCTGATTTCTAATGATTTAAA 780
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QY 789 TCCTCTCCCTAGGGTCTGTAGTGTAAACAGTCAAAATCTGATTTCTAATGATTTAAA 848
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QY 841 AGCCCACTGGATACTCTGATGCTTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
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DB 1209 GTGTGTGGTGTGCTCTTCTTTCTGTCTGTGGACTCCATACCAATTTTGGAGTCTGTCA 1268
QY 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGTCTGGGATCATGTATGC 1260
DB 1269 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGTCTGGGATCATGTATGC 1328
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DB 1329 ATTGCTCTAGCATCTGCAATAGTGTCTTTAATCCCTTCTTTATGCGCTCTTGGGAAA 1388
QY 1321 GATTTTAGGAGAAAGCAAGCAGTCCATTTCAGGAAATCTGGAGGACGCTTCAGTGCAG 1380
DB 1389 GATTTTAGGAGAAAGCAAGCAGTCCATTTCAGGAAATCTGGAGGACGCTTCAGTGCAG 1448
QY 1381 GAGCTCACAGTCTCCACCCTGCTCCCTCAAACTATGTCATTTTCAGAAAGAAATAGTACA 1440
DB 1449 GAGCTCACAGTCTCCACCCTGCTCCCTCAAACTATGTCATTTTCAGAAAGAAATAGTACA 1508
QY 1441 ACTGTGTGA 1449
DB 1509 ACTGTGTGA 1517

RESULT 4
LOCUS CR623914
DEFINITION full-length cDNA clone CSODI016YJ19 of Placentia Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR623914
VERSION CR623914.1 GI:50504721
KEYWORDS HTC; CNSLT cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1899)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Redwood City, CA 94065
REFERENCE 2 (bases 1 to 1899)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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ORIGIN
Query Match 100.0%; Score 1449; DB 3; Length 1899;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGCTTTTCTCTGTCTGAGACCAATTCAACTACTCTCAGCCATGGAATGAG 60
DB 68 ATGGCGCTTTTCTCTGTCTGAGACCAATTCAACTACTCTCAGCCATGGAATGAG 127
QY 61 CCCCCAGTAATCTCTCCATGCTCATCTCCAGCCTTACTTTTACTGGATTGCCAGC 120

128	Db	 CCCCCAGTAAATCTCTCATGSGTCATTCTCAGCGCTTACTTTTCTACTGGGATGCGCAGGC	187
121	Qy	AATGGGCTGCTGTGTGGGTGGCTGAGATGCAGCGGACAGTGAACAAATTTGG	180
188	Db	AATGGGCTGCTGTGTGGGTGGCTGAGATGCAGCGGACAGTGAACAAATTTGG	247
181	Qy	TTCTCTCACCTCACCTTTGGCGGACCTCTCTGTCTGCTCTCTCTTGGCCCTTCTCGCTGGCT	240
248	Db	TTCTCTCACCTCACCTTTGGCGGACCTCTCTGTCTGCTCTCTCTTGGCCCTTCTCGCTGGCT	307
241	Qy	CACCTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCTATGCGAAGCTCATCCCTCC	300
308	Db	CACCTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTCTATGCGAAGCTCATCCCTCC	367
301	Qy	ATCATTTGCTCTCAACATGTTTGGCAGTGCTCTCTCTGTACTGCCATTAAGCTTGGATCGC	360
368	Db	ATCATTTGCTCTCAACATGTTTGGCAGTGCTCTCTCTGTACTGCCATTAAGCTTGGATCGC	427
361	Qy	TGTCTTTGTGGTATTCAGGCCAATCTGGTGTGAGAATCATCGCAATGTAGGGATGGCTGC	420
428	Db	TGTCTTTGTGGTATTCAGGCCAATCTGGTGTGAGAATCATCGCAATGTAGGGATGGCTGC	487
421	Qy	TCTATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTTCTGTGTAC	480
488	Db	TCTATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTCTGTGTTCTGTGTAC	547
481	Qy	CGGGAATCTTCACTACAGACAACCAATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540
548	Db	CGGGAATCTTCACTACAGACAACCAATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	607
541	Qy	TCATTAGATTATCCAGACTTTTATGGAGATCCCACTAGAAAAAGGCTCTCTTGAACAAAT	600
608	Db	TCATTAGATTATCCAGACTTTTATGGAGATCCCACTAGAAAAAGGCTCTCTTGAACAAAT	667
601	Qy	GTTTCAGCGCTCGAGAAATGAATGATGATTAGATCTTCTCTCTTTCAAAACAAAATGAT	660
668	Db	GTTTCAGCGCTCGAGAAATGAATGATGATTAGATCTTCTCTCTTTCAAAACAAAATGAT	727
661	Qy	CATCTTTGGACAGTCCCACTGTCTTCCAACTTCAAAATTTCAAAGACCTTCTGCAGAT	720
728	Db	CATCTTTGGACAGTCCCACTGTCTTCCAACTTCAAAATTTCAAAGACCTTCTGCAGAT	787
721	Qy	TCATCTCCTTAGGGTCTCTGCTAGGTTAAACAAGTCAAAATCTGTATTTCTAATGATTTAAA	780
788	Db	TCATCTCCTTAGGGTCTCTGCTAGGTTAAACAAGTCAAAATCTGTATTTCTAATGATTTAAA	847
781	Qy	CTGTCTGATGTGCTCACCTAAATCCCAGTGGGTTTCTATATGAAGATCACGAAACC	840
848	Db	CTGTCTGATGTGCTCACCTAAATCCCAGTGGGTTTCTATATGAAGATCACGAAACC	907
841	Qy	AGCCCACTGATTAATCTGATGCTTTTCTCTCTACTATTTAAAGCTGTTCCTTAGGCT	900
908	Db	AGCCCACTGATTAATCTGATGCTTTTCTCTCTACTATTTAAAGCTGTTCCTTAGGCT	967
901	Qy	TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTTA	960
968	Db	TCTAGCAATTCCTTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTTA	1027
961	Qy	GGCCAAATTCACAGATGACGATCAAGTGCACCAACCCCTGTGGCAATTAACGATCACTAGG	1020
1028	Db	GGCCAAATTCACAGATGACGATCAAGTGCACCAACCCCTGTGGCAATTAACGATCACTAGG	1087
1021	Qy	CTAGTGTGGGTTTCTGCTGCCCTCTGTATCATGATAGCCGTGTACAGCTTCATTGTC	1080
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1081	Qy	TTCCGAATGCAAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCAGTGGGCGTG	1140
1148	Db	TTCCGAATGCAAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCAGTGGGCGTG	1207
1141	Qy	GTGGTGGTGGCTGTCTTTCTTGTCTGTGATCCATACACATTTTGTGGATCCTGTCA	1200

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Qy	1201	TTGCTTTACTGACCCAGAAACTCCCTTTGGGGAAACCTCTGATGTCTCTGGGATCATGTATGC	1260
Db	1268	TTGCTTTACTGACCCAGAAACTCCCTTTGGGGAAACCTCTGATGTCTCTGGGATCATGTATGC	1327
Qy	1261	ATTGCTCTAGCATCTGCGAATAGTTGCTTTTAATCCCTTTATGTCCTTTATGCCCTCTTTGGGGAAA	1320
Db	1328	ATTGCTCTAGCATCTGCGAATAGTTGCTTTTAATCCCTTTATGTCCTTTATGCCCTCTTTGGGGAAA	1387
Qy	1321	GATTTTATAGGAAGAAACGACAGGAGTCCATTTACAGGGAATTTCTGAGGAGCAGCCTTCAGTNGAG	1380
Db	1388	GATTTTATAGGAAGAAACGACAGGAGTCCATTTACAGGGAATTTCTGAGGAGCAGCCTTCAGTNGAG	1447
Qy	1381	GAGCTCACACGTTTCCACCCACTGCTCCCTCAAAACAATGTCAATTTACAGAAAGAAATAGTACA	1440
Db	1448	GAGCTCACACGTTTCCACCCACTGCTCCCTCAAAACAATGTCAATTTACAGAAAGAAATAGTACA	1507
Qy	1441	ACTGTGTGA 1449	
Db	1508	ACTGTGTGA 1516	
RESULT 5			
CR591233			
LOCUS			
DEFINITION			
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VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
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REMARK			
REFERENCE			
AUTHORS			
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JOURNAL			
COMMENT			
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ORIGIN			
Query Match			
Best Local Similarity			
Matches 1449; Conservative			
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Db	79	ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGAATGAG	138
Qy	61	CCCCAGTAATCTCTCATGGTTCATTTCTCAGCGCTACTCTTTTACTGGGAATGCCAGGC	120

139 CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTTTACTGGGATGCCAGGC 198
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841 AGCCCACTGGATACTCTGATGCTTTTCTCTACTCTATTTAAAGCTGTTCCCTAGCGCT 900
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1219 GTGCTGGTGGTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1278

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1399 GATTTTAGGAAGAAGCAAGCAGTCCATTAGGGAATTTGGAGGAGCCCTTCAGTGAG 1458
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1459 GAGCTCACACCTTCCACCCACTGTCTCTCAAACTGTCTTTTTCAGAAAGAAATAGTACA 1518
1441 ACTGTGTGA 1449
1519 ACTGTGTGA 1527

RESULT 6
CR609272
LOCUS
DEFINITION CR609272 1951 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1061YC05 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR609272
VERSION CR609272.1 GI:50490079
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1951)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1951)
REFERENCE
AUTHORS
TITLE Direct Submission
JOURNAL Genoscope.
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGCTTTTCTCTGCTGAGACCAATTTCAACTGACCTTACTCTCACAGCCATGGAATGAG 60
Db 68 ATGGCGCTTTTCTCTGCTGAGACCAATTTCAACTGACCTTACTCTCACAGCCATGGAATGAG 127
Qy 61 CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTTTACTGGGATGCCAGGC 120
Db 128 CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTTTACTGGGATGCCAGGC 187


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QY 181 TTCTTCCACCTCACCTTCGGGACCTCTCTGTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
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QY 301 ATCATTGTCTCAACATGTTTGGCAGTGTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCT 360
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DB 848 CCTGCTGATGTGCTCACTCACTAAATCCCAAGTGGTTCCTCTCTCTCTCTCTCTCTCT 907
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DB 968 TCTAGCAATCTCTCTACAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTTA 1027
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DB 1208 GTGTGTGGTGTCTCTCTCTGTCTGTGAGCTCCATACCACTTTTGGAGTCTCTGTCA 1267
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QY 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGGAATACTCTGATGTCTCTGGATCATGTATGC 1260
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QY 1381 GAGCTTCACAGTTCACCCCACTGTCCCTCAAACTATGTCTTTCAGAAAGAAATAGTACA 1440
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QY 1441 ACTGTGTGA 1449
DB 1508 ACTGTGTGA 1516

RESULT 7
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LOCUS Pan troglodytes C3AR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AV410248
VERSION AV410248.1 GI:39766216
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1449)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1449)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM3827"

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Best Local Similarity 98.2%; Pred. No. 0;
Matches 1423; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 181 TTCTCCACCTCACCCTGGGAGACCTCTCTGTGCTGCTCTCTGTGCTGCTCTCTGTGCT 240
Db 249 TTCTCCACCTCACCCTGGGAGACCTCTCTGTGCTGCTCTCTGTGCTGCTCTCTGTGCT 308
Qy 241 CACTTGGCTCTCCAGGAGACCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 300
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Qy 301 ATCATTTGCTCTCAACATGTTTGCAGTGTCTTCTGCTTACTTGCATTTAGCTGGATGCC 360
Db 369 ATCATTTGCTCTCAACATGTTTGCAGTGTCTTCTGCTTACTTGCATTTAGCTGGATGCC 428
Qy 361 TGTCTTGGTATTTCAAGCAATCTGGTGTGATGATGATGATGATGATGATGATGATGAT 420
Db 429 TGTCTTGGTATTTCAAGCAATCTGGTGTGATGATGATGATGATGATGATGATGATGAT 488
Qy 421 TCTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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Qy 481 CGGGAATCTTCACTACAGACATTAATAGATGATGATGATGATGATGATGATGATGAT 540
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Qy 541 TCATTAGATTTACAGATTTTATGGAGATCCACTAGAAACAGATGCTCTTGAACAAT 600
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RESULT 9
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LOCUS BX381444 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1065YH15 5-PRIME, mRNA sequence.
ACCESSION BX381444
VERSION BX381444.2 GI:46622125
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1092)
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AUTHORS
TITLE
JOURNAL
COMMENT

Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30454945.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6632.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1065CD08QPI&c=6632.r.

FEATURES
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 62.9%; Score 911.4; DB 5; Length 1092;
Best Local Similarity 96.4%; Pred. No. 2.8e-260; Indels 5; Gaps 3;
Matches 953; Conservative 10; Mismatches 21;
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Db 79 ATGGCGTCTTCTCTGCTGAGACCAATTCACACTGACCTACTCTCACGCCATGGAATGAG 138
Qy 61 CCCCAGTAATCTCTCCATGGTCAATTCAGCCTTACTTTTTTACTGGGATGCCAGC 120
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Qy 181 TTCTCCACCTCACCCTTGGCGGACCTCTCTGTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db 259 TTCTCCACCTCACCCTTGGCGGACCTCTCTGTGCTCTCTCTGCTGCTCTCTGCTGCT 318
Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACCGGAGTTTCTATGCAAGCTCATTCCTCC 300
Db 319 CACTTGGCTCTCCAGGACAGTGGCCCTTACCGGAGTTTCTATGCAAGCTCATTCCTCC 378
Qy 301 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTGCGCATAGCTGATCGC 360
Db 379 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTGCGCATAGCTGATCGC 438
Qy 361 TGTCTTGGTATTTCAAGCAATCTGGTGTGATGATGATGATGATGATGATGATGATGAT 420
Db 439 TGTCTTGGTATTTCAAGCAATCTGGTGTGATGATGATGATGATGATGATGATGATGAT 498
Qy 421 TCTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 499 TCTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 558
Qy 481 CGGGAATCTTCACTACAGACATTAATAGATGATGATGATGATGATGATGATGATGAT 540
Db 559 CGGGAATCTTCACTACAGACATTAATAGATGATGATGATGATGATGATGATGATGAT 618
Qy 541 TCATTAGATTTACAGATTTTATGGAGATCCACTAGAAACAGATGCTCTTGAACAAT 600
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Qy 601 GTTCAGCGCCTGGAGAAATGAATGATAGTTAGATCCTCTCTTTTCCAAACAAATGAT 660
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Qy 721 TCACCTCCCTAGGGTCTGCTAGGTTAACTAAGTCAAAATCTGATCTTAATGATTTAAA 780
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Db 919 AGCCACCTGGATTAATCTGATGCTTTCTCTCTACTCAATTTAAAGCTTCCCTAGCGCT 978
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RESULT 10

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BX396411 1137 bp mRNA linear EST 28-APR-2004
LOCUS BX396411 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1016YJ19 5-PRIME, mRNA sequence.
ACCESSION BX396411
VERSION BX396411.2 GI:46843657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1137)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30609095.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6632.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0D1016CE10QPI&c=6632.r.

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FEATURES

source

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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized."

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ORIGIN

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Query Match 61.9%; Score 897; DB 5; Length 1137;
Best Local Similarity 95.7%; Pred. No. 5.6e-256;
Matches 929; Conservative 12; Mismatches 27; Indels 3; Gaps 2;
Qy 1 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCAGACCCATGGAATGAG 60
Db 68 ATGGCGTCTTMTCTGCTGAGACCAATCAACTGACCTACTCTCAGACCCATGGAATGAG 127
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Qy 121 AATGGGCTGTGTGCTGGTGGCTGAGATGAGGAGCAGTGAACACAAATTTGG 180
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Qy 181 TTCTCTCACTCACCCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db 248 TTCTCTCACTCACCCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 307
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Qy 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTATGAGCTTGGATGCG 360
Db 368 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTATGAGCTTGGATGCG 427
Qy 361 TGTCTGTGCTTCAAGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Qy 421 TCTATCTGTGATGATATCTGGTGGTGGCTTTTGTGATGTGCAATCTCTGTTGCTGTAC 480
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Qy 721 TCATCTCCCTAGGGTCTGCTAGGTTAACTAAGTCAAAATCTGATCTTAATGATTTAAA 780
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Qy 781 CCTGCTGATGTGCTCACTCACTTAAATCCCAAGTGGTTCCTATTGAAGATCAAGAAACC 840
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Qy 961 GGCAATTCAC 971
Db 1025 ATYMARATGAS 1035

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DEFINITION BX381109 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
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ACCESSION  BX381109
VERSION     BX381109.2 GI:46573448
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1035)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30448938.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6632.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DI061AB03QPI&c=6632.r.
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ORIGIN
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Best Local Similarity 97.8%; Pred. No. 6.4e-244;
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DB 188 AATGGCTGGTCTGCTGGGCTGGCTGAGATGAGCGGACAGTGAACACAAATTTGG 247
QY 181 TTCTCCACCTCACCCTGGCGGACCTCTGCTGCTGCTCTCTGCTGCTCTGCTGCTGCT 240
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DB 308 CACTTGGCTCTCCAGGACAGTGGGCTTACGGCAGGTTTCTATGCAAGCTCATCTCCCTCC 367
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728 CATCTTGGACAGTCCCACTGCTCTCCAACTCAAACTTTCAAGACCTTCTGCGAGAT 787
721 TCATCTCCCTA-GGGGTTCTGCTAGGTTAAACAAGTCAAAATCTGTATTTCTAATGTTTAA 779
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840 CAGCCCACTGATTAACCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTTCCCTAGCGC 899
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900 T 900
967 T 967

BM562131 1112 bp mRNA linear EST 20-FEB-2002
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BM562131
VERSION BM562131.1 GI:18807958
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1112)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
            Email: csapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12768 Row: h Column: 06
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and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
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ORIGIN

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Query Match 57.3%; Score 830.4; DB 4; Length 1112;
Best Local Similarity 94.2%; Pred. No. 4.4e-236;
Matches 950; Conservative 0; Mismatches 47; Indels 12; Gaps 8;

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DB |||||||
QY 104 ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAATGAG 163
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QY 61 CCCCAGTAATCTCTCATGCTGATCTCAGCTTACTTTTACTGGATGCCAGC 120
DB |||||||
QY 164 CCCCAGTAATCTCTCATGCTGATCTCAGCTTACTTTTACTGGATGCCAGC 223
DB |||||||
QY 121 AATGGCTGGTCTGCTGGTGGCTGCTGAGATGACGCGACAGTGAACACAAATGG 180
DB |||||||
QY 224 AATGGCTGGTCTGCTGGTGGCTGCTGAGATGACGCGACAGTGAACACAAATGG 283
DB |||||||
QY 181 TTCTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
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QY 284 TTCTCCACCTCACCTTGGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 343
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QY 241 CACTTGGCTCTCCAGGACAGTGGCTTACCGAGTTCCTATGCAAGCTCATCCCTCC 300
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QY 404 ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTGCTTCTGCTGCTGCTGCTG 463
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QY 361 TGTCTTGGTATTTCAAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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QY 464 TGTCTTGGTATTTCAAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
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QY 421 TCTATCTGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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QY 524 TCTATCTGCTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
DB |||||||
QY 481 CGGAAATCTTCTACACACCAATTAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
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QY 584 CGGAAATCTTCTACACACCAATTAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 643
DB |||||||
QY 541 TCATTAGATATCAGACTTTTATGGAGATCCACTAGAAACAGGCTCTTTGAAACATT 600
DB |||||||
QY 644 TCATTAGATATCAGACTTTTATGGAGATCCACTAGAAACAGGCTCTTTGAAACATT 703
DB |||||||
QY 601 GTTCAGCGCTGAGAAATGAATGATAGTGTAGATCTCTCTCTCTTCCAAACAAATGAT 660
DB |||||||
QY 704 GTTCAGCGCTGAGAAATGAATGATAGTGTAGATCTCTCTCTCTTCCAAACAAATGAT 763
DB |||||||
QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTCAAACTTCAAGACCTTCTGCAGAT 720
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QY 764 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTCAAACTTCAAGACCTTCTGCAGAT 823
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QY 721 TCACT-CCCTAGGGTCTGCTAGGTTAAAGTCAAACTGTAATCTGTAATGTAATTA 779
DB |||||||
QY 824 TCACTCCCTAGGGGCTGCTAGGTTAAAGTCAAACTGTAATCTGTAATGTAATTA 883
DB |||||||
QY 780 ACCTGCTGATGTGCTCTCACTTAAATCCCC- --AGTGGGTTTCTTCTTGAAGATCACGA 836
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QY 884 ACCTGCTGATGTGCTCTCACTTAAATCCCCATTTGGGTTTCTTCTTGAAGATCCCCA 943
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QY 837 AACCA-GCCACTGGAFAACT-CTGATGCTTTTCTCTCTACTCATTTAAAG--CTGTTC 892
DB |||||||
QY 944 AACAGGCCCCACTGATAAATCCGAGGCTTTTCTCTACTCCATTTAAGGCTTTCC 1003
DB |||||||
QY 893 CTAGGCTTTCTA-GCAATTTCTCTTACGAGTCTGAGC--TACCACAAGGTTTCCAGGATT 949
DB |||||||
QY 1004 CTAGGCTTTCTAGCAATTTCTTCTACGAGTCTGAGCTTACCCCAAGGTTTTCGGGATT 1063
DB |||||||
QY 950 ATTAC-AATTTAGGCCAATTCACAGATGACGATCAAGTCCCAACACCC 997
DB |||||||
QY 1064 ATTACAATTTAGGCCAATTTCCCGGAGGACCATCAAGGGCCCAAAACCC 1112
DB |||||||
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RESULT 13
BX337391
LOCUS
DEFINITION BX337391 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1041Y11 5-PRIME, mRNA sequence.
ACCESSION BX337391
VERSION BX337391.2 GI:46283013
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30346958.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6632.f
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For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSOD1041Y11AA06QP1&c=6632.f>.

FEATURES

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/clone="CSOD1041Y11"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

```
Query Match 57.1%; Score 827.4; DB 5; Length 934;
Best Local Similarity 99.6%; Pred. No. 3.3e-235;
Matches 850; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAATGAG 60
DB |||||||
QY 79 ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAATGAG 138
DB |||||||
QY 61 CCCCAGTAATCTCTCCATGCTGCTCAGCTTACTTTTACTGGATGCCAGC 120
DB |||||||
QY 139 CCCCAGTAATCTCTCCATGCTGCTCAGCTTACTTTTACTGGATGCCAGC 198
DB |||||||
QY 121 AATGGGCTGCTGCTGCTGGTGGCTGCGCTGAAGATGACGCGGACAGTGAACACAAATTTGG 180
DB |||||||
QY 199 AATGGGCTGCTGCTGCTGGTGGCTGCGCTGAAGATGACGCGGACAGTGAACACAAATTTGG 258
DB |||||||
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Db	788	ATTCACTCCCTAGGGGTTCTGCTAGGTAAACAAGTCAAAATCTGTATTTCTTAATGTATTTA	847
Qy	779	AACTCTCTGATGTGTCCTACCTAAATCCCAAGTGGTTCCTATTGAAGATCAGAAA	838
Db	848	AAMCTCTGATGTGTCACCTAAATCCCAAGTGGTTCCTATTGAAGATCAGAAA	907
Qy	839	CGAGCCCACTGAATAACTCTGANGCTTTTCTCTACTCATTTAAAGCTGTTCCTCTA	895
Db	908	-CAGTCCCACTGGAATATYGGAWGYGTTT--YYCYATCTATKAAACYGTTTCCGMA	961

RESULT 15
BM920604
LOCUS
BM920604 1093 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6709588 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750634
DEFINITION
5', mRNA sequence.

EM920604.1 GI:19370983
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1093)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. Scalability: The model is designed to scale efficiently, handling large volumes of data and complex tasks without significant performance degradation.	2. Scalability: The model is designed to scale efficiently, handling large volumes of data and complex tasks without significant performance degradation.
3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying reasoning and identify potential biases or errors.	3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying reasoning and identify potential biases or errors.
4. Robustness: The model is highly robust to adversarial attacks and noisy data, maintaining stable performance even in challenging environments.	4. Robustness: The model is highly robust to adversarial attacks and noisy data, maintaining stable performance even in challenging environments.
5. Efficiency: The model is optimized for fast inference and low resource consumption, making it suitable for deployment in resource-constrained environments.	5. Efficiency: The model is optimized for fast inference and low resource consumption, making it suitable for deployment in resource-constrained environments.

Query Match	55.3%;	Score 809.4;	DB 5;	Length 1093;
Best Local Similarity	93.4%;	Pred. No. 8.3e-230;		
Matches 955; Conservative	0;	Mismatches 56;	Indels 12;	Gaps 10;

Search completed: April 11, 2005, 07:07:10
Job time : 5123 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 07:07:15 ; Search time 841 Seconds
(without alignments)
10199.412 Million cell updates/sec

Title: US-10-764-649-1

Perfect score: 1449

Sequence: 1 atggcgctttctctgtga.....gaaatagacaactgtgtga 1449

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	1449	6	Abk86860 Human ana
2	1449	100.0	1449	8	ACA64730 Chemoatr
3	1449	100.0	1449	8	ABZ42643 Human com
4	1449	100.0	1449	10	ADF43377 Chemoatr
5	1449	100.0	1449	13	Adr05359 Human cDN
6	1449	100.0	1449	13	AdS09203 Complem
7	1449	100.0	1449	10	AdC86208 Human GPC
8	1449	100.0	2040	2	Aav03250 Homo sapi
9	1449	100.0	2096	12	AdQ23545 Human sof
10	1398	96.5	1449	12	AdO29820 Human GPC
11	1398	96.5	1956	6	AbL67676 Oesophagu
12	1398	96.5	1970	2	Aat64946 cDNA enco
13	1398	96.5	2040	2	Aat36375 Human G-p
14	1398	96.5	2040	9	AdC26620 cDNA enco
15	1398	96.5	2040	10	AdE84844 Farnesy1
16	1398	96.5	2040	12	AdL22831 Human C3a
17	1398	96.5	2040	12	AdQ19274 Human sof
18	1347	93.0	2040	3	Aaf18195 Lung canc
19	1245	85.9	1449	5	AbI97972 Non-endog
20	1153	79.6	1893	13	ACn42148 Human dia

21	1140	78.7	1446	2	AAT70001	Aat70001 C5a anaph	
22	1140	78.7	1446	2	AAT45873	Aat45873 C5a-like	
23	330	22.8	453	9	ACH26794	Ach26794 Human acu	
c	24	198	625	10	ADe85150	AdE85150 Farnesy1	
25	173	11.9	453	3	AAAS2668	Aaas2668 Bosinophi	
c	26	163	611	10	ADe85151	AdE85151 Farnesy1	
27	60	4.1	60	6	ABN42114	Abn42114 Human spl	
28	50	3.5	50	6	ABZ02606	Abz02606 Human leu	
29	47	3.2	200	6	ABK13747	Abk13747 Targeting	
30	47	3.2	1434	12	ADL22833	AdL22833 Murine C3	
31	47	3.2	1434	12	ADO30111	Ado30111 Mouse GPC	
32	47	3.2	2657	6	ABK13745	Abk13745 Mouse ana	
33	47	3.2	2657	13	ADRO5367	Adr05367 Mouse cDN	
34	47	3.2	3329	5	ADAO2458	Ada02458 Mouse C3a	
c	35	28	1.9	37	AB197584	Ab197584 Endogenou	
36	25	1.7	25	13	ADSO9207	Adso9207 Complemen	
37	25	1.7	7449	6	ABL32276	AbL32276 Human imm	
38	24	1.7	24	2	AAT44038	Aat44038 Primer 2	
39	24	1.7	24	2	AAT45875	Aat45875 Human C5a	
c	40	24	1.7	7449	6	ABL32277	AbL32277 Human imm
c	41	23	1.6	23	2	AAT44037	Aat44037 Primer 1
c	42	23	1.6	23	2	AAT45874	Aat45874 Human C5a
c	43	22	1.5	40	5	AB197777	Ab197777 Non-endog
c	44	22	1.5	40	5	AB197778	Ab197778 Non-endog
45	22	1.5	65	6	ABN54524	Abn54524 Mouse spl	
46	21	1.4	32	13	ADSO9205	Adso9205 Complemen	
47	21	1.4	32	2	AAT36376	Aat36376 Human G-p	
48	21	1.4	32	9	ACD26621	AcD26621 Putative	
49	21	1.4	586	6	ABN73390	Abn73390 Bovine em	
50	21	1.4	586	6	ABN73300	Abn73300 Bovine em	
51	21	1.4	644	12	ADG27903	AdG27903 Rice vari	
52	21	1.4	1071	3	AAA30775	Aaa30775 DNA encod	
53	21	1.4	1071	3	AAA30756	Aaa30756 Human G p	
54	21	1.4	1071	8	ABZ42848	Abz42848 Human G p	
55	21	1.4	1071	10	ADC22788	Adc22788 Human G p	
56	21	1.4	1071	10	ADC22764	Adc22764 Human G p	
57	21	1.4	1071	10	ADH14261	Adh14261 Mutated h	
58	21	1.4	1071	10	ADH14237	Adh14237 Human GPR	
59	21	1.4	1071	12	ADG19667	AdG19667 G protein	
60	21	1.4	1071	12	ADO05703	Ado05703 Human G p	
61	21	1.4	1071	12	ADO30071	Ado30071 Human GPC	
62	21	1.4	1785	10	ADF70598	Adf70598 Orphan re	
63	21	1.4	1797	10	ADC24765	Adc24765 cDNA enco	
64	21	1.4	1797	12	ADG19665	Adg19665 Human G p	
c	65	20	1.4	20	ADSO9206	Adso9206 Complemen	
66	20	1.4	1379	13	ADR24460	Adr24460 Breast ca	
67	20	1.4	1475	6	ABQ60999	Abq60999 FLJ21773	
68	20	1.4	1579	6	ABA91938	Abq60999 Human his	
69	20	1.4	1755	8	ACC00501	Acc00501 Human his	
70	20	1.4	1966	3	AAC76633	Aac76633 Human ORF	
c	71	19	1.3	32	2	AAT36377	Aat36377 Human G-p
c	72	19	1.3	32	5	AB197583	Ab197583 Endogenou
c	73	19	1.3	32	9	ACD26622	AcD26622 Putative
74	19	1.3	200	6	ABK13746	Abk13746 Targeting	
75	19	1.3	487	4	AAI15502	Aai15502 Probe #54	
76	19	1.3	487	4	ABAS7374	Abas7374 Human foe	
77	19	1.3	487	4	ABAS7374	Abas7374 Human foe	
78	19	1.3	487	4	AAI36919	Aai36919 Probe #56	
79	19	1.3	487	4	ABA26907	Abas26907 Probe #53	
80	19	1.3	487	4	AAK31008	Aak31008 Human bon	
81	19	1.3	487	4	AAK05409	Aak05409 Human bra	
82	19	1.3	487	4	ABAS30686	Abas30686 Human liv	
83	19	1.3	487	6	ABSO5757	Abso5757 Human gen	
c	84	19	1.3	520	12	ACH68998	Ach68998 Human gen
c	85	19	1.3	614	5	ABV49971	Abv49971 Human pro
c	86	19	1.3	752	5	AAAS6765	Aas6765 DNA encod
c	87	19	1.3	1149	12	ADO30211	Ado30211 Mouse GPC
c	88	19	1.3	2037	8	ADA70727	Ada70727 Rice gene
c	89	19	1.3	2204	3	AZ43769	Aaz43769 Human end
c	90	19	1.3	2633	12	AQD21390	Adq21390 Human sof
c	91	19	1.3	2870	5	AAAS5322	Aas5322 DNA encod
c	92	19	1.3	3268	12	ADQ25250	Adq25250 Human sof
c	93	19	1.3	3574	13	ADRO6620	Adr06620 Full leng
c	93	19	1.3	4236	2	AAx58676	Aax58676 Human CII

C 94	19	1.3	6698	13	ADRL14130	Adrl14130 Human NF-	167	18	1.2	1157	8	ABZ42527	Abz42527 Human gal
C 95	19	1.3	6698	13	ADP22957	Adp22957 PRO polyp	168	18	1.2	1157	9	ADB67675	ADB67675 Human gal
C 96	19	1.3	6762	4	AAK79970	AAk79970 Human imm	169	18	1.2	1157	10	ADE31658	Ade31658 Human 437
C 97	19	1.3	34337	6	ABL55857	AbL55857 Human GAB	C 170	18	1.2	1158	8	ADA70836	Ada70836 Rice gene
C 98	19	1.3	34337	10	ADG88376	Adg88376 Human tra	C 171	18	1.2	1191	10	ABZ39047	Abz39047 N. gonorr
C 99	19	1.3	34337	10	ADG88376	Adg88376 Human tra	C 172	18	1.2	1275	12	ADL16269	Adl16269 Human typ
C 100	19	1.3	57728	4	AAK87588	Aak87588 Human 9p1	173	18	1.2	1275	12	ADQ35153	Adq35153 Human Gal
C 101	19	1.3	62782	9	ADAD58282	Adad58282 Human tum	174	18	1.2	1275	12	ADQ35153	Adq35153 Human Gal
C 102	19	1.3	62782	9	ADAD58282	Adad58282 Human tum	175	18	1.2	1335	3	AAK47331	Aak47331 Ftsz homo
C 103	19	1.3	73100	12	ADP44145	Adp44145 Human TEK	C 176	18	1.2	1335	8	ABQ77446	Abq77446 Murine hu
C 104	19	1.3	84073	11	ACN44322	Acn44322 Human gen	C 177	18	1.2	1350	10	ACF57838	Acf57838 Hu007 ant
C 105	19	1.3	135800	11	ACN44446	Acn44446 Human gen	C 178	18	1.2	1350	10	ACF57838	Acf57838 Hu007 ant
C 106	19	1.3	143973	11	ACN44142	Acn44142 Human gen	C 179	18	1.2	1374	8	ACA25103	Aca25103 Prokaryot
C 107	19	1.3	163998	6	ADAD36511	Adad36511 Human Her	180	18	1.2	1417	6	AAV27893	Aav27893 Human hyp
C 108	19	1.3	197496	6	ABN85584	Abn85584 Human RGF	181	18	1.2	1417	6	AAV27893	Aav27893 Human hyp
C 109	19	1.3	209083	13	ABD32854	Abd32854 Human can	182	18	1.2	1417	6	AAV27893	Aav27893 Human hyp
C 110	19	1.3	226475	9	ADAD58279	Adad58279 Human can	183	18	1.2	1417	6	AAV27893	Aav27893 Human hyp
C 111	18	1.2	29	2	AAT36381	Aat36381 Human G-p	C 184	18	1.2	1469	4	AAK69478	Aak69478 Human imm
C 112	18	1.2	29	2	AAT36381	Aat36381 Human G-p	C 185	18	1.2	1469	4	AAK69478	Aak69478 Human imm
C 113	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 186	18	1.2	1469	4	AAK69478	Aak69478 Human imm
C 114	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 187	18	1.2	1611	12	ADN74240	Adn74240 Thale cre
C 115	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 188	18	1.2	2000	6	ABZ15556	Abz15556 Arabidops
C 116	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 189	18	1.2	2082	2	AAQ55789	Aaq55789 Sequence
C 117	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 190	18	1.2	2179	13	ACN41605	Acn41605 Human dia
C 118	18	1.2	30	2	AAT33908	Aat33908 Human G-p	C 191	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 119	18	1.2	204	4	AAK91699	Aak91699 I-Ab epit	C 192	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 120	18	1.2	212	6	ABN79538	Abn79538 Human ORF	C 193	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 121	18	1.2	225	12	ADG20373	Adg20373 Beta 2-mi	C 194	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 122	18	1.2	349	8	AAH99845	Aah99845 Human pro	C 195	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 123	18	1.2	360	8	ABQ77442	Abq77442 Murine mu	C 196	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 124	18	1.2	360	8	ABQ77442	Abq77442 Murine mu	C 197	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 125	18	1.2	377	4	AAK57624	Aak57624 Human imm	C 198	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 126	18	1.2	378	12	ACH81767	Ach81767 Human gen	C 199	18	1.2	2218	6	ABL64747	AbL64747 Lung can
C 127	18	1.2	438	6	ABT07167	Abt07167 Human ova	C 200	18	1.2	2382	2	AAQ10238	Aaq10238 Encodes m
C 128	18	1.2	438	6	ABT07167	Abt07167 Human ova	C 201	18	1.2	2393	13	ACN41601	Acn41601 Human dia
C 129	18	1.2	490	9	ADA50209	Ada50209 CMV/MIP-3	C 202	18	1.2	2464	10	ADC86018	Adc86018 Human GPC
C 130	18	1.2	493	9	ADA50213	Ada50213 CMV/SDF-1	C 203	18	1.2	2543	3	AAA52774	Aaa52774 Soybean p
C 131	18	1.2	499	9	ADA50211	Ada50211 CMV/TCA-3	C 204	18	1.2	2543	3	AAA52774	Aaa52774 Soybean p
C 132	18	1.2	499	9	ADA50207	Ada50207 CMV/MIP-1	C 205	18	1.2	2593	2	RAT33487	Rat33487 Aspergill
C 133	18	1.2	506	12	ADL85135	Adl85135 DNA up-re	C 206	18	1.2	2795	4	AAK89086	Aak89086 Human dig
C 134	18	1.2	506	12	ADL85135	Adl85135 DNA up-re	C 207	18	1.2	2825	5	AAK89086	Aak89086 Human dig
C 135	18	1.2	518	12	ADL85146	Adl85146 DNA up-re	C 208	18	1.2	2934	9	ADA48441	Ada48441 Rice gene
C 136	18	1.2	518	12	ADL85146	Adl85146 DNA up-re	C 209	18	1.2	3513	8	ABV73339	Abv73339 M. sexta
C 137	18	1.2	543	12	ACH68065	Ach68065 Human gen	C 210	18	1.2	3736	2	AAK84918	Aak84918 Rat brain
C 138	18	1.2	569	4	ABA64081	AbA64081 Human foe	C 211	18	1.2	3736	2	AAK84918	Aak84918 Rat brain
C 139	18	1.2	569	4	AAI44226	Aai44226 Probe #12	C 212	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 140	18	1.2	569	4	AAK12565	Aak12565 Human bon	C 213	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 141	18	1.2	569	4	AAK12565	Aak12565 Human bon	C 214	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 142	18	1.2	569	4	AAK12565	Aak12565 Human bon	C 215	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 143	18	1.2	569	4	AAK12565	Aak12565 Human bon	C 216	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 144	18	1.2	569	4	AAK12565	Aak12565 Human bon	C 217	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 145	18	1.2	580	4	ABA60656	AbA60656 Human foe	C 218	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 146	18	1.2	580	4	AAI40545	Aai40545 Probe #92	C 219	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 147	18	1.2	580	4	ABA28756	AbA28756 Probe #72	C 220	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 148	18	1.2	580	4	AAK34829	Aak34829 Human bon	C 221	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 149	18	1.2	580	4	AAK08938	Aak08938 Human bon	C 222	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 150	18	1.2	580	4	ABE34592	AbE34592 Human liv	C 223	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 151	18	1.2	580	6	ABE09372	AbE09372 Human gen	C 224	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 152	18	1.2	582	4	AAK23421	Aak23421 Candida a	C 225	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 153	18	1.2	582	4	AAK23421	Aak23421 Candida a	C 226	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 154	18	1.2	735	10	ABZ39048	Abz39048 N. gonorr	C 227	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 155	18	1.2	941	3	AAZ44871	Aaz44871 C. vulgar	C 228	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 156	18	1.2	993	12	ADP28528	Adp28528 Human sec	C 229	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 157	18	1.2	1077	12	ADJ75766	Adj75766 Marker ge	C 230	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 158	18	1.2	1077	12	ADJ75766	Adj75766 Marker ge	C 231	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 159	18	1.2	1083	3	AAA47330	Aaa47330 Ftsz homo	C 232	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 160	18	1.2	1083	3	AAA47330	Aaa47330 Ftsz homo	C 233	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 161	18	1.2	1104	12	ADO80873	Ado80873 DNA encod	C 234	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 162	18	1.2	1107	2	AAK87382	Aak87382 Human gal	C 235	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 163	18	1.2	1107	10	ABZ81595	Abz81595 Human gal	C 236	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 164	18	1.2	1107	10	ADO29894	Ado29894 Human GPC	C 237	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 165	18	1.2	1119	10	ADF83692	Adf83692 Human-mou	C 238	18	1.2	3857	10	ADF83691	Adf83691 Human-mou
C 166	18	1.2	1119	12	AAK52478	Aak52478 HLA-A24-I	C 239	18	1.2	3857	10	ADF83691	Adf83691 Human-mou

240	18	1.2	79528	6	AA150814	Human can	AA150814 Human can	c 313	17	1.2	418	3	AAH30897	Human col
241	18	1.2	79528	12	ADQ19802	Human sof	Adq19802 Human sof	314	17	1.2	422	9	ACH17497	Human adu
c 242	18	1.2	110000	3	AAH81490.07	Continuation (8 of	Continuation (8 of	c 315	17	1.2	424	4	AA111392	Human bre
243	18	1.2	110000	10	ADG70184.0	ADG70184 DNA of BA	Adg70184 DNA of BA	316	17	1.2	431	2	AAV88768	EST clone
244	18	1.2	110000	11	ACN43998.0	ACN43998 Human gen	Acn43998 Human gen	c 317	17	1.2	432	10	ADH87117	Human pan
245	18	1.2	110000	12	ADQ97050.1	Continuation (2 of	Continuation (2 of	c 318	17	1.2	439	4	AA115391	Human bre
246	18	1.2	110000	13	ABD32908.3	Continuation (4 of	Continuation (4 of	c 319	17	1.2	441	4	AA115391	Human bre
c 247	18	1.2	139904	6	ABK83362	ABK83362 Human CDN	Abk83362 Human CDN	c 320	17	1.2	441	4	AA115391	Human bre
248	18	1.2	140167	6	ABT10146	ABT10146 Human bre	Abt10146 Human bre	c 321	17	1.2	441	4	AA115391	Human bre
c 249	18	1.2	166181	12	ADQ20461	ADQ20461 Human sof	Adq20461 Human sof	c 322	17	1.2	441	4	AA150344	Probe #19
c 250	18	1.2	166181	12	ADQ19633	ADQ19633 Human sof	Adq19633 Human sof	c 323	17	1.2	441	4	AA150344	Probe #19
c 251	18	1.2	169659	12	ADQ59434	ADQ59434 Human can	Adq59434 Human can	c 324	17	1.2	441	4	AA187087	Human bon
c 252	18	1.2	185555	11	ACN45180	ACN45180 Mouse gen	Acn45180 Mouse gen	c 325	17	1.2	441	4	AA187087	Human bon
c 253	18	1.2	243390	11	ABD33366	ABD33366 Human can	Abd33366 Human can	c 326	17	1.2	441	4	AA187087	Human bon
c 254	18	1.2	254087	11	ACN43996	ACN43996 Mouse gen	Acn43996 Mouse gen	c 327	17	1.2	441	6	ABT08833	Human bre
c 255	18	1.2	349980	13	AA121608	AA121608 Neisseria	Aa121608 Neisseria	c 328	17	1.2	441	6	ABT08833	Human bre
c 256	17	1.2	23	3	AAH87836	AAH87836 Oligonucle	Aah87836 Oligonucle	c 329	17	1.2	441	6	ABT08833	Human bre
c 257	17	1.2	30	2	AAH33909	AAH33909 Human G-P	Aat33909 Human G-P	c 330	17	1.2	441	10	ABT32991	Human tum
c 258	17	1.2	30	3	AAZ60125	AAZ60125 PCR prime	Aaz60125 PCR prime	c 331	17	1.2	441	11	ADL92898	Human bre
c 259	17	1.2	30	3	AAH70777	AAH70777 Primer #2	Aah70777 Primer #2	c 332	17	1.2	441	12	ADL92898	Human bre
c 260	17	1.2	30	9	ACH00364	ACH00364 PCR prime	Ach00364 PCR prime	c 333	17	1.2	455	4	ABAS7592	Probe #58
c 261	17	1.2	47	4	AAH39552	AAH39552 Human SNP	Aah39552 Human SNP	c 334	17	1.2	455	4	AA137154	Probe #58
c 262	17	1.2	50	6	AB202282	AB202282 Human leu	Ab202282 Human leu	c 335	17	1.2	455	4	AAK31254	Human bon
c 263	17	1.2	58	2	AAH36379	AAH36379 Human G-P	Aat36379 Human G-P	c 336	17	1.2	455	4	AAK05645	Human bra
c 264	17	1.2	58	9	ACD26624	ACD26624 Putative	Ac26624 Putative	c 337	17	1.2	455	4	ABT18943	Human liv
c 265	17	1.2	80	12	ADP49395	ADP49395 Oligonucle	Adp49395 Oligonucle	c 338	17	1.2	455	6	ABT18943	Human liv
c 266	17	1.2	81	6	ABK85000	ABK85000 DNA encod	Abk85000 DNA encod	c 339	17	1.2	455	6	ABT18943	Human liv
c 267	17	1.2	113	6	ABQ96187	ABQ96187 Tumour su	Abq96187 Tumour su	c 340	17	1.2	455	6	ABT18943	Human liv
c 268	17	1.2	115	6	ABQ96190	ABQ96190 Tumour su	Abq96190 Tumour su	c 341	17	1.2	458	11	ACN81593	Breast ca
c 269	17	1.2	115	6	ABQ96201	ABQ96201 Tumour su	Abq96201 Tumour su	c 342	17	1.2	462	8	ABT18943	Breast ca
c 270	17	1.2	122	6	ABQ96188	ABQ96188 Tumour su	Abq96188 Tumour su	c 343	17	1.2	472	2	AAQ10375	Aspergill
c 271	17	1.2	135	6	ABQ96193	ABQ96193 Tumour su	Abq96193 Tumour su	c 344	17	1.2	473	9	ACH37880	Plasmid p
c 272	17	1.2	141	6	ABQ96189	ABQ96189 Tumour su	Abq96189 Tumour su	c 345	17	1.2	474	10	AD122566	Human end
c 273	17	1.2	174	4	ABL27543	ABL27543 Drosophi	Ab127543 Drosophi	c 346	17	1.2	481	9	ACH27340	Rat liver
c 274	17	1.2	177	6	ABQ97718	ABQ97718 Mouse ES	Abq97718 Mouse ES	c 347	17	1.2	486	9	ACH15599	Human adu
c 275	17	1.2	183	10	ADH83187	ADH83187 Enterococ	Adh83187 Enterococ	c 348	17	1.2	486	10	ACD92422	Human col
c 276	17	1.2	232	3	AAH70359	AAH70359 Single nu	Aac70359 Single nu	c 349	17	1.2	495	5	AAH52199	Human AFP
c 277	17	1.2	232	3	AAH70350	AAH70350 Single nu	Aac70350 Single nu	c 350	17	1.2	496	11	ADT96282	Colon can
c 278	17	1.2	240	3	AAH40731	AAH40731 Wild type	Aaa40731 Wild type	c 351	17	1.2	497	3	AAH77178	Human ORF
c 279	17	1.2	240	5	AAH76043	AAH76043 CD36 muta	Aah76043 CD36 muta	c 352	17	1.2	502	6	ABK39425	DNA encod
c 280	17	1.2	240	5	AAH76078	AAH76078 CD36 gene	Aah76078 CD36 gene	c 353	17	1.2	502	8	ACA11754	Human lun
c 281	17	1.2	241	5	AAH76042	AAH76042 CD36 muta	Aah76042 CD36 muta	c 354	17	1.2	502	8	ACA02940	Lung canc
c 282	17	1.2	248	6	ABN23616	ABN23616 Human ORF	Abn23616 Human ORF	c 355	17	1.2	502	10	ADH46982	Human lun
c 283	17	1.2	287	6	ABQ58741	ABQ58741 Human col	Abq58741 Human col	c 356	17	1.2	502	10	ADH46982	Human lun
c 284	17	1.2	303	4	AAH53937	AAH53937 Murine tr	Aah53937 Murine tr	c 357	17	1.2	502	13	ADJ20901	Human lun
c 285	17	1.2	305	3	AAH53937	AAH53937 Murine tr	Aah53937 Murine tr	c 358	17	1.2	513	13	ADQ56965	Novel can
c 286	17	1.2	319	3	AAH53937	AAH53937 Murine tr	Aah53937 Murine tr	c 359	17	1.2	513	13	ADQ52351	Novel can
c 287	17	1.2	327	6	ABL71038	ABL71038 Corn tass	Ab171038 Corn tass	c 360	17	1.2	530	12	ADL88192	DNA up-re
c 288	17	1.2	333	8	ACA19143	ACA19143 Prokaryot	Aca19143 Prokaryot	c 361	17	1.2	530	12	ADL88192	DNA up-re
c 289	17	1.2	335	8	ABX45534	ABX45534 Bovine ES	Abx45534 Bovine ES	c 362	17	1.2	560	10	ADP90585	Human hep
c 290	17	1.2	341	9	ACH31853	ACH31853 Human bon	Ach31853 Human bon	c 363	17	1.2	563	5	ADL43023	Human ova
c 291	17	1.2	345	6	ABQ85913	ABQ85913 Arabidops	Abq85913 Arabidops	c 364	17	1.2	563	5	ADL43023	Human ova
c 292	17	1.2	351	10	ADD33106	ADD33106 Human mit	Ad33106 Human mit	c 365	17	1.2	565	5	AAH64735	Human sec
c 293	17	1.2	353	6	ABL83087	ABL83087 Human ova	Ab183087 Human ova	c 366	17	1.2	567	12	ACH87262	Human gen
c 294	17	1.2	360	6	ABL82554	ABL82554 Human ova	Ab182554 Human ova	c 367	17	1.2	572	3	AAH48585	Arabidops
c 295	17	1.2	369	3	AAA40747	AAA40747 Wild type	Aaa40747 Wild type	c 368	17	1.2	572	3	AAH48585	Arabidops
c 296	17	1.2	369	3	AAA40749	AAA40749 Wild type	Aaa40749 Wild type	c 369	17	1.2	574	3	AAH48585	Arabidops
c 297	17	1.2	369	8	ACA64747	ACA64747 LDL or ox	Aca64747 LDL or ox	c 370	17	1.2	575	6	ABT10941	Human bre
c 298	17	1.2	369	10	ADL43417	ADL43417 Macrophag	Adf43417 Macrophag	c 371	17	1.2	575	6	ABN96018	Gene #251
c 299	17	1.2	369	10	ADL13543	ADL13543 Osteoarth	Adl13543 Osteoarth	c 372	17	1.2	575	8	ABT20763	Aspergill
c 300	17	1.2	369	12	ADM34116	ADM34116 Human CD3	Adm34116 Human CD3	c 373	17	1.2	582	12	ACH87351	Human gen
c 301	17	1.2	369	12	ADM11313	ADM11313 Human CD3	Adm11313 Human CD3	c 374	17	1.2	589	4	AA115523	Human bre
c 302	17	1.2	375	4	AAH39315	AAH39315 Novel hum	Aah39315 Novel hum	c 375	17	1.2	591	13	ACN53406	Cotton an
c 303	17	1.2	380	4	AAH39315	AAH39315 Novel hum	Aah39315 Novel hum	c 376	17	1.2	591	13	ACN53406	Cotton an
c 304	17	1.2	383	6	AAH39316	AAH39316 Human pap	Aah39316 Human pap	c 377	17	1.2	598	13	ACN60649	Cotton gy
c 305	17	1.2	395	12	ADP57064	ADP57064 Maize car	Adp57064 Maize car	c 378	17	1.2	599	5	AAH88744	Human dig
c 306	17	1.2	399	4	AAH20291	AAH20291 Human bre	Aah20291 Human bre	c 379	17	1.2	599	5	AAH88744	Human dig
c 307	17	1.2	400	4	AAH37355	AAH37355 Novel hum	Aah37355 Novel hum	c 380	17	1.2	599	5	AAH88744	Human dig
c 308	17	1.2	410	3	AAH30509	AAH30509 Human col	Aah30509 Human col	c 381	17	1.2	601	13	ACN60861	Cotton gy
c 309	17	1.2	410	5	ADL36639	ADL36639 Human ova	Adl36639 Human ova	c 382	17	1.2	602	4	AA124612	Human bre
c 310	17	1.2	410	5	ADL36639	ADL36639 Human ova	Adl36639 Human ova	c 383	17	1.2	616	3	AAH11311	Aspergill
c 311	17	1.2	415	3	AAH11772	AAH11772 Aspergill	Aah11772 Aspergill	c 384	17	1.2	619	12	ACH87573	Human gen
c 312	17	1.2	418	3	AAH31113	AAH31113 Human col	Aah31113 Human col	c 385	17	1.2	619	13	ADR62135	Cotton CD

386	17	1.2	622	6	ABZ35313	Abz35313 Human gen	459	17	1.2	1128	2	AAQ82870	Aac82870 Rat STX 8
387	17	1.2	625	4	AAK93445	Aak93445 Human CDN	c 460	17	1.2	1154	9	AD57353	Aad57353 Human kin
388	17	1.2	625	4	AAK92179	Aak92179 Human CDN	c 461	17	1.2	1154	9	AA57578	Aal57578 Human ami
389	17	1.2	625	12	ADL28606	Adl28606 5' end of	c 462	17	1.2	1161	5	AA572466	Aal572466 DNA encod
390	17	1.2	625	12	ADL29872	Adl29872 5' end of	c 463	17	1.2	1188	13	AD556027	Ad556027 Bacterial
391	17	1.2	628	4	AAI24237	Aai24237 Human bre	c 464	17	1.2	1190	3	AA385828	Aac385828 Arabidops
392	17	1.2	637	11	ACN92164	Acn92164 Breast ca	c 465	17	1.2	1222	2	AAQ37204	Aac37204 Delta-ami
393	17	1.2	638	4	AAI24229	Aai24229 Human bre	c 466	17	1.2	1227	2	AAI14478	Aax14478 H. pylori
394	17	1.2	647	4	AAI24200	Aai24200 Human bre	c 467	17	1.2	1232	3	AA34814	Aac34814 Arabidops
395	17	1.2	660	10	ADK11787	Adk11787 Breast ca	c 468	17	1.2	1239	3	AA99087	Aaa99087 Hepatitis
396	17	1.2	664	4	AAK88850	Aak88850 Human dig	c 469	17	1.2	1240	5	AA563153	Aae63153 Human pur
397	17	1.2	665	4	AAI16538	Aai16538 Human nov	c 470	17	1.2	1328	6	ABZ12054	Abz12054 Human pol
398	17	1.2	665	4	AA534878	Aa534878 CDNA enco	c 471	17	1.2	1328	12	ADMA4572	Adm44572 Novel hum
399	17	1.2	665	6	AB564128	Ab564128 Human apo	c 472	17	1.2	1328	12	ADN96017	Adn96017 Human NOV
400	17	1.2	665	10	ADC46036	Adc46036 Human neo	c 473	17	1.2	1332	6	ABQ76514	Abq76514 C. albica
401	17	1.2	665	10	AD660437	Ad660437 Human sec	c 474	17	1.2	1332	12	ADP98677	Adp98677 C. albica
402	17	1.2	667	8	ABT18349	Abt18349 Aspergill	c 475	17	1.2	1363	12	ADH70089	Adh70089 Human Vbe
403	17	1.2	669	9	AD585560	Ad585560 Human thy	c 476	17	1.2	1363	11	ABD14989	Abd14989 Pseudomon
404	17	1.2	671	6	ABX65594	Abx65594 Helicobac	c 477	17	1.2	1365	12	ADO71726	Ado71726 Human gen
405	17	1.2	687	13	ADR26808	Adr26808 Breast ca	c 478	17	1.2	1365	12	ADO71726	Ado71726 Human gen
406	17	1.2	690	4	AAI15383	Aai15383 Human bre	c 479	17	1.2	1389	9	ACD06238	AcD06238 Human CDN
407	17	1.2	692	11	ACN88268	Acn88268 Breast ca	c 480	17	1.2	1389	9	ACD06237	AcD06237 Human CDN
408	17	1.2	705	6	ABK36103	Abk36103 CDNA sequ	c 481	17	1.2	1389	9	ACD06204	AcD06204 Human CDN
409	17	1.2	712	5	AA566460	Aa566460 DNA encod	c 482	17	1.2	1389	12	ADN96085	Adn96085 Human NOV
410	17	1.2	722	3	AAAC46860	Aac46860 Arabidops	c 483	17	1.2	1390	4	AAK70283	Aak70283 Human 1mm
411	17	1.2	739	2	AAK03015	Aax03015 Human IL-	c 484	17	1.2	1401	9	ACD06241	AcD06241 Human CDN
412	17	1.2	742	9	ADB82962	AdB82962 Human CDN	c 485	17	1.2	1401	9	ACD06243	AcD06243 Human CDN
413	17	1.2	743	5	ABV29603	Abv29603 Human pro	c 486	17	1.2	1401	9	ACD06242	AcD06242 Human CDN
414	17	1.2	743	5	ABV23730	Abv23730 Human pro	c 487	17	1.2	1401	9	ACD06239	AcD06239 Human CDN
415	17	1.2	750	4	AAI96135	Aai96135 Human neu	c 488	17	1.2	1401	9	ACD06240	AcD06240 Human CDN
416	17	1.2	751	11	ACN85378	Acn85378 Breast ca	c 489	17	1.2	1401	12	ADN96089	Adn96089 Human NOV
417	17	1.2	754	4	AAI24367	Aai24367 Human bre	c 490	17	1.2	1401	12	ADN96091	Adn96091 Human NOV
418	17	1.2	770	4	AAI21822	Aai21822 Human bre	c 491	17	1.2	1419	10	ADL13538	Adl13538 Osreoeath
419	17	1.2	782	4	AAI81913	Aai81913 Single ch	c 492	17	1.2	1422	4	AAI12497	Aai12497 Probe #24
420	17	1.2	783	8	ACA19281	AcA19281 Prokaryot	c 493	17	1.2	1422	4	AAI133852	Aai133852 Probe #25
421	17	1.2	802	6	ABQ89923	Abq89923 Human pro	c 494	17	1.2	1422	4	AAK27918	Aak27918 Human bon
422	17	1.2	807	11	ACN92228	Acn92228 Breast ca	c 495	17	1.2	1422	4	AAK02479	Aak02479 Human bra
423	17	1.2	813	11	ACN88258	Acn88258 Breast ca	c 496	17	1.2	1438	6	ABZ34990	Abz34990 Human gen
424	17	1.2	815	10	AD87116	Ad87116 Human pan	c 497	17	1.2	1438	10	ADB84848	AdB84848 Farnesyl
425	17	1.2	819	2	AAK39702	Aax39702 Gastric c	c 498	17	1.2	1438	10	ACA56828	AcA56828 Human sig
426	17	1.2	825	12	ADP28483	Adp28483 Human sec	c 499	17	1.2	1438	10	AD156624	Adi56624 Human pol
427	17	1.2	830	11	ACN85711	Acn85711 Breast ca	c 500	17	1.2	1439	12	ADH89021	Adh89021 Human POL
428	17	1.2	840	4	AAH05683	Aah05683 Human CDN	c 501	17	1.2	1441	5	AA501219	Aae01219 DNA encod
429	17	1.2	852	13	AD585589	Ad585589 Cotton cd	c 502	17	1.2	1441	9	ACD06232	AcD06232 Human CDN
430	17	1.2	862	8	ABV76807	Abv76807 Human nuc	c 503	17	1.2	1441	9	ACD06235	AcD06235 Human CDN
431	17	1.2	870	4	AAI15768	Aai15768 Human bre	c 504	17	1.2	1441	12	ADN96073	Adn96073 Human NOV
432	17	1.2	893	11	ACN85386	Acn85386 Breast ca	c 505	17	1.2	1449	13	ADQ86621	Adq86621 Human tum
433	17	1.2	941	6	ABX66620	Abx66620 Helicobac	c 506	17	1.2	1449	13	ADQ85493	Adq85493 Prokaryot
434	17	1.2	948	11	ABD15359	Abd15359 Pseudomon	c 507	17	1.2	1470	8	ACA38687	AcA38687 Prokaryot
435	17	1.2	953	8	ABT20165	Abt20165 Aspergill	c 508	17	1.2	1473	8	ACA40446	AcA40446 Prokaryot
436	17	1.2	953	10	ADG32856	Adg32856 Human DNA	c 509	17	1.2	1475	10	ADC30480	Adc30480 Human nov
437	17	1.2	993	4	AAAF72866	Aaf72866 ALAD codi	c 510	17	1.2	1489	4	ADF90731	Adf90731 Human hep
438	17	1.2	993	13	ADQ89853	Adq89853 Antagonis	c 511	17	1.2	1498	4	AAF74446	Aaf74446 Human PRO
439	17	1.2	1024	6	ABL46292	AbL46292 Human ant	c 512	17	1.2	1498	9	ACD06231	AcD06231 Human CDN
440	17	1.2	1068	3	AAA30580	Aaa30580 Human G p	c 513	17	1.2	1498	12	ADN96071	Adn96071 Human NOV
441	17	1.2	1068	3	AAA30709	Aaa30709 DNA encod	c 514	17	1.2	1500	3	AAK74371	Aak74371 Human sec
442	17	1.2	1068	4	AAI21688	Aai21688 Probe #11	c 515	17	1.2	1500	8	ABZ73562	Abz73562 Secreted
443	17	1.2	1068	4	AAI46977	Aai46977 Probe #15	c 516	17	1.2	1500	10	ADC20238	Adc20238 Human sec
444	17	1.2	1068	4	AAK40922	Aak40922 Human bon	c 517	17	1.2	1500	10	ABZ67159	Abz67159 Human sec
445	17	1.2	1068	4	AAK15197	Aak15197 Human bra	c 518	17	1.2	1533	10	ADF01197	Adf01197 Bacterial
446	17	1.2	1068	8	ABZ42726	Abz42726 Human G p	c 519	17	1.2	1545	6	AAAD23674	Aad23674 Human cal
447	17	1.2	1068	10	ADC22682	Adc22682 Human G p	c 520	17	1.2	1581	2	AAZ10804	Aaz10804 Polynucle
448	17	1.2	1068	10	ADC32520	Adc32520 Human G p	c 521	17	1.2	1581	2	AAZ59260	Aaz59260 Human CDN
449	17	1.2	1068	10	ADH14155	Adh14155 Mutated h	c 522	17	1.2	1581	6	ABA90929	AbA90929 Human pol
450	17	1.2	1068	10	ADH13993	Adh13993 Human GPR	c 523	17	1.2	1581	6	ABA90929	AbA90929 Human pol
451	17	1.2	1068	12	ADO29900	Ado29900 Human GPC	c 524	17	1.2	1584	4	AAAD15666	Aad15666 Human nov
452	17	1.2	1078	11	ACN85512	Acn85512 Breast ca	c 525	17	1.2	1584	6	AB564156	Ab564156 Human apo
453	17	1.2	1082	11	ACN85739	Acn85739 Breast ca	c 526	17	1.2	1584	10	ADC46550	Adc46550 Human neo
454	17	1.2	1086	11	ABD15251	Abd15251 Pseudomon	c 527	17	1.2	1584	10	AAAD60465	Aad60465 Human sec
455	17	1.2	1087	4	ABA09391	AbA09391 Human sec	c 528	17	1.2	1605	3	AAAC54148	Aac54148 Arabidops
456	17	1.2	1107	13	ADR64215	Adr64215 Cotton cd	c 529	17	1.2	1607	3	AAAC35942	Aac35942 Arabidops
457	17	1.2	1122	6	ABL39748	AbL39748 Human NS	c 530	17	1.2	1620	8	ABV76806	Abv76806 Human nuc
458	17	1.2	1128	2	AAQ47960	Aaq47960 Sialyltra	c 531	17	1.2	1635	4	AAH14149	Aah14149 Human CDN

532	17	1.2	1647	3	AAA40746	Aaa40746 Wild type	c 605	17	1.2	1958	4	AAI34489	Aai34489 Probe #31
533	17	1.2	1673	2	AAQ22749	Aaq22749 Class II	c 606	17	1.2	1958	4	ABA44387	Ab444387 Human bre
534	17	1.2	1673	2	AAT93789	Aat93789 Class II	c 607	17	1.2	1958	4	ABA24602	Ab24602 Probe #30
535	17	1.2	1673	2	AAT77315	Aat77315 Class II	c 608	17	1.2	1958	4	AAK28566	Aak28566 Human bra
536	17	1.2	1673	2	AAV58011	Aav58011 Achromoba	c 609	17	1.2	1958	4	AAK03113	Aak03113 Human bra
537	17	1.2	1673	2	AAD09755	Aad09755 Achromoba	c 610	17	1.2	1958	4	ABs28163	Ab28163 Human liv
538	17	1.2	1673	10	AAD060591	Aad060591 Achromoba	c 611	17	1.2	1958	5	AAI03042	Aai03042 Human liv
539	17	1.2	1677	2	AAV06059	Aav06059 Human imi	c 612	17	1.2	1958	6	ABs03076	Ab3076 Human gen
540	17	1.2	1689	13	ACN40107	Acn40107 Tumour-as	c 613	17	1.2	1971	5	AAAS80749	Aas80749 DNA encod
541	17	1.2	1699	2	AAQ65605	Aaq65605 Porcine z	c 614	17	1.2	1972	4	AAH14077	Aah14077 Human CDN
542	17	1.2	1699	2	AAV64787	Aav64787 Porcine z	c 615	17	1.2	2000	8	ADA72798	Ada72798 Rice gene
543	17	1.2	1699	2	AAZ22710	Aaz22710 Porcine z	c 616	17	1.2	2001	6	ADA723675	Ada723675 Human Cal
544	17	1.2	1699	3	AAZ33244	Aaz33244 Porcine z	c 617	17	1.2	2024	2	AAT17383	Aat17383 G-protein
545	17	1.2	1699	3	AAZ95647	Aaz95647 Porcine z	c 618	17	1.2	2024	2	AAV55772	Aav55772 Human C5a
546	17	1.2	1699	3	AAZ46255	Aaz46255 Porcine o	c 619	17	1.2	2024	6	AAAD22063	Aad22063 Human mat
547	17	1.2	1699	3	AAZ37799	Aaz37799 Porcine z	c 620	17	1.2	2024	8	ABX95600	Abx95600 Human CDN
548	17	1.2	1699	9	ACF05479	Acf05479 Pig zona	c 621	17	1.2	2025	12	ADQ85695	Adq85695 Human tum
549	17	1.2	1707	5	AAAS85320	Aas85320 DNA encod	c 622	17	1.2	2025	13	ADQ86771	Adq86771 Human tum
550	17	1.2	1725	9	ACD06203	Acd06203 Human CDN	c 623	17	1.2	2036	5	AAAS72868	Aas72868 DNA encod
551	17	1.2	1725	12	ADN96015	Adn96015 Human NOV	c 624	17	1.2	2040	13	ADP56413	Adp56413 Human PRO
552	17	1.2	1734	12	ACH87711	Ach87711 Human gen	c 625	17	1.2	2055	13	ADN60271	Adn60271 Human ZIP
553	17	1.2	1735	4	AAI22373	Aai22373 Probe #12	c 626	17	1.2	2055	13	ADN83403	Adn83403 Human ZIP
554	17	1.2	1735	4	ABA67449	Ab67449 Human foe	c 627	17	1.2	2078	13	ACN40732	Acn40732 Tumour-as
555	17	1.2	1735	4	AAI47664	Aai47664 Probe #16	c 628	17	1.2	2079	4	AAK94258	Aak94258 Human ful
556	17	1.2	1735	4	ABA49540	Ab49540 Human bre	c 629	17	1.2	2079	10	ABX77160	Abx77160 DNA seque
557	17	1.2	1735	4	ABA34529	Ab34529 Probe #12	c 630	17	1.2	2079	12	ADQ30841	Adq30841 Full leng
558	17	1.2	1735	4	AAK41623	Aak41623 Human bon	c 631	17	1.2	2079	13	ADQ68012	Adq68012 Recombina
559	17	1.2	1735	4	AAK15878	Aak15878 Human bra	c 632	17	1.2	2082	10	ADES8909	Ades8909 Human gen
560	17	1.2	1735	4	ABS41213	Ab41213 Human liv	c 633	17	1.2	2088	4	AAH16743	Aah16743 Human CDN
561	17	1.2	1735	5	AAI08059	Aai08059 Probe #80	c 634	17	1.2	2093	12	ADM87030	Adm87030 Human pro
562	17	1.2	1735	6	ABS15630	Ab15630 Human gen	c 635	17	1.2	2099	12	ADQ70390	Adq70390 Respirato
563	17	1.2	1748	6	ABT03047	Abt03047 Human bre	c 636	17	1.2	2104	12	ADQ84258	Adq84258 Human tum
564	17	1.2	1818	13	ACN37314	Acn37314 Tumour-as	c 637	17	1.2	2104	13	ADQ85644	Adq85644 Human tum
565	17	1.2	1820	3	AAA40755	Aaa40755 Wild type	c 638	17	1.2	2104	13	ADQ86740	Adq86740 Human tum
566	17	1.2	1820	6	AAD38654	Aad38654 Human CD3	c 639	17	1.2	2105	6	ABV72291	Abv72291 Nucleotid
567	17	1.2	1820	11	ADI31705	Adi31705 Human CDN	c 640	17	1.2	2105	13	ADNG0267	Adng0267 Human dea
568	17	1.2	1820	12	ADM34097	Adm34097 Human CD3	c 641	17	1.2	2105	13	ADNG0269	Adng0269 Human ZIP
569	17	1.2	1820	12	ADM11294	Adm11294 Human CDN	c 642	17	1.2	2105	13	ADR83493	Adr83493 Human dea
570	17	1.2	1823	2	AAZ33602	Aaz33602 Human bre	c 643	17	1.2	2132	2	AAAX34656	Aax34656 Human ZIP
571	17	1.2	1838	12	ADI40932	Adi40932 Human kin	c 644	17	1.2	2132	8	ACA90235	Aca90235 Deatch as
572	17	1.2	1846	4	ABL09201	AbL09201 Drosophil	c 645	17	1.2	2132	12	ADO09424	Ado09424 Novel hum
573	17	1.2	1851	10	ADB53752	Ab23752 Primary r	c 646	17	1.2	2138	4	AAH18492	Aah18492 Human CDN
574	17	1.2	1857	6	ABZ32148	Abz32148 Candida a	c 647	17	1.2	2158	12	ADH13777	Adh13777 Human ENZ
575	17	1.2	1860	10	ADC08236	Adc08236 Rice DNA	c 648	17	1.2	2159	4	ABL20010	AbL20010 Drosophil
576	17	1.2	1860	10	ADC08058	Adc08058 Rice DNA	c 649	17	1.2	2174	4	ABL27542	AbL27542 Drosophil
577	17	1.2	1860	12	ADJ40524	Adj40524 Plant CDN	c 650	17	1.2	2196	13	ADSL49240	Adsl49240 Bacterial
578	17	1.2	1865	2	AAV81212	Aav81212 Human CD3	c 651	17	1.2	2203	2	AAZ06247	Aaz06247 Human sec
579	17	1.2	1870	2	AAQ21177	Aaq21177 Human CD3	c 652	17	1.2	2206	5	ADL62916	AdL62916 Human ova
580	17	1.2	1870	2	AAT14716	Aat14716 Human put	c 653	17	1.2	2209	3	AAC78100	Aac78100 Human can
581	17	1.2	1870	2	AAV63455	Aav63455 Human CD3	c 654	17	1.2	2216	3	AAA40752	Aaa40752 Wild type
582	17	1.2	1870	3	AAAS0591	Aas0591 Human cel	c 655	17	1.2	2216	6	ABL66667	AbL66667 Lung canc
583	17	1.2	1870	3	AAA40754	Aaa40754 Wild type	c 656	17	1.2	2216	6	ABN95939	Abn95939 Gene #243
584	17	1.2	1870	4	AAAS03185	Aas03185 Human lym	c 657	17	1.2	2216	10	ADL13537	AdL13537 Osteoearth
585	17	1.2	1870	5	AAH76045	Aah76045 CD36 gene	c 658	17	1.2	2216	10	ADK61408	Adk61408 Ovarian c
586	17	1.2	1870	12	ADO49360	Ado49360 Human CD3	c 659	17	1.2	2216	12	ADM34118	Adm34118 Human CD3
587	17	1.2	1888	6	AAD34456	Aad34456 Human 264	c 660	17	1.2	2216	12	ADM11315	Adm11315 Human CDN
588	17	1.2	1936	12	ADH35355	Adh35355 ENZM enco	c 661	17	1.2	2216	13	ADR87640	Adr87640 Human CD3
589	17	1.2	1941	4	ABA83374	Aab83374 Human sec	c 662	17	1.2	2217	10	ADL13553	AdL13553 Osteoearth
590	17	1.2	1941	4	ABA83374	Aab83374 Human sec	c 663	17	1.2	2222	12	ADH35356	Adh35356 ENZM enco
591	17	1.2	1941	9	ACH04875	Ach04875 Novel hum	c 664	17	1.2	2224	4	AAH16158	Aah16158 Human CDN
592	17	1.2	1941	9	ACD44685	Acd44685 Human CDN	c 665	17	1.2	2224	5	AAH18068	Aah18068 Human kin
593	17	1.2	1942	3	AAA40753	Aaa40753 Wild type	c 666	17	1.2	2225	13	ADR07342	Adr07342 Full leng
594	17	1.2	1942	10	ACA56593	Aca56593 Human Big	c 667	17	1.2	2225	13	ADRS34569	Adrs34569 POSH prot
595	17	1.2	1942	12	ADI56389	Adi56389 Human pol	c 668	17	1.2	2226	10	ADD29770	Add29770 Human tum
596	17	1.2	1942	12	ADM34117	Adm34117 Human CD3	c 669	17	1.2	2237	4	AAK94489	Aak94489 Human ful
597	17	1.2	1942	12	ADM11314	Adm11314 Human CDN	c 670	17	1.2	2237	12	ADL31291	AdL31291 Full leng
598	17	1.2	1944	10	ADJ56278	Adj56278 Human CDN	c 671	17	1.2	2240	6	AAD26460	Aad26460 Human kin
599	17	1.2	1951	6	AAAS62304	Aas62304 cDNA sequ	c 672	17	1.2	2244	2	AAT99965	Aat99965 Gene for
600	17	1.2	1952	6	ABL68003	AbL68003 Ovary can	c 673	17	1.2	2245	12	ADL35545	AdL35545 Human kar
601	17	1.2	1952	6	ABL63315	AbL63315 Breast ca	c 674	17	1.2	2280	3	AAC77630	Aac77630 Human can
602	17	1.2	1954	2	AAZ28368	Aaz28368 Human imi	c 675	17	1.2	2286	12	ADI40930	Adi40930 Human kin
603	17	1.2	1958	4	AAI11317	Aai11317 Probe #30	c 676	17	1.2	2287	10	ADB63385	AdB63385 Human cDN
604	17	1.2	1958	4	ABA54835	AbA54835 Human foe	c 677	17	1.2	2311	10	ADF38036	Adf38036 Synchroni

C 678	17	1.2	2316	12	ADH35354	Adh35354 ENZM enco	751	17	1.2	2953	8	ABT19569	Abt19569 Aspergill
C 679	17	1.2	2319	12	ADH35353	Adh35353 ENZM enco	752	17	1.2	2961	12	ADN96075	Adn96075 Human NOV
C 680	17	1.2	2326	4	APF55436	Aaf55436 Nucleotid	753	17	1.2	2982	5	ADL45719	Adl45719 Human ova
C 681	17	1.2	2340	11	ADI31033	Adi31033 Human cDN	754	17	1.2	3012	9	ACD06234	AcD06234 Human cDN
C 682	17	1.2	2347	6	ADP35108	Adp35108 Human chr	755	17	1.2	3012	12	ADN96077	Adn96077 Human NOV
C 683	17	1.2	2347	13	ADR96743	Adr96743 Human chr	756	17	1.2	3021	9	ACD06233	AcD06233 Human cDN
C 684	17	1.2	2362	8	ABA00720	AbA00720 Human KPP	757	17	1.2	3032	4	AAH98711	Aah98711 Human EST
C 685	17	1.2	2389	2	AAT96470	Aat96470 MSRV-1 cl	758	17	1.2	3032	4	RAA22857	Raa22857 Human cDN
C 686	17	1.2	2389	2	AAV43161	Aav43161 Multiple	759	17	1.2	3063	1	AAH91438	Aah91438 DNA enco
C 687	17	1.2	2389	9	ADB84343	AdB84343 MSRV-1 en	760	17	1.2	3064	13	ADRA45327	Adr45327 Serine/th
C 688	17	1.2	2389	12	ADG14789	Adg14789 MSRV-1 cl	761	17	1.2	3064	13	ADRA45206	Adr45206 Serine/th
C 689	17	1.2	2392	8	ACC46230	Acc46230 Human dit	762	17	1.2	3078	9	ACD06236	AcD06236 Human cDN
C 690	17	1.2	2436	5	ABV30123	Abv30123 Human pro	763	17	1.2	3078	12	ADN96081	Adn96081 Human NOV
C 691	17	1.2	2436	8	ABV76805	Abv76805 Human nuc	764	17	1.2	3078	13	ADR25578	Adr25578 Breast ca
C 692	17	1.2	2439	12	ADH35358	Adh35358 ENZM enco	765	17	1.2	3085	10	ADB62223	AdB62223 Human cDN
C 693	17	1.2	2466	6	ABK49562	Abk49562 Human cDN	766	17	1.2	3088	2	AAK35741	Aak35741 cDNA enco
C 694	17	1.2	2473	5	ADL63822	Adl63822 Human ova	767	17	1.2	3139	12	ADJ39889	Adj39889 Plant cDN
C 695	17	1.2	2473	10	ADE57910	Ade57910 Rat gene	768	17	1.2	3155	6	AAH94847	Aah94847 Human DNA
C 696	17	1.2	2484	10	ABX70672	Abx70672 Human cDN	769	17	1.2	3204	4	AAK94369	Aak94369 Human ful
C 697	17	1.2	2487	2	AAQ45332	Aaq45332 Human epi	770	17	1.2	3204	12	ADL31062	Adl31062 Full leng
C 698	17	1.2	2488	2	AAT95987	Aat95987 DNA for e	771	17	1.2	3224	13	ADRA4049	Adr44049 Human kid
C 699	17	1.2	2488	6	ABL67780	AbL67780 Oesophagu	772	17	1.2	3236	6	AAK93298	Aak93298 cDNA of t
C 700	17	1.2	2488	6	ABK84049	Abk84049 Human cDN	773	17	1.2	3263	6	ABQ55014	Abq55014 Human ova
C 701	17	1.2	2488	13	ADR73463	Adr73463 Human flo	774	17	1.2	3309	3	AAF21886	Aaf21886 Human bre
C 702	17	1.2	2503	12	ADM18456	Adm18456 Human chr	775	17	1.2	3315	12	ADQ67491	Adq67491 Novel hum
C 703	17	1.2	2505	6	ABS67744	Abs67744 Human int	776	17	1.2	3316	3	AAV76526	Aav76526 Human ORF
C 704	17	1.2	2520	6	ABK64801	Abk64801 Human ben	777	17	1.2	3317	2	AAV06060	Aav06060 Human imi
C 705	17	1.2	2520	6	ABN97190	Abn97190 Gene #368	778	17	1.2	3318	2	AAK28369	Aak28369 Human imi
C 706	17	1.2	2529	5	AAH85655	Aah85655 DNA enco	779	17	1.2	3336	4	AAF74445	Aaf74445 Human PRO
C 707	17	1.2	2532	12	ADN96097	Adn96097 Human NOV	780	17	1.2	3336	9	ACD06230	AcD06230 Human cDN
C 708	17	1.2	2560	9	ACD06245	AcD06245 Human cDN	781	17	1.2	3348	8	ACA38191	ACA38191 Prokaryot
C 709	17	1.2	2560	12	ADN96099	Adn96099 Human NOV	782	17	1.2	3350	4	AAAD08345	Aad08345 Human sec
C 710	17	1.2	2577	4	AAK35740	Aak35740 cDNA enco	783	17	1.2	3352	12	ADQ35957	Adq35957 Novel mou
C 711	17	1.2	2586	4	AAF44665	Aaf44665 Novel pro	784	17	1.2	3389	2	AAK28367	Aak28367 Human imi
C 712	17	1.2	2586	12	ADI29363	Adi29363 Human MAR	785	17	1.2	3405	5	AAH81784	Aah81784 Human dif
C 713	17	1.2	2592	9	ACD06244	AcD06244 Human cDN	786	17	1.2	3416	12	ADQ18747	Adq18747 Human sof
C 714	17	1.2	2620	12	ADQ22546	Adq22546 Human sof	787	17	1.2	3424	10	ADA53066	Ada53066 Human cod
C 715	17	1.2	2623	4	ABL11529	AbL11529 Drosophil	788	17	1.2	3456	12	ADN96069	Adn96069 Human NOV
C 716	17	1.2	2629	10	ADB58673	AdB58673 Toxicity-	789	17	1.2	3472	12	ADQ64600	Adq64600 Novel hum
C 717	17	1.2	2629	10	ABT42252	Abt42252 Toxicity	790	17	1.2	3528	13	ADRO7865	Adr07865 Full leng
C 718	17	1.2	2635	4	ABR84521	AbR84521 Human sec	791	17	1.2	3580	4	ABL18862	AbL18862 Drosophil
C 719	17	1.2	2635	4	ABR83304	AbR83304 Human sec	792	17	1.2	3604	10	ADA52845	Ada52845 Human cod
C 720	17	1.2	2635	9	ACH04805	Ach04805 Novel hum	793	17	1.2	3677	4	ABA09142	AbA09142 Human ST7
C 721	17	1.2	2635	9	ACD44615	AcD44615 Human cDN	794	17	1.2	3694	2	AAZ00356	Aaz00356 Nucleotid
C 722	17	1.2	2660	13	ADL14030	AdL14030 Human NF-	795	17	1.2	3694	5	AAF89018	Aaf89018 Human FAT
C 723	17	1.2	2667	8	ABT17755	Abt17755 Aspergill	796	17	1.2	3704	2	AAZ00352	Aaz00352 Nucleotid
C 724	17	1.2	2686	13	ADP55714	AdP55714 Human PRO	797	17	1.2	3704	5	AAF89010	Aaf89010 Human FAT
C 725	17	1.2	2693	4	AAK94347	Aak94347 Human ful	798	17	1.2	3708	5	ABV23245	Abv23245 Human pro
C 726	17	1.2	2693	4	AAK16565	Aak16565 Human nov	799	17	1.2	3708	5	ABV29089	Abv29089 Human pro
C 727	17	1.2	2693	4	AAK16568	Aak16568 Human nov	800	17	1.2	3809	4	ABK42271	Abk42271 Genomic s
C 728	17	1.2	2693	4	AAK16567	Aak16567 Human nov	801	17	1.2	3809	9	ADB60427	AdB60427 Connectiv
C 729	17	1.2	2693	4	AAK35109	Aak35109 DNA #59 e	802	17	1.2	3837	9	ADQ23166	Adq23166 Human sof
C 730	17	1.2	2693	4	AAK35110	Aak35110 DNA #60 e	803	17	1.2	3891	3	AAK76424	Aak76424 Human ORF
C 731	17	1.2	2693	4	AAK35107	Aak35107 DNA #57 e	804	17	1.2	3930	5	AAZ44744	Aaz44744 Human Klf
C 732	17	1.2	2693	6	ABS64155	AbS64155 Human apo	805	17	1.2	3930	5	AAAD08139	Aaad08139 Human kin
C 733	17	1.2	2693	6	ABS64158	AbS64158 Human apo	806	17	1.2	3930	10	ADG63389	Adg63389 Human cDN
C 734	17	1.2	2693	6	ABS64157	AbS64157 Human apo	807	17	1.2	3930	5	ABA21203	AbA21203 Human ner
C 735	17	1.2	2693	10	ADC46549	Adc46549 Human neo	808	17	1.2	3956	5	ABA21203	AbA21203 Human ner
C 736	17	1.2	2693	10	ADC46551	Adc46551 Human neo	809	17	1.2	3960	8	ACC42329	Acc42329 Human MAP
C 737	17	1.2	2693	10	ADC46552	Adc46552 Human neo	810	17	1.2	3975	6	AAAD26455	Aaad26455 Human kin
C 738	17	1.2	2693	10	AAAD60466	Aaad60466 Human sec	811	17	1.2	3985	10	ADJ56279	Adj56279 Human cDN
C 739	17	1.2	2693	10	AAAD60467	Aaad60467 Human sec	812	17	1.2	3993	4	AAF44688	Aaf44688 Novel pro
C 740	17	1.2	2693	10	AAAD60464	Aaad60464 Human sec	813	17	1.2	3993	12	ADI29386	Adi29386 Human MAR
C 741	17	1.2	2693	12	ADL31018	AdL31018 Full leng	814	17	1.2	3994	8	ACC42330	Acc42330 Human MAP
C 742	17	1.2	2701	4	AAH17862	Aah17862 Human cDN	815	17	1.2	3996	8	ACA39373	AcA39373 Prokaryot
C 743	17	1.2	2729	6	ABL90664	AbL90664 Human pol	816	17	1.2	4000	6	ABK92257	AbK92257 Prostate
C 744	17	1.2	2737	6	ABK88008	AbK88008 cDNA enco	817	17	1.2	4000	10	ADD18977	Add18977 Human dis
C 745	17	1.2	2739	6	AAI49803	Aai49803 Murine ch	818	17	1.2	4083	12	ADO20150	Ado20150 Human PRO
C 746	17	1.2	2739	10	ADF69745	Adf69745 cDNA enco	819	17	1.2	4083	13	ADP25176	Adp25176 PRO polyp
C 747	17	1.2	2739	10	AAAD69750	Aaad69750 Mouse CLC	820	17	1.2	4121	13	ABD32993	Abd32993 Human can
C 748	17	1.2	2787	5	AAH85323	Aah85323 DNA enco	821	17	1.2	4121	13	ABD32994	Abd32994 Human can
C 749	17	1.2	2795	13	ACN38734	Acn38734 Tumour-as	822	17	1.2	4187	10	ADE87204	Ade87204 Human pan
C 750	17	1.2	2877	13	ADS09828	AdS09828 Human the	823	17	1.2				

c 824	17	1.2	4223	8	ABX111199	Abx111199 cDNA enco	c 897	17	1.2	6182	12	ADQ25403	Adq25403 Human sof
c 825	17	1.2	4231	6	AA594798	AA594798 Human DNA	c 898	17	1.2	6545	2	AAZ00020	AAZ00020 osi+ DNA
c 826	17	1.2	4246	13	ADR14374	Adr14374 Human NF-	c 899	17	1.2	6545	12	ADN07069	Adn07069 Neurospor
c 827	17	1.2	4246	13	ADP54834	Adp54834 Human PRO	c 900	17	1.2	6689	8	ACD40375	AcD40375 Human ary
c 828	17	1.2	4246	13	ADP24271	Adp24271 PRO poly	c 901	17	1.2	6694	6	ABL67791	AbL67791 Oesophagu
c 829	17	1.2	4338	3	AA57197	AA57197 Human sub	c 902	17	1.2	6694	6	ABL64103	AbL64103 Breast ca
c 830	17	1.2	4338	6	AD24182	Ad24182 Human sit	c 903	17	1.2	6742	4	AAK66424	AaK66424 Human imm
c 831	17	1.2	4338	10	ADG32883	Adg32883 Human DNA	c 904	17	1.2	6742	4	ABL11528	AbL11528 Drosophi
c 832	17	1.2	4338	13	ADR25092	Adr25092 Breast ca	c 905	17	1.2	7000	8	ABZ74421	AbZ74421 Secreted
c 833	17	1.2	4447	12	ADM86963	Adm86963 Human pro	c 906	17	1.2	7000	10	ADC20884	AdC20884 Human sec
c 834	17	1.2	4450	4	AAK90986	AaK90986 Human dig	c 907	17	1.2	7000	10	ABZ67978	AbZ67978 Human sec
c 835	17	1.2	4450	5	AA532021	AA532021 Human liv	c 908	17	1.2	7222	8	ABT42544	AbT42544 Human nuc
c 836	17	1.2	4450	6	ABN90376	ABn90376 Human liv	c 909	17	1.2	7428	4	ABL10064	AbL10064 Drosophi
c 837	17	1.2	4454	11	ADJ15289	Adj15289 Human liv	c 910	17	1.2	7430	6	AAZ34173	AaZ34173 Pugu rubr
c 838	17	1.2	4454	4	AAK90985	AaK90985 Human dig	c 911	17	1.2	7592	13	ACN37313	AcN37313 Tumour-as
c 839	17	1.2	4454	5	AA532020	AA532020 Human liv	c 912	17	1.2	8570	12	ADO20320	AdO20320 Human PRO
c 840	17	1.2	4454	6	ABN90375	ABn90375 Human liv	c 913	17	1.2	8570	13	ADP55596	AdP55596 Human PRO
c 841	17	1.2	4454	11	ADJ15288	Adj15288 Human liv	c 914	17	1.2	8790	12	ADG65229	AdG65229 Mgf1 codi
c 842	17	1.2	4736	6	AA562248	AA562248 cDNA sequ	c 915	17	1.2	8867	10	ADE56784	AdE56784 Rat gene
c 843	17	1.2	4739	5	AA584367	AA584367 DNA enco	c 916	17	1.2	9016	8	ABX63507	AbX63507 Human CDN
c 844	17	1.2	4744	4	AAK69578	AaK69578 Human imm	c 917	17	1.2	9151	8	ABZ74514	AbZ74514 Secreted
c 845	17	1.2	4744	4	AAK68384	AaK68384 Human imm	c 918	17	1.2	9151	8	ADA98912	AdA98912 Human sec
c 846	17	1.2	4744	4	AAK68315	AaK68315 Human imm	c 919	17	1.2	9151	10	ABZ68050	AbZ68050 Human sec
c 847	17	1.2	4747	4	AAK69579	AaK69579 Human imm	c 920	17	1.2	9157	6	ABL33500	AbL33500 Human imm
c 848	17	1.2	4747	4	AAK68385	AaK68385 Human imm	c 921	17	1.2	9267	6	ABL33853	AbL33853 Human imm
c 849	17	1.2	4755	12	ADM44013	Adm44013 Novel hum	c 922	17	1.2	9273	8	ABZ74515	AbZ74515 Secreted
c 850	17	1.2	4782	12	ADQ97218	Adq97218 Human can	c 923	17	1.2	9273	8	ADA98913	AdA98913 Human sec
c 851	17	1.2	4836	6	AB211494	AB211494 Human pol	c 924	17	1.2	9273	10	ABZ68051	AbZ68051 Human sec
c 852	17	1.2	4836	12	ADM44012	Adm44012 Novel hum	c 925	17	1.2	9377	6	ABA97530	AbA97530 Human ami
c 853	17	1.2	4859	5	ABV29317	ABv29317 Human pro	c 926	17	1.2	9689	4	AAI199218	AaI199218 Human exc
c 854	17	1.2	4859	5	ABV23122	ABv23122 Human pro	c 927	17	1.2	9689	5	AAI63568	AaI63568 Human kid
c 855	17	1.2	4859	5	ABV23459	ABv23459 Human pro	c 928	17	1.2	9760	5	AA2F8598	Aa2F8598 Human sec
c 856	17	1.2	4880	5	ABV28963	ABv28963 Human pro	c 929	17	1.2	10053	4	AAK73765	AaK73765 Japanese
c 857	17	1.2	4880	4	ABL10065	ABL10065 Drosophi	c 930	17	1.2	10067	10	ADD48596	AdD48596 Human gen
c 858	17	1.2	5107	4	AAH18489	AaH18489 Human CDN	c 931	17	1.2	10149	4	AAK75769	AaK75769 Human imm
c 859	17	1.2	5128	9	ABX78274	ABx78274 Human imi	c 932	17	1.2	10772	4	AAK66425	AaK66425 Human imm
c 860	17	1.2	5128	12	ADM41039	Adm41039 Human mam	c 933	17	1.2	10901	4	AAI03236	AaI03236 Human rep
c 861	17	1.2	5132	11	ADN95739	Adn95739 Human BEC	c 934	17	1.2	11524	8	ABX76362	AbX76362 Lung canc
c 862	17	1.2	5132	13	ACN37945	AcN37945 Tumour-as	c 935	17	1.2	11524	11	ADN39475	AdN39475 Cancer/an
c 863	17	1.2	5132	13	ADP23236	ADp23236 PRO poly	c 936	17	1.2	11524	11	ADN38858	AdN38858 Cancer/an
c 864	17	1.2	5175	2	AAZ00022	AAZ00022 osi DNA n	c 937	17	1.2	12354	8	ABV76801	AbV76801 Nucleotid
c 865	17	1.2	5175	12	ADN07071	Adn07071 Neurospor	c 938	17	1.2	12638	4	AAK70641	AaK70641 Human imm
c 866	17	1.2	5193	8	ABV76804	ABv76804 Human nuc	c 939	17	1.2	15059	13	ADP55625	AdP55625 Human PRO
c 867	17	1.2	5203	5	AA584366	AA584366 DNA enco	c 940	17	1.2	15202	2	AAZ28371	AaZ28371 Human ini
c 868	17	1.2	5316	6	ABL68498	ABL68498 Kidney ca	c 941	17	1.2	15295	10	ABX77181	AbX77181 Genomic D
c 869	17	1.2	5316	6	ABL66912	ABL66912 Lung canc	c 942	17	1.2	16720	6	ABL32414	AbL32414 Human imm
c 870	17	1.2	5316	10	ADO15873	Ado15873 Leukaemia	c 943	17	1.2	16720	6	AA561118	Aa561118 Human gen
c 871	17	1.2	5316	12	ADO19287	Ado19287 Human PRO	c 944	17	1.2	16738	4	AAK70864	AaK70864 Human imm
c 872	17	1.2	5316	13	ADP25668	ADp25668 Breast ca	c 945	17	1.2	16946	5	ABA20324	AbA20324 Human ner
c 873	17	1.2	5316	13	ADP54353	ADp54353 Human PRO	c 946	17	1.2	20001	13	ACN37208	AcN37208 Human per
c 874	17	1.2	5319	6	ABN83974	ABn83974 Human gen	c 947	17	1.2	20693	4	ABL16740	AbL16740 Drosophi
c 875	17	1.2	5320	4	AAH57557	AaH57557 Human bra	c 948	17	1.2	23241	4	AAK87225	AaK87225 Human imm
c 876	17	1.2	5338	6	ABZ35279	ABz35279 Human gen	c 949	17	1.2	23241	4	AAK84291	AaK84291 Human imm
c 877	17	1.2	5344	4	AAH14375	AaH14375 Human CDN	c 950	17	1.2	25756	10	AD63866	Ad63866 Human gen
c 878	17	1.2	5362	2	AAZ02980	AAZ02980 Human IL-	c 951	17	1.2	25756	10	AD63863	Ad63863 Human gen
c 879	17	1.2	5393	10	ADL15058	ADl15058 Human mal	c 952	17	1.2	25970	6	ABQ75118	AbQ75118 Human SMS
c 880	17	1.2	5420	4	ABL11538	ABL11538 Drosophi	c 953	17	1.2	26016	2	AA534624	Aa534624 Human fla
c 881	17	1.2	5421	12	ADQ25213	AdQ25213 Human sof	c 954	17	1.2	27289	5	AA34624	Aa34624 Human DNA
c 882	17	1.2	5465	5	AA579378	Aa579378 DNA enco	c 955	17	1.2	27811	10	ABX77186	AbX77186 Genomic D
c 883	17	1.2	5467	4	AAH98343	AaH98343 Human EST	c 956	17	1.2	28506	6	ABK90191	AbK90191 Human fla
c 884	17	1.2	5468	4	AAH98411	AaH98411 Human EST	c 957	17	1.2	28564	10	AD63874	Ad63874 Human gen
c 885	17	1.2	5495	12	ADQ21577	AdQ21577 Human sof	c 958	17	1.2	28772	6	ABK83555	AbK83555 Human cDN
c 886	17	1.2	5495	13	ADR52991	ADR52991 Drug ther	c 959	17	1.2	28772	12	ADQ19885	AdQ19885 Human sof
c 887	17	1.2	5599	6	ABQ93376	ABq93376 Human CDN	c 960	17	1.2	29340	13	ABD33482	AbD33482 Human can
c 888	17	1.2	5697	2	AAZ00023	AAZ00023 osi genom	c 961	17	1.2	30196	6	ABQ75119	AbQ75119 Human tum
c 889	17	1.2	5697	12	ADN07072	Adn07072 Neurospor	c 962	17	1.2	31314	4	AAI37510	AaI37510 Human mus
c 890	17	1.2	5701	4	ABL09200	ABL09200 Drosophi	c 963	17	1.2	31314	8	ABX60498	AbX60498 cDNA enco
c 891	17	1.2	5816	11	ACN91561	AcN91561 Breast ca	c 964	17	1.2	31314	12	ADJ31248	AdJ31248 Human mus
c 892	17	1.2	5972	13	ADP55023	ADp55023 Human PRO	c 965	17	1.2	31718	4	AAK90359	AaK90359 Human dig
c 893	17	1.2	5994	12	ADQ97216	AdQ97216 Human can	c 966	17	1.2	31718	4	AAK90360	AaK90360 Human dig
c 894	17	1.2	6034	6	ABQ60978	ABq60978 Human mRN	c 967	17	1.2	31718	4	AAK73104	AaK73104 Human imm
c 895	17	1.2	6063	2	AAQ37205	AAq37205 Delta-ami	c 968	17	1.2	31718	4	AAK87573	AaK87573 Human imm
c 896	17	1.2	6121	3	AAA07779	AAA07779 DNA seque	c 969	17	1.2	31718	4	AAK73120	AaK73120 Human imm

Db 481 CGGGAATCTTCACTACAGACCAACCAATAGATGGCTACAAATTTGGTCTCTCCAGC 540
QY 541 TCATTAGATATTCAGACTTTTATAGGAGATCCACTAGAAAACAGGTCTCTTGAACAATTT 600
Db 541 TCATTAGATATTCAGACTTTTATAGGAGATCCACTAGAAAACAGGTCTCTTGAACAATTT 600
QY 601 GTTCAGCCGCTGGAGAAATGAATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 660
Db 601 GTTCAGCCGCTGGAGAAATGAATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 660
QY 661 CATCTCTGGACAGTCCCACTCTCTTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACT 720
Db 661 CATCTCTGGACAGTCCCACTCTCTTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACT 720
QY 721 TCATCTCTAGGGTCTCTAGGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 780
Db 721 TCATCTCTAGGGTCTCTAGGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 780
QY 781 CCTGCTGATGCTCTCACTTAAATCCCACTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Db 781 CCTGCTGATGCTCTCACTTAAATCCCACTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
QY 841 AGCCCACTGGATAAATCTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900
Db 841 AGCCCACTGGATAAATCTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900
QY 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATTAATTAATTAATTAATTA 960
Db 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATTAATTAATTAATTAATTA 960
QY 961 GGCCTAATTCACAGATGACATCAAGTCCCACTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
Db 961 GGCCTAATTCACAGATGACATCAAGTCCCACTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
QY 1021 CTAGTGGTGGTCTTCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080
Db 1021 CTAGTGGTGGTCTTCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080
QY 1081 TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAACTTTCGAGTGGCGCTG 1140
Db 1081 TTCCGAATGCAAGGGGCGCTTCCGCAAGTCTCAGAGCAAACTTTCGAGTGGCGCTG 1140
QY 1141 GTGGTGGTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
Db 1141 GTGGTGGTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
QY 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1260
Db 1201 TTGCTTACTGACCCAGAACTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1260
QY 1261 ATTGCTTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1261 ATTGCTTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
QY 1321 GATTTTGAAGAAAGCAGGAGGAGTCCATTCAGGGAATCTCGAGGAGCCTTTCAGTGAG 1380
Db 1321 GATTTTGAAGAAAGCAGGAGGAGTCCATTCAGGGAATCTCGAGGAGCCTTTCAGTGAG 1380
QY 1381 GAGCTCACAGCTTCCACCACTGTCTTCCCTCAAACTATGTCTTCAAGAAATAGTATAGTATAGT 1440
Db 1381 GAGCTCACAGCTTCCACCACTGTCTTCCCTCAAACTATGTCTTCAAGAAATAGTATAGTATAGT 1440
QY 1441 ACTGTGTGA 1449
Db 1441 ACTGTGTGA 1449

RESULT 2

ACA64730

ID ACA64730 standard; DNA; 1449 BP.

XX

ACA64730;

XX

DT 18-JUN-2003 (first entry)
XX Chemoattractant gene.
DE Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;
XX apoptosis; gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
XX Unidentified.
XX US2002177551-A1.
XX 28-NOV-2002.
XX 30-MAY-2001; 2001US-00870759.
XX 31-MAY-2000; 2000US-0208128P.
XX (TERM/) TERMAN D S.
XX Terman DS;
XX WPI; 2003-361759/34.
XX P-PSDB; ABU79122.
XX A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.
XX Example 2; Page; 167pp; English.
XX The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phospholipolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidal APC population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipid to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The

PR 19-DEC-2000; 2000US-0257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPI: 2003-046718/04.
 XX P-PSDB; ABP81797.
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABP42523 to ABP42869 encode
 CC GPCR proteins given in ABP1675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 1449; DB 8; Length 1449;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGCTCTTCTGCTGAGACCAATTCACCTGACCTACTCTACAGCCATGGATGAG 60
 DB 1 ATGGCGCTCTTCTGCTGAGACCAATTCACCTGACCTACTCTACAGCCATGGATGAG 60
 QY 61 CCCACAGTAATCTCTCCATGCTGATCTCTACGCTTACTTTTACTGGGATGCGAGGC 120
 DB 61 CCCACAGTAATCTCTCCATGCTGATCTCTACGCTTACTTTTACTGGGATGCGAGGC 120
 QY 121 AATGGCGTGGTCTGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 180
 DB 121 AATGGCGTGGTCTGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 180
 QY 181 TTCTCTCAGCTACCTCTGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
 DB 181 TTCTCTCAGCTACCTCTGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
 QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGCTTCTATGCAAGCTCATCCCTCC 300
 DB 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGCTTCTATGCAAGCTCATCCCTCC 300
 QY 301 ATCATTTGCTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGCATAGCTGATGCG 360
 DB 301 ATCATTTGCTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGCATAGCTGATGCG 360
 QY 361 TGTCTTGTGGTATTCAAGCCAAATCTGGGTGTCAGAAATCATGCAATGTAGGGATGGCCTGC 420

DB 361 TGTCTTGTGGTATTCAAGCCAAATCTGGGTGTCAGAAATCATGCAATGTAGGGATGGCCTGC 420
 QY 421 TCTATCTGTGGATGATCTCTGGGTGGTGGCTTTTGTGATGTGCATTTCTGTGTCTGTGTAC 480
 DB 421 TCTATCTGTGGATGATCTCTGGGTGGTGGCTTTTGTGATGTGCATTTCTGTGTCTGTGTAC 480
 QY 481 CGGGAATCTTCACTACAGACCAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 DB 481 CGGGAATCTTCACTACAGACCAACATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAACTT 600
 DB 541 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAACTT 600
 QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTCCAAACAAATGAT 660
 DB 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTCCAAACAAATGAT 660
 QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 DB 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 QY 721 TCACCTCCCTAGGGTCTCTGCTAGTTAACTAGTCAAAATCTGATTTCTAAATGATTTAAA 780
 DB 721 TCACCTCCCTAGGGTCTCTGCTAGTTAACTAGTCAAAATCTGATTTCTAAATGATTTAAA 780
 QY 781 CCTGCTGATGTGCTCTCACTAAATCCCAAGTGGTTCCTTATTTGAAGATCAAGAAACC 840
 DB 781 CCTGCTGATGTGCTCTCACTAAATCCCAAGTGGTTCCTTATTTGAAGATCAAGAAACC 840
 QY 841 AGCCACCTGGATTAATCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
 DB 841 AGCCACCTGGATTAATCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT 900
 QY 901 TCTAGCAATCTCTCTAGAGTCTGAGTCAACAGGTTTCCAGGATTTATTACAAATTTA 960
 DB 901 TCTAGCAATCTCTCTAGAGTCTGAGTCAACAGGTTTCCAGGATTTATTACAAATTTA 960
 QY 961 GGCCAAATTCACAGATGACGATCAAGTGCCAAACCCCTCGTGGCAATTAACGATCACTAGG 1020
 DB 961 GGCCAAATTCACAGATGACGATCAAGTGCCAAACCCCTCGTGGCAATTAACGATCACTAGG 1020
 QY 1021 CTAGTGTGGTGTCTGCTGCTGCTCTGTTTATCATGATAGCTGTTTCAAGCTTCAATGTC 1080
 DB 1021 CTAGTGTGGTGTCTGCTGCTGCTCTGTTTATCATGATAGCTGTTTCAAGCTTCAATGTC 1080
 QY 1081 TTCCGAATGCAAGAGGGGCGCTTCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 DB 1081 TTCCGAATGCAAGAGGGGCGCTTCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
 QY 1141 GTGGTGGTGGTGTCTTTCTTGTCTGCTGGACTCCATACCAATTTTGGAGTCTCTGCA 1200
 DB 1141 GTGGTGGTGGTGTCTTTCTTGTCTGCTGGACTCCATACCAATTTTGGAGTCTCTGCA 1200
 QY 1201 TTGCTTACTACCCAGAAAACTCCCTTGGGAAAAACTCTGATGTCTGCGGATCATGTATGC 1260
 DB 1201 TTGCTTACTACCCAGAAAACTCCCTTGGGAAAAACTCTGATGTCTGCGGATCATGTATGC 1260
 QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCTTATGCTTGGGAAA 1320
 DB 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTATGCTTATGCTTGGGAAA 1320
 QY 1321 GATTTTAGGAAGAAAGCAAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
 DB 1321 GATTTTAGGAAGAAAGCAAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
 QY 1381 GAGTCTACACCTTCCACCCACTGCTCCCTCAAACTGTCATTTCAGAAAGAAATAGTACA 1440
 DB 1381 GAGTCTACACCTTCCACCCACTGCTCCCTCAAACTGTCATTTCAGAAAGAAATAGTACA 1440
 QY 1441 ACTGTGTGA 1449
 |||||

Db	1441	ACTGTGTGA 1449	Db	241	CACTTGGCTCTCCAGGACAGTGGCCCTAGGCGAGTTCTTATGCAAGCTCATCCCTCC	300
RESULT 4						
ADF43377						
ID	ADF43377	standard; DNA; 1449 BP.	Qy	301	ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATTTAGCTGGATGCG	360
XX	XX		Db	301	ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATTTAGCTGGATGCG	360
AC	ADF43377;		Qy	361	TGCTCTGTGTATTCAAGCCCAATCTGGTGTGTCAGAAATCATGCAATGTAGGATGGCCCTGC	420
XX	XX		Db	361	TGCTCTGTGTATTCAAGCCCAATCTGGTGTGTCAGAAATCATGCAATGTAGGATGGCCCTGC	420
DT	12-FEB-2004	(first entry)	Qy	421	TCTATCTGTGATGTATCTGGGTGGTCTTTTGTGATGTGTCATTTCTGTGTTTCTGTGAC	480
DE	XX	Chemoattractant polynucleotide seq id 97.	Db	421	TCTATCTGTGATGTATCTGGGTGGTCTTTTGTGATGTGTCATTTCTGTGTTTCTGTGAC	480
XX	XX	receptor; lipid-based tumour associated antigen; cytostatic;	Qy	481	CGGGAATCTTCACTACAGACAACCAATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540
KW	antimicrobial; gene therapy; neoplastic disease; tumour; cancer;		Db	481	CGGGAATCTTCACTACAGACAACCAATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540
KW	infectious disease; chemoattractant; ds.					
XX	OS	Unidentified.				
XX	PN	US2003157113-A1.	Qy	541	TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT	600
XX	PD	21-AUG-2003.	Db	541	TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT	600
XX	PF	28-DEC-2000; 2000US-00751708.	Qy	601	GTTCAGCGCTCGAGAAAAATGAATGATAGTGTAGATCCTTCTCTTTTCCAAACAAATGAT	660
XX	PR	28-DEC-1999; 99US-0173371P.	Db	601	GTTCAGCGCTCGAGAAAAATGAATGATAGTGTAGATCCTTCTCTTTTCCAAACAAATGAT	660
XX	PA	(TERM/) Terman D S.	Qy	661	CATCCTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAGACCTTCTTCAGAT	720
XX	PI	Terman DS;	Db	661	CATCCTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAGACCTTCTTCAGAT	720
XX	XX		Qy	721	TCACCTCCCTAGGGTCTCTGCTAGGTAAACAACTCAAAATCTGATTTCTTAATGATTTTAAA	780
DR	WPI; 2003-787326/74.		Db	721	TCACCTCCCTAGGGTCTCTGCTAGGTAAACAACTCAAAATCTGATTTCTTAATGATTTTAAA	780
DR	P-PSDB; ADF43378.		Qy	781	CCTGCTGATGTGTCTCACCTTAAATCCCAAGTGGTTCCTTATTTGAAGATCACGAAACC	840
PT	New receptor in a mammalian cell that inhibits regular activation by		Db	781	CCTGCTGATGTGTCTCACCTTAAATCCCAAGTGGTTCCTTATTTGAAGATCACGAAACC	840
PT	receptors specific for lipid-based tumor associated antigens, useful for		Qy	841	AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT	900
PT	treating a neoplastic disease or tumor, and infectious diseases.		Db	841	AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT	900
XX	Example 3; SEQ ID NO 97; 151pp; English.		Qy	901	TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTTACAATTTA	960
XX	The invention describes a receptor in a mammalian cell that inhibits		Db	901	TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTTACAATTTA	960
CC	regular activation by receptors specific for lipid-based tumour		Qy	961	GGCCAAATTCACAGATGACGATCAAGTGCACACCCCTCGTGGCAATAACGATCACTAGG	1020
CC	associated antigen. The receptor has cytostatic and antimicrobial		Db	961	GGCCAAATTCACAGATGACGATCAAGTGCACACCCCTCGTGGCAATAACGATCACTAGG	1020
CC	properties and is suitable for use in gene therapy. The receptors,		Qy	1021	CTAGTGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCATTTGTC	1080
CC	methods and compositions are useful for treating a neoplastic disease or		Db	1021	CTAGTGTGGGTTTCTGCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCATTTGTC	1080
CC	tumour (cancer), and infectious diseases. This sequence represents a		Qy	1081	TTCCGAATGCAAGGGGCGCTTGGCCAAAGTCTCAGACAAAACCTTTGAGTGGCCGTG	1140
CC	chemoattractant polynucleotide, a cell surface moiety, the DNA of which		Db	1081	TTCCGAATGCAAGGGGCGCTTGGCCAAAGTCTCAGACAAAACCTTTGAGTGGCCGTG	1140
CC	can be transfected into a cell with superantigen DNA to generate		Qy	1141	GTGGTGTGGTGTCTTTTCTGTGTGGAATCCATACCAATTTTGGAGTCTCTGTCA	1200
CC	antitumour immunity.		Db	1141	GTGGTGTGGTGTCTTTCTTCTGTGTGGAATCCATACCAATTTTGGAGTCTCTGTCA	1200
XX	Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;		Qy	1201	TTGCTTACTGACCCGAAACTCCCTTGGGAAAACCTGATGTCCTGGGATCATGTATGC	1260
XX	Query Match 100.0%; Score 1449; DB 10; Length 1449;		Db	1201	TTGCTTACTGACCCGAAACTCCCTTGGGAAAACCTCTGATGTCCTGGATCATGTATGC	1260
XX	Best Local Similarity 100.0%; Pred. No. 0;		Qy	1261	ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCCTCTTGGGAAA	1320
XX	Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db	1261	ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCCTCTTGGGAAA	1320
Qy	1	ATGGCGCTCTTCTGCTGAGACCAATTCACCTGACCTACTCTACAGCCATGGATGAG	60			
Db	1	ATGGCGCTCTTCTGCTGAGACCAATTCACCTGACCTACTCTACAGCCATGGATGAG	60			
Qy	61	CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTACTTTTACTGGGATGCGAGGC	120			
Db	61	CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTACTTTTACTGGGATGCGAGGC	120			
Qy	121	AATGGCTGTGCTGTGGGTGGCTGGCTGAGATGCGCGGACAGTGAACAATTTGG	180			
Db	121	AATGGCTGTGCTGTGGGTGGCTGGCTGAGATGCGCGGACAGTGAACAATTTGG	180			
Qy	181	TTCTCCACCTACCTTGGCGGACCTCTCTGCTGCTCTCTGCTTCTGCTGCTGCT	240			
Db	181	TTCTCCACCTACCTTGGCGGACCTCTCTGCTGCTCTCTGCTTCTGCTGCTGCT	240			
Qy	241	CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGGTTCTTATGCAAGCTCATCCCTCC	300			

Db 601 GTTACGCCCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTTCCAAACAAATGAT 660
Qy 661 CATCTTGGACAGTCCCACTGCTTTCAACCTCAACATTTCAAGACCTTTCGCAGAT 720
Db 661 CATCTTGGACAGTCCCACTGCTTTCAACCTCAACATTTCAAGACCTTTCGCAGAT 720
Qy 721 TCATCTCCCTAGGGTTCTGCTAGGTTAAACAGTCAAAATCTGTATTTAAATGATTTAAA 780
Db 721 TCATCTCCCTAGGGTTCTGCTAGGTTAAACAGTCAAAATCTGTATTTAAATGATTTAAA 780
Qy 781 CCTGCTGATGCTCTACCTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAC 840
Db 781 CCTGCTGATGCTCTACCTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAC 840
Qy 841 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCAATTTAAAGCTCTCCCTAGCGCT 900
Db 841 AGCCCACTGGATACTCTGATGCTTTCTCTCTACTCAATTTAAAGCTCTCCCTAGCGCT 900
Qy 901 TCTAGCAATCTCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATT 960
Db 901 TCTAGCAATCTCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATT 960
Qy 961 GGCCAAATCACAGATGACATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1020
Db 961 GGCCAAATCACAGATGACATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1020
Qy 1021 CTAGTGGTGGGTTTCTCTGCTGCCCTCTGTATCATGATGAGCTGTTACAGCTTCAATGTC 1080
Db 1021 CTAGTGGTGGGTTTCTCTGCTGCCCTCTGTATCATGATGAGCTGTTACAGCTTCAATGTC 1080
Qy 1081 TTCCGAATGCAAAAGGGCGGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
Db 1081 TTCCGAATGCAAAAGGGCGGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
Qy 1141 GTGTTGGTGGCTGCTTTCTGCTGGACTCATACCAATTTTGGAGTCTCTGCA 1200
Db 1141 GTGTTGGTGGCTGCTTTCTGCTGGACTCATACCAATTTTGGAGTCTCTGCA 1200
Qy 1201 TTGCTTACTGACCCAGAACTCCCTTGGGAAAACCTCTGATGCTCTGGGATCATGTATGC 1260
Db 1201 TTGCTTACTGACCCAGAACTCCCTTGGGAAAACCTCTGATGCTCTGGGATCATGTATGC 1260
Qy 1261 ATTGCTCTAGCATGTCGCAATAGTGTCTTTAATCCCTTTCCTTTATGCCCCTCTTGGGAAA 1320
Db 1261 ATTGCTCTAGCATGTCGCAATAGTGTCTTTAATCCCTTTCCTTTATGCCCCTCTTGGGAAA 1320
Qy 1321 GATTTTGGGAAGAGGAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
Db 1321 GATTTTGGGAAGAGGAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
Qy 1381 GAGCTCACACGTTCCACCCACTGTCCTTCAACCAATGTCATTTCAAGAAAGAAATAGTACA 1440
Db 1381 GAGCTCACACGTTCCACCCACTGTCCTTCAACCAATGTCATTTCAAGAAAGAAATAGTACA 1440
Qy 1441 ACTGTGTGA 1449
Db 1441 ACTGTGTGA 1449

RESULT 6

ID ADS09203 standard; DNA; 1449 BP.
XX AC ADS09203;
XX DT 16-DEC-2004 (first entry)
XX DE Complement component 3a receptor 1, C3AR1, coding sequence, SEQ ID 1.
XX KW Antianemic; Antiinflammatory; Cardiovascular; Gastrointestinal;
KW Hepatotropic; Neuroprotective; Respiratory; Gene therapy;
KW Cardiovascular disease; Gastrointestinal disease; liver disease;

KW inflammatory disease; hematological disease; respiratory disease;
KW neurological disease; complement component 3a receptor 1; C3AR1;
XX C3a anaphylatoxin receptor; G protein coupled receptor; human; gene; ds.
XX Homo sapiens.
FH Key Location/Qualifiers
CDS 1..1449
FT /*tag= a
FT /product= "C3AR1"
FT /transl_except= (pos:607..609,aa:Arg)
XX WO2004082566-A2.
XX 30-SEP-2004.
XX 04-MAR-2004; 2004WO-EP002173.
XX 17-MAR-2003; 2003EP-00005468.
XX (FARB) BAYER HEALTHCARE AG.
XX Golz S, Brueggemeier U, Summer H;
XX WPI; 2004-690917/67.
DR P-ESDB; ADS09204.
DR GENBANK; NM_004054.
XX Screening for agents for treating e.g., cardiovascular, liver, or
PT neurological diseases, comprises detecting agents which modulate the
PT expression or activity of the G protein coupled receptor C3AR1
XX (complement component 3a receptor 1).
PS Disclosure; SEQ ID NO 1; 121bp; English.
XX The present invention relates to a method (M1) for screening for
CC therapeutic agents for treating a cardiovascular, gastrointestinal,
CC liver, inflammatory, hematological, respiratory or neurological disease
CC in a mammal. The method comprises detecting binding of a test compound to
CC a complement component 3a receptor 1 (C3AR1) polypeptide (ADS09204) or
CC polynucleotide (ADS09203), or detecting an affect on C3AR1 activity.
CC C3AR1 (also known as C3a anaphylatoxin receptor, is a seven transmembrane
CC G protein coupled receptor. Compositions comprising agents identified by
CC M1 or C3AR1 polynucleotides and polypeptides are useful for treating the
CC diseases. The present sequence is the coding sequence for human C3AR1,
CC used in the method of the invention.
SQ Sequence 1449 BP; 331 A; 380 C; 310 G; 428 T; 0 U; 0 Other;
Query Match 100.0%; Score 1449; DB 13; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGCTTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAATGAG 60
Db 1 ATGGCGCTTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGAATGAG 60
Qy 61 CCCCCAGTAATTTCTCCATGCTCATTTCTAGCCCTTACTTTTTTACTGGGATTGCCAGGC 120
Db 61 CCCCCAGTAATTTCTCCATGCTCATTTCTAGCCCTTACTTTTTTACTGGGATTGCCAGGC 120
Qy 121 AATGGGCTGGTGTGTTGGGTGGCTGCTGAAGATGACGGGACAGTGAAACAAATTTGG 180
Db 121 AATGGGCTGGTGTGTTGGGTGGCTGCTGAAGATGACGGGACAGTGAAACAAATTTGG 180
Qy 181 TTCTTCCACCTCACCTTGGCGGACCTCTCTGCTGCCCTCTCTTCTCGCTGGCT 240
Db 181 TTCTTCCACCTCACCTTGGCGGACCTCTCTGCTGCCCTCTCTTCTCGCTGGCT 240
Qy 241 CACTTGGCTCTCCAGGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 300
Db 241 CACTTGGCTCTCCAGGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 300

QY 301 ATCATGTCCTCAACATGTTGGCAGTGTCTTCTGCTTACTGCAATAGCCTGGATCGC 360
 Db 301 ATCATGTCCTCAACATGTTGGCAGTGTCTTCTGCTTACTGCAATAGCCTGGATCGC 360
 QY 361 TGTCTTGTGGTATTCAAGCAATCTGGTGTGAGATCATCGCAATGAGGATGCGCTGC 420
 Db 361 TGTCTTGTGGTATTCAAGCAATCTGGTGTGAGATCATCGCAATGAGGATGCGCTGC 420
 QY 421 TCTATCTGTGGATGATCTGGGTGTGCTTTTGTGATGTGCATTCCTGTGTGTGTAC 480
 Db 421 TCTATCTGTGGATGATCTGGGTGTGCTTTTGTGATGTGCATTCCTGTGTGTGTAC 480
 QY 481 CGGGAATCTTCACTACAGCAACATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 540
 Db 481 CGGGAATCTTCACTACAGCAACATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 540
 QY 541 TCATTAGATTTCCAGACTTTTATCGAGATCCACTAGAAAACAGCTCTCTGAAAACATT 600
 Db 541 TCATTAGATTTCCAGACTTTTATCGAGATCCACTAGAAAACAGCTCTCTGAAAACATT 600
 QY 601 GTTCAGCCGCTGGAGAAATGAATAGTTAGATCTTCTCTTTTCCAAACAAATGAT 660
 Db 601 GTTCAGCCGCTGGAGAAATGAATAGTTAGATCTTCTCTTTTCCAAACAAATGAT 660
 QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 Db 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAGACCTTCTGCAGAT 720
 QY 721 TCACCTCCCTAGGGGTTCTGAGTTTAAACAGTCAAAATCTGATTTCTAATGATTTAAA 780
 Db 721 TCACCTCCCTAGGGGTTCTGAGTTTAAACAGTCAAAATCTGATTTCTAATGATTTAAA 780
 QY 781 CCTGCTGATGTGCTCACTAAATCCCAAGTGGGTTTCTTATGAAAGATCAGAAACC 840
 Db 781 CCTGCTGATGTGCTCACTAAATCCCAAGTGGGTTTCTTATGAAAGATCAGAAACC 840
 QY 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTAGCGCT 900
 Db 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTAGCGCT 900
 QY 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGATATTATCAATTTA 960
 Db 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGATATTATCAATTTA 960
 QY 961 GGCCAAATTCAGATGACATCAAGTGCCAAACCCCTCGTGGCAATTAACGATCACTAGG 1020
 Db 961 GGCCAAATTCAGATGACATCAAGTGCCAAACCCCTCGTGGCAATTAACGATCACTAGG 1020
 QY 1021 CTAGTGTGGGTTTCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCAATGTC 1080
 Db 1021 CTAGTGTGGGTTTCTGCTGCTCTGTTATCATGATAGCTGTTACAGCTTCAATGTC 1080
 QY 1081 TTCCCAATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
 Db 1081 TTCCCAATGCAAAAGGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
 QY 1141 GTGTGTGGTGTCTTTCTTGTCTGTGAGTCCATACCAATTTTGGAGTCTCTGTCA 1200
 Db 1141 GTGTGTGGTGTCTTTCTTGTCTGTGAGTCCATACCAATTTTGGAGTCTCTGTCA 1200
 QY 1201 TTGCTTACTGACCAAGAACTCCCTTGGGAAACCTCTGATGTCTGGGATCATGTATGC 1260
 Db 1201 TTGCTTACTGACCAAGAACTCCCTTGGGAAACCTCTGATGTCTGGGATCATGTATGC 1260
 QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTTAACTCCCTTATGCTTATGCTTGGGAAA 1320
 Db 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTTAACTCCCTTATGCTTATGCTTGGGAAA 1320
 QY 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTTAGGGAATTTCTGGAGGACGCTTCAAGTGA 1380
 Db 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTTAGGGAATTTCTGGAGGACGCTTCAAGTGA 1380
 QY 1381 GAGCTCACACGTTCCACCACTGTCTCCCTCAAAACATATGTCATTTTCAGAAAGAAATAGTACA 1440

Db 1381 GAGCTCACACGTTCCACCACTGTCTCCCTCAAAACATATGTCATTTTCAGAAAGAAATAGTACA 1440
 QY 1441 ACTGTGTGA 1449
 Db 1441 ACTGTGTGA 1449
 RESULT 7
 ADC86208
 ID ADC86208 standard; DNA; 1849 BP.
 XX
 AC ADC86208;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 Human GPCR gene SEQ ID NO:661.
 DE
 ds; gene; human; GPCR;
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1270724-A2.
 XX
 PD 02-JAN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Asai K, Akiyama Y, Aburatani H;
 XX
 DR WPI; 2003-315783/31.
 DR P-FSDB; ADC86209.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
 PT
 XX
 PS Claim 1; SEQ ID NO 661; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the invention.
 CC
 XX
 SQ Sequence 1849 BP; 462 A; 451 C; 395 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1449; DB 10; Length 1849;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGCTTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGAATGAG 60
 Db 201 ATGGCGCTTTTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGAATGAG 260
 QY 61 CCCCCAGTAATTCCTCCATGTCATTCCTCAGCCCTTACTTTTACTGGGATTCGAGGC 120
 Db 261 CCCCCAGTAATTCCTCCATGTCATTCCTCAGCCCTTACTTTTACTGGGATTCGAGGC 320
 QY 121 AATGGCTGTGTGTGTGGTGGCTGAGATGAGCGGACAGTGAACACAAATTTGG 180
 Db 321 AATGGCTGTGTGTGTGGTGGCTGAGATGAGCGGACAGTGAACACAAATTTGG 380
 QY 181 TTCCTCCACCTCACCTTGGCGGACCTCTCTGTGCTCTCTCTGCTGCTCTCTGCTGCTGCT 240

Db 381 TTCTCCACCTACCTTGGGACCTCTCTGCTGCTCTCTGCTCTCTGCTCTCTGCTGCT 440
Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTACCGCAGGTTCCTATGCAAGCTCATCCCTCC 300
Db 441 CACTTGGCTCTCCAGGACAGTGGCCCTACCGCAGGTTCCTATGCAAGCTCATCCCTCC 500
Qy 301 ATCATTTGCTCCAAATGTTTGGCCAGTGTCTCTGCTTACTGCGCATAGCTGATGCG 360
Db 501 ATCATTTGCTCCAAATGTTTGGCCAGTGTCTCTGCTTACTGCGCATAGCTGATGCG 560
Qy 361 TGTCTTGTGGTATTCAGGCAATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC 420
Db 561 TGTCTTGTGGTATTCAGGCAATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC 620
Qy 421 TCTATCTGTGATGATCTGGTGTGCTTTTGTGATGATGATCTCTGCTGCTGCTGAC 480
Db 621 TCTATCTGTGATGATCTGGTGTGCTTTTGTGATGATGATCTCTGCTGCTGCTGAC 680
Qy 481 CGGGAATCTTCACTACAGAACCAATATAGATGCTGCTCAAAATTTGGTCTCTCCAGC 540
Db 681 CGGGAATCTTCACTACAGAACCAATATAGATGCTGCTCAAAATTTGGTCTCTCCAGC 740
Qy 541 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGCTCTCTTGAACAACTT 600
Db 741 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGCTCTCTTGAACAACTT 800
Qy 601 GTTACGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTCTCTCTCTCTCTCT 660
Db 801 GTTACGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTCTCTCTCTCTCTCT 860
Qy 661 CATCTTGGAGAGTCCCACTGCTCTTCCAACTCAAACTTCAAGACCTCTCTGACAT 720
Db 861 CATCTTGGAGAGTCCCACTGCTCTTCCAACTCAAACTTCAAGACCTCTCTGACAT 920
Qy 721 TCATCTCTAGGGTCTCTGCTAGTTAAAGTCAAAATCTGTAATCTTAATGATTTAA 780
Db 921 TCATCTCTAGGGTCTCTGCTAGTTAAAGTCAAAATCTGTAATCTTAATGATTTAA 980
Qy 781 CCTGCTGATGCTCTCACTTAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 981 CCTGCTGATGCTCTCACTTAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
Qy 841 AGCCCACTGGATACTCTGATGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 1041 AGCCCACTGGATACTCTGATGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1100
Qy 901 TCTAGCAATCTCTCTACAGTCTGAGCTACCAAGGTTTCCAGGATTTTCAAAATTA 960
Db 1101 TCTAGCAATCTCTCTACAGTCTGAGCTACCAAGGTTTCCAGGATTTTCAAAATTA 1160
Qy 961 GGCCAAATTCAGATGAGTCAAGTGCACACCCCTCTGCGCAATTAACGATCACTAGG 1020
Db 1161 GGCCAAATTCAGATGAGTCAAGTGCACACCCCTCTGCGCAATTAACGATCACTAGG 1220
Qy 1021 CTAGTGTGGTGTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1221 CTAGTGTGGTGTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1280
Qy 1081 TTCCGAATGCAAGGGCGCTTCTGCAAGTCTCAGACAAACCTTTTGGAGTGGCGGTG 1140
Db 1281 TTCCGAATGCAAGGGCGCTTCTGCAAGTCTCAGACAAACCTTTTGGAGTGGCGGTG 1340
Qy 1141 GTGTGTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1341 GTGTGTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400
Qy 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1260
Db 1401 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1460
Qy 1261 ATTCTCTAGCATCTGCAATAGTGTCTTTTAACTCCCTCTCTCTCTCTCTCTCTCT 1320

Db 1461 ATTCTCTAGCATCTGCCAATAGTTGCTTTTAACTCCCTTCTTATGCCCTCTTGGGAA 1520
Qy 1321 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCGGAGGAGCCCTTCAGTGAG 1380
Db 1521 GATTTTAGAAGAAAGCAAGGAGTCCATTCAGGGAATTCGGAGGAGCCCTTCAGTGAG 1580
Qy 1381 GAGCTCACACCTTCCACCCACTGCTCCCTCAACCAATGTCATTTCAAGAAGAAATAGTACA 1440
Db 1581 GAGCTCACACCTTCCACCCACTGCTCCCTCAACCAATGTCATTTCAAGAAGAAATAGTACA 1640
Qy 1441 ACTGTGTGA 1449
Db 1641 ACTGTGTGA 1649

RESULT 8
AAV03250
ID AAV03250 standard; cDNA; 2040 BP.
XX AC AAV03250;
XX XX
DT 08-JUN-1998 (first entry)
XX Homo sapiens cDNA encoding C3a receptor.
DE C3a receptor; treatment; diagnosis; atherosclerosis; chronic;
KW polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's;
KW disease; acute inflammatory disease; Crohn's disease; food; allergies;
KW non-bronchial allergies; osteoarthritis; osteoporosis; thyroid disease;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 153..1601
FT FT /*tag= a
FT FT /product= "C3a receptor"
XX
PN EP814158-A2.
XX
PD 29-DEC-1997.
XX
PF 17-JUN-1997; 97EP-00304250.
XX
PR 17-JUN-1996; 96US-0019627P.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Ames RS, Bergsma DU, Foley JJ, Kumar C, Sarau HM;
XX
XX WPI; 1998-044336/05.
XX P-PSDB; AAW42376.
XX
XX C3a receptor agonists, antibodies and antagonists - useful for diagnosis
XX of disease related to expression of C3a receptor, e.g. acute inflammatory
XX disease, atherosclerosis, chronic polyarthritis, etc.
XX
XX Disclosure; Fig 1; 43pp; English.
XX
XX The sequence is that encoding the C3a receptor. It can be used in a
XX process for diagnosing a disease or susceptibility to a disease related
XX to expression of the C3a receptor. This process involves determining the
XX presence of a mutation in the nucleic acid sequence encoding the
XX polypeptide, the disease being selected from acute inflammatory disease,
XX atherosclerosis, chronic polyarthritis, systemic vasculitis, multiple
XX sclerosis, Alzheimer's Disease, CNS inflammatory disease, Crohn's
XX Disease, food allergies, non-bronchial allergies, osteoarthritis,
XX Erythematous SLE-associated nephritis, coronary heart disease, Systemic Lupus
XX erythematosus, thyroid disease, rheumatoid arthritis, Behcet's syndrome, juvenile
XX rheumatoid arthritis, Sjogren's syndrome, myasthenia gravis, cerebral
XX lupus, Guillain-Barre syndrome, pemphigus/pemphigoid, phototoxic
XX reactions, vasculitis, post-bypass syndrome, catheter reactions, sepsis,

and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 6365; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 2096 BP; 559 A; 498 C; 439 G; 600 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1449;	DB 12;	Length 2096;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1449;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ATGGCGTCTTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGATGAG	60		
DB 156	ATGGCGTCTTCTGCTGAGACCAATTCACCTGACCTACTCTCACGCCATGGATGAG	215		
QY 61	CCCCAGTAATCTCCATGGTCAATCTCAGCCCTACTTTTACTGGGATGCGAGGC	120		
DB 216	CCCCAGTAATCTCCATGGTCAATCTCAGCCCTACTTTTACTGGGATGCGAGGC	275		
QY 121	AATGGCTGCTGCTGGGTGGCTGGCTGAGAGTGCAGCGACAGTGAACACAAATTTGG	180		
DB 276	AATGGCTGCTGCTGGGTGGCTGGCTGAGAGTGCAGCGACAGTGAACACAAATTTGG	335		
QY 181	TTCTCCACCTCACCTTGGCGGACCTCCTCTGCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT	240		
DB 336	TTCTCCACCTCACCTTGGCGGACCTCCTCTGCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT	395		
QY 241	CACCTGGCTCTCCAGGACAGTGGCCCTACGGCAGTTCTATGCAAGCTATCCCTCC	300		
DB 396	CACCTGGCTCTCCAGGACAGTGGCCCTACGGCAGTTCTATGCAAGCTATCCCTCC	455		
QY 301	ATCATTGCTCAACATGTTGGCCAGTCTCTCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCT	360		
DB 456	ATCATTGCTCAACATGTTGGCCAGTCTCTCTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCT	515		
QY 361	TGCTTGTGGTATTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC	420		
DB 516	TGCTTGTGGTATTCAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC	575		
QY 421	TCTATCTGAGTATCTGGGTGGTGGCTTTTGTGATGTCATCTCTGTTGTGTGATC	480		
DB 576	TCTATCTGAGTATCTGGGTGGTGGCTTTTGTGATGTCATCTCTGTTGTGTGATC	635		
QY 481	CGGGAATCTTCACTACAGAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540		
DB 636	CGGGAATCTTCACTACAGAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC	695		
QY 541	TCATTAGATATCCAGATCTTTATGGAGATCCATGAGAAACACAGTCTCTTTGAAACAT	600		
DB 696	TCATTAGATATCCAGATCTTTATGGAGATCCATGAGAAACACAGTCTCTTTGAAACAT	755		
QY 601	GTTCCAGCGCTGGAGAAATCAATGATAGTATCTCTCTCTTCCAAACAAATGAT	660		
DB 756	GTTCCAGCGCTGGAGAAATCAATGATAGTATCTCTCTCTTCCAAACAAATGAT	815		
QY 661	CATCTTGGACAGTCCCTGCTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGAT	720		
DB 816	CATCTTGGACAGTCCCTGCTCTTCCAACTCAACATTTCAAGACCTTCTGCGAGAT	875		

QY 721	TCATCCCTAGGGTTCCTAGGTAAACAAGTCAAAATCTGTATTTCTAATGATTTAAA	780
DB 876	TCATCCCTAGGGTTCCTAGGTAAACAAGTCAAAATCTGTATTTCTAATGATTTAAA	935
QY 781	CCTGCTGATGGTCTCACCTAAATCCCAAGTGGTTCCTATTGAAGATCACGAAACC	840
DB 936	CCTGCTGATGGTCTCACCTAAATCCCAAGTGGTTCCTATTGAAGATCACGAAACC	995
QY 841	AGCCCATGGATACTCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT	900
DB 996	AGCCCATGGATACTCTGATGCTTTCTCTACTCATTTAAAGCTGTTCCCTAGCGCT	1055
QY 901	TCTAGCAATTCCTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTTACAAATTA	960
DB 1056	TCTAGCAATTCCTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTTACAAATTA	1115
QY 961	GGCCAAATTCAGATGAGTCAAGTGCACACCCCTCTGTCGCAATTAACGATCCTAGG	1020
DB 1116	GGCCAAATTCAGATGAGTCAAGTGCACACCCCTCTGTCGCAATTAACGATCCTAGG	1175
QY 1021	CTAGTGGTGGTTCCTGCTGCTGCTCTGTTATCATGATAGCTGTACAGCTTCATTTGC	1080
DB 1176	CTAGTGGTGGTTCCTGCTGCTGCTCTGTTATCATGATAGCTGTACAGCTTCATTTGC	1235
QY 1081	TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCCAGTGGCCGTG	1140
DB 1236	TTCCGAATGCAAGGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTTCCAGTGGCCGTG	1295
QY 1141	GTGCTGGTGGTCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200
DB 1296	GTGCTGGTGGTCTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1355
QY 1201	TTGCTTACTGACCCAGCAAACTCCCTTGGGAAACTCTGATGCTCTGGATCATGTATGC	1260
DB 1356	TTGCTTACTGACCCAGCAAACTCCCTTGGGAAACTCTGATGCTCTGGATCATGTATGC	1415
QY 1261	ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTTCCCTTTATGCTGCTTGGGAAA	1320
DB 1416	ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTTCCCTTTATGCTGCTTGGGAAA	1475
QY 1321	GATTTTAGAAGAAGCAAGCAGTCCATTGAGGAAATCTGGAGGAGCCCTCAGTGAG	1380
DB 1476	GATTTTAGAAGAAGCAAGCAGTCCATTGAGGAAATCTGGAGGAGCCCTCAGTGAG	1535
QY 1381	GAGCTCACGCTTCCACCCACTGCTCCCTCAAACTGTCATTTCAGAAAGAAATAGTACA	1440
DB 1536	GAGCTCACGCTTCCACCCACTGCTCCCTCAAACTGTCATTTCAGAAAGAAATAGTACA	1595
QY 1441	ACTGTGTA 1449	
DB 1596	ACTGTGTA 1604	

RESULT 10

ADO29820
ID ADO29820 standard; cDNA; 1449 BP.

XX ADO29820;

XX 29-JUL-2004 (first entry)

XX Human GPCR C3AR1 polynucleotide, SEQ ID NO:922.

G protein-coupled receptor; GPCR; drug screening; diagnosis;
transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disorder;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;

Db 322 CACTTGGCTCTCCAGGACAGTGGCCCTAGCCAGGTTCTATGCAAGCTCATCCCTCC 381
QY 301 ATCAATGCTCTCAACATGTTCCAGTGTCTTCCTGCTTACTGCAATAGCCTGATGCG 360
Db 382 ATCAATGCTCTCAACATGTTCCAGTGTCTTCCTGCTTACTGCAATAGCCTGATGCG 441
QY 361 TGTCTTGTGGTATTCAAGCCATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC 420
Db 442 TGTCTTGTGGTATTCAAGCCATCTGGTGTGAGATCATCGCAATGTAGGATGCGCTGC 501
QY 421 TCTATCTGTGGATGATCTGGGTGGTGGCTTTTGTGATGTGATTCCTGTGTTCTGTGTAC 480
Db 502 TCTATCTGTGGATGATCTGGGTGGTGGCTTTTGTGATGTGATTCCTGTGTTCTGTGTAC 561
QY 481 CGGGAAATCTTCACATACAGAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 562 CGGGAAATCTTCACATACAGAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGCTCTCTTGAACATT 600
Db 622 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGCTCTCTTGAACATT 681
QY 601 GTTCAGCGCTCGGAGAAATGAATAGATGTAGATCCTTCTCTTTTCAAAACAATGAT 660
Db 682 GTTCAGCGCTCGGAGAAATGAATAGATGTAGATCCTTCTCTTTTCAAAACAATGAT 741
QY 661 CATCTTGGAGATGCTCCACTCTCTTCCAACTCCAACTCAAAATTTCAAGACCTTCTCGAGAT 720
Db 742 CATCTTGGAGATGCTCCACTCTCTTCCAACTCCAACTCAAAATTTCAAGACCTTCTCGAGAT 801
QY 721 TCACCTCCCTAGGGTCTGTAGTATTACAACTCAAAATCTGTATTTCTAAATGATTAA 780
Db 802 TCACCTCCCTAGGGTCTGTAGTATTACAACTCAAAATCTGTATTTCTAAATGATTAA 861
QY 781 CTGCTGTGATGTGCTCTCACTAAATCCCGAGTGGTTCCTTATTTGAAGATCACGAAACC 840
Db 862 CTGCTGTGATGTGCTCTCACTAAATCCCGAGTGGTTCCTTATTTGAAGATCACGAAACC 921
QY 841 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCACTTTAAAGCTGTTCCTAGCGCT 900
Db 922 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCACTTTAAAGCTGTTCCTAGCGCT 981
QY 901 TCTAGCAATTCCTTCTAGAGTCTGAGCTTACACAGGTTTCCAGGATTTATCAATTTA 960
Db 982 TCTAGCAATTCCTTCTAGAGTCTGAGCTTACACAGGTTTCCAGGATTTATCAATTTA 1041
QY 961 GGCCTAATTCACAGATGACATCAAGTGCCAAACACCCCTGCTGGCAATACGATCACTAGG 1020
Db 1042 GGCCTAATTCACAGATGACATCAAGTGCCAAACACCCCTGCTGGCAATACGATCACTAGG 1101
QY 1021 CTAGTGTGGTGTCTCTGCTGCCCTCTGTTATCATGATAGCCTGTTCAGCTTCATTGTC 1080
Db 1102 CTAGTGTGGTGTCTCTGCTGCCCTCTGTTATCATGATAGCCTGTTCAGCTTCATTGTC 1161
QY 1081 TTCCGAATTCAGAGGGGCGCTTCGCCAGTCTCAGGCAAACTTTCGAGTGGCGCTG 1140
Db 1162 TTCCGAATTCAGAGGGGCGCTTCGCCAGTCTCAGGCAAACTTTCGAGTGGCGCTG 1221
QY 1141 GTGGTGGTGGCTGTCTTCTCTGCTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1200
Db 1222 GTGGTGGTGGCTGTCTTCTCTGCTGGACTCCATACCAATTTTGGAGTCTCTGTCA 1281
QY 1201 TTGCTTACTGACCCAGAACTCCCTTGGGAAACTCTGATGTCCTGGGATCATGTATGC 1260
Db 1282 TTGCTTACTGACCCAGAACTCCCTTGGGAAACTCTGATGTCCTGGGATCATGTATGC 1341
QY 1261 ATTGCTTAGCATCTGCCAATAGTGTCTTTATCCCTTATGCTCCCTCTTGGGAA 1320
Db 1342 ATTGCTTAGCATCTGCCAATAGTGTCTTTATCCCTTATGCTCCCTCTTGGGAA 1401
QY 1321 GATTTTGAAGAAAGCAGGAGTCCATTTCTAGGGAATTTCTGGAGCAGCTTTCAGTGAG 1380
Db 1402 GATTTTGAAGAAAGCAGGAGTCCATTTCTAGGGAATTTCTGGAGCAGCTTTCAGTGAG 1461

QY 1381 GAGCTCACACGTTTCCACCCACTGTCCTTCAAAACAATGTCTATTTGAGAAAGAAATAGTACA 1440
Db 1462 GAGCTCACACGTTTCCACCCACTGTCCTTCAAAACAATGTCTATTTGAGAAAGAAATAGTACA 1521
QY 1441 ACTGTGTGA 1449
Db 1522 ACTGTGTGA 1530

RESULT 12

AAT64946

ID AAT64946 standard; cDNA, 1970 BP.

AC AAT64946;

XX 30-MAR-1998 (first entry)

XX cDNA encoding a novel G-protein coupled receptor.

XX G-protein coupled receptor; enlarged extracellular loop;
KW inflammatory disease; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; multiple sclerosis; antibody; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 5'UTR 1..81

FT /*tag= b 82..1530

FT CDS /*tag= a

XX WO9728188-A1.

XX 07-AUG-1997.

XX 30-JAN-1997; 97WO-US001736.

XX 30-JAN-1996; 96US-0010808P.

XX (SCRI) SCRIPPS RES INST.

XX Ye RD;

XX WPI; 1997-402552/37.

XX P-PSDB; AAW23367.

G-protein-coupled receptor with enlarged extracellular domain - between fourth and fifth transmembrane domains, also nucleic acid and antibodies useful for treating inflammation and neurological disease.

XX Claim 11; Fig 1; 54pp; English.

The present cDNA sequence encodes a novel G-protein coupled receptor that has an enlarged extracellular loop between the fourth and fifth transmembrane domains. It was isolated from a human granulocyte cDNA library prepared from differentiated HL-60 granulocyte mRNA. The library was screened with a probe made from human N-formyl peptide receptor (FPR) cDNA. Antibodies generated against the protein encoded by the present sequence revealed expression in a variety of tissues, including heart, lung and placenta. Diseases or conditions mediated by the G-protein coupled receptor can be treated by administering reagents such as the present sequence, antisense nucleic acid or antibodies generated against the receptor. Reagents may comprise a molecule binding to the receptor but not transmitting a signal across the cell membrane or reducing effectiveness of binding of the natural ligand. The reagent may also alter the interaction of the receptor with the G-protein with which it naturally reacts e.g. by altering phosphorylation sites in intracellular domains of the receptor. Inflammatory diseases or conditions mediated by the novel receptor which can be treated include e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, multiple sclerosis. The antibody can also be used to diagnose these diseases e.g. in brain tissue from patients with suspected neurological disease, especially

XX	DNA encoding G-protein coupled receptor - and antagonists and agonists, useful to treat asthma and transplant rejection, and immunodeficiency and severe infections, respectively.	4
XX	Claim 7; Page 44-45; 63pp; English.	
XX	This cDNA encodes a 482 AA sequence of a human G-protein coupled receptor. This sequence may be expressed in a host cell using a vector, for production of the recombinant protein. The DNA and the protein can be used to treat patients in need of G-protein coupled receptor. A disease or susceptibility to a disease can be diagnosed by detecting a mutation in this sequence, in a sample from a host	
XX	Sequence 2040 BP; 530 A; 493 C; 433 G; 584 T; 0 U; 0 Other;	
SQ	Query Match 96.5%; Score 1398; DB 2; Length 2040; Best Local Similarity 99.9%; Pred. No. 0; Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	1 ATGGGGTCTTTCTGTGTGAGACCAATTCAACTGACCTCTCACAGCCATGGGAATGAG 60	
DB	153 ATGGGGTCTTTCTGTGTGAGACCAATTCAACTGACCTCTCTCACAGCCATGGGAATGAG 212	
QY	61 CCCCAGATAATTCTCCATGGTCATTCAGCCTTACTTTTTTACTGGGATGCCAGGC 120	
DB	213 CCCCAGATAATTCTCCATGGTCATTCAGCCTTACTTTTTTACTGGGATGCCAGGC 272	
QY	121 AATGGGCTGGTCTGTGGGTGGCTGGCTGAAGATGACGGGACAGTGAACAAATTTGG 180	
DB	273 AATGGGCTGGTCTGTGGGTGGCTGGCTGAAGATGACGGGACAGTGAACAAATTTGG 332	
QY	181 TTCTCTCCACCTCACCTTGGCGGACCTCTCTGTGTCCTCTCTTGGCCCTTCTCGTGGCT 240	
DB	333 TTCTCTCCACCTCACCTTGGCGGACCTCTCTGTGTCCTCTCTTGGCCCTTCTCGTGGCT 392	
QY	241 CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGTTCCTATGCAAGCTCATGCCCTCC 300	
DB	393 CACTTGGCTCTCCAGGACAGTGGCCCTACGGCAGTTCCTATGCAAGCTCATGCCCTCC 452	
QY	301 ATCATGTGCTCACAATGTTTGGCAGTGTCTTCTGCTTACTGCGCATAGCCTGGATCGC 360	
DB	453 ATCATGTGCTCACAATGTTTGGCAGTGTCTTCTGCTTACTGCGCATAGCCTGGATCGC 512	
QY	361 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGACAAATCATCGCAATGATGGGATGGCTGC 420	
DB	513 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGACAAATCATCGCAATGATGGGATGGCTGC 572	
QY	421 TCTATCTGTGGATGATCTGGGTGGTGGCTTTGTGATGCAATCCTGTGTTCTGTGTAC 480	
DB	573 TCTATCTGTGGATGATCTGGGTGGTGGCTTTGTGATGCAATCCTGTGTTCTGTGTAC 632	
QY	481 CGGGAATCTTCACCTACAGACAAACATAATAGATGGGCTACAAATTTGGTCTCTCCAGC 540	
DB	633 CGGGAATCTTCACCTACAGACAAACATAATAGATGGGCTACAAATTTGGTCTCTCCAGC 692	
QY	541 TCATTAGATATTCCAGACTTTTATGGAGATCCACTAGAAAAAGGTCTCTTGAAAAACATT 600	
DB	693 TCATTAGATATTCCAGACTTTTATGGAGATCCACTAGAAAAAGGTCTCTTGAAAAACATT 752	
QY	601 GTTCAGCCGCTGGGAAATGAATGATAGGTATGATCCTTCTCTTTCCAAACAAATGAT 660	
DB	753 GTTCAGCCGCTGGGAAATGAATGATAGGTATGATCCTTCTCTTTCCAAACAAATGAT 812	
QY	661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAAGACCTTCTGAGAT 720	
DB	813 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAAGACCTTCTGAGAT 872	
QY	721 TCATCTCCCTPAGGGTTCGTAGGTAAACAGTCAAAATCTGTATTCTAATGATTATTA 780	
DB	873 TCATCTCCCTPAGGGTTCGTAGGTAAACAGTCAAAATCTGTATTCTAATGATTATTA 932	
QY	781 CCTGTGTGATGGTCTCACCTAAAAATCCCCAGTGGGTTTCTTATTGAAGATCAGGAACC 840	

XX 30-JAN-2003.
 PD 30-SEP-2002; 2002US-00259521.
 PF 17-FEB-1995; 95WO-US001992.
 PR 05-JUN-1995; 95US-00462314.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Li Y, Rosen CA;
 XX WPI; 2003-531445/50.
 PI P-PSDB; ABU62861.
 XX New G-protein coupled receptor polypeptides and polynucleotide, useful
 PT for screening receptor agonists and/or antagonists and/or receptor
 PT ligands, in chromosome identification, and in for producing antibodies.
 XX Disclosure; Fig 1A-D; 26pp; English.
 PS The invention describes an isolated polynucleotide (I) comprising a
 CC sequence which: (a) encodes a polypeptide having a sequence of 482 amino
 CC acids (II) given in the specification; (b) encodes a mature polypeptide
 CC encoded or expressed by the DNA contained in ATCC deposit number 75982;
 CC (c) is capable of hybridizing to and which is at least 70% identical to
 CC (a) or (b); or (d) a fragment of (a), (b) or (c). The G-protein coupled
 CC receptors (GPCR) are useful for screening receptor agonists and/or
 CC antagonists and/or receptor ligands. GPCR agonists are useful for
 CC stimulating GPCR for the treatment of conditions related to the under-
 CC expression of GPCR, e.g. bacterial or viral infection, immunodeficiency
 CC diseases and severe infections. GPCR antagonists are useful for
 CC inhibiting the action of GPCR for treating conditions associated with
 CC over-expression of the GPCR, e.g. asthma, bronchial allergy, chronic
 CC inflammation, systemic lupus erythematosus, gout, transplant rejection,
 CC hypertension, abnormal cell growth, and neurological diseases. The GPCR
 CC genes are also useful in diagnostic assays for detecting diseases or
 CC susceptibility to diseases related to the presence of mutations in the
 CC GPCR genes. These may also be used in chromosome identification. The
 CC polypeptides are useful as immunogens for producing antibodies. This
 CC sequence encodes a putative mature human G protein coupled receptor
 XX
 SQ Sequence 2040 BP; 530 A; 493 C; 433 G; 584 T; 0 U; 0 Other;
 Query Match 96.5%; Score 1398; DB 9; Length 2040;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCCATGGAATGAG 60
 DB 153 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCCATGGAATGAG 212
 QY 61 CCCCAGTAATCTCTCATGGTCAATCTCAGCCTTACTTTTACTGGGATGCCAGGC 120
 DB 213 CCCCAGTAATCTCTCATGGTCAATCTCAGCCTTACTTTTACTGGGATGCCAGGC 272
 QY 121 AATGGCTGGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 180
 DB 273 AATGGCTGGTGTGGTGGCTGGCTGAAGATGAGCGGACAGTGAACACAAATTTGG 332
 QY 181 TTCCTCACCTCACTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTCGCTGGCT 240
 DB 333 TTCCTCACCTCACTTGGCGGACCTCTCTGTGCTGCTCTCTTGGCCCTTCTCGCTGGCT 392
 QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTAGCGGAGTTCCTATGCAAGCTCATCCCTCC 300
 DB 393 CACTTGGCTCTCCAGGACAGTGGCCCTAGCGGAGTTCCTATGCAAGCTCATCCCTCC 452
 QY 301 ATCAATGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTTACTGCT 360
 DB 453 ATCAATGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCTTACTGCT 512
 QY 361 TGTCTTGGTATTCAAGCCAAATCTGGTGTGAGATCATCGAATCATCGAATGTAGGATGGCCTGC 420

DB 513 TGTCTTGGTATTCAAGCCAAATCTGGTGTGAGATCATCGAATGTAGGATGGCCTGC 572
 QY 421 TCTATCTGTGATGTATCTGGTGTGCTTTTGTGATGTGATCTCTGTGTCTGTGTAC 480
 DB 573 TCTATCTGTGATGTATCTGGTGTGCTTTGTGTGATGTGATCTCTGTGTCTGTGTAC 632
 QY 481 CCGGAAATCTTCACTACAGACCAACATAATAGATGTGCTTCAAAATTTGGTCTCTCCAGC 540
 DB 633 CCGGAAATCTTCACTACAGACCAACATAATAGATGTGCTTCAAAATTTGGTCTCTCCAGC 692
 QY 541 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAAAT 600
 DB 693 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAAAT 752
 QY 601 GTTCAGCGCTGGAGAAATCAATGATAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 DB 753 GTTCAGCGCTGGAGAAATCAATGATAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 812
 QY 661 CATCTTGGACAGTCCCACCTCTCTCAACCTCAAAACATTTCAAGACCTTCTGCGAGAT 720
 DB 813 CATCTTGGACAGTCCCACCTCTCTCAACCTCAAAACATTTCAAGACCTTCTGCGAGAT 872
 QY 721 TCACCTCCCTAGGGTCTCTGTAGTTCACAGTCAAAATCTGTATTTCTAATGATTTAAA 780
 DB 873 TCACCTCCCTAGGGTCTCTGTAGTTCACAGTCAAAATCTGTATTTCTAATGATTTAAA 932
 QY 781 CCTGCTGATGTGCTCACCTCAAAATCCCAAGTGGGTTTCTCTTATGAAGATCAAGAAC 840
 DB 933 CCTGCTGATGTGCTCACCTCAAAATCCCAAGTGGGTTTCTCTTATGAAGATCAAGAAC 992
 QY 841 AGCCCACTGATTAATCTGTATGCTTTCTCTACTCAATTTAAAGCTTTCCCTAGCGCT 900
 DB 993 AGCCCACTGATTAATCTGTATGCTTTTCTCTACTCAATTTAAAGCTTTCCCTAGCGCT 1052
 QY 901 TCTAGCAATTTCTTCTACGAGTCTGAGTACCAAGTTCACAGATTTTACCAATTTA 960
 DB 1053 TCTAGCAATTTCTTCTACGAGTCTGAGTACCAAGTTCACAGATTTTACCAATTTA 1112
 QY 961 GGCAATTTACAGATGAGTCAAGTGGCAACCCCTCTGGCAATAACGATCACTAGG 1020
 DB 1113 GGCAATTTACAGATGAGTCAAGTGGCAACCCCTCTGGCAATAACGATCACTAGG 1172
 QY 1021 CTAGTGTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1173 CTAGTGTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 QY 1081 TTCGGAATGCAAGGGGCGCTTTCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1140
 DB 1233 TTCGGAATGCAAGGGGCGCTTTCGCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCGGTG 1292
 QY 1141 GTGGTGGTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1293 GTGGTGGTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
 QY 1201 TTGCTTACTGACCCAGAAATCTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1260
 DB 1353 TTGCTTACTGACCCAGAAATCTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1412
 QY 1261 ATTGCTTACTGACCCAGAAATCTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1320
 DB 1413 ATTGCTTACTGACCCAGAAATCTCCCTTGGGGAATCTCTGATGCTCTGGGATCATGTATGC 1472
 QY 1321 GATTTTAGGAAGAAAGCAGGAGTCCATTCAGGGAATCTTGGAGGAGGAGGAGGAGGAGGAGGAG 1380
 DB 1473 GATTTTAGGAAGAAAGCAGGAGTCCATTCAGGGAATCTTGGAGGAGGAGGAGGAGGAGGAGGAG 1532
 QY 1381 GAGCTCACAGCTTCCAGCACTGCTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA 1440
 DB 1533 GAGCTCACAGCTTCCAGCACTGCTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA 1592
 QY 1441 ACTGTGTGA 1449

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 07:11:45 ; Search time 6433 Seconds

(without alignment)
10914.287 Million cell updates/sec

Title: US-10-764-649-1

Perfect score: 1449

Sequence: 1 atggcgctttctctgtga.....gaaatagatacaactgtgtga 1449

Scoring table: Oligo NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sv.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	1449	6	CQ719960 Sequence
2	1449	100.0	1449	6	CQ880087 Sequence
3	1449	100.0	1449	6	AX548792 Sequence
4	1449	100.0	1449	6	AX741648 Sequence
5	1449	100.0	1449	6	BD017452 C3a recep
6	1449	100.0	1449	9	AY268431 Homo sapi
7	1449	100.0	1449	9	HSC3AAREC
8	1449	100.0	1849	6	AX646469 Sequence
9	1449	100.0	1849	9	AB065870 Homo sapi
10	1449	100.0	1985	9	BC020742 Homo sapi
11	1449	100.0	12053	9	AY455929 Homo sapi
12	1449	100.0	186321	9	AC006511 Homo sapi
13	1398	96.5	1956	6	AX335504 Sequence
14	1398	96.5	1956	6	HS028488 Human putat
15	1398	96.5	1970	6	AR281967 Sequence
16	1398	96.5	2040	6	AX774747 Sequence
17	1398	96.5	2040	9	HS062027
18	1245	85.9	1449	6	AX280841 Sequence
19	695	48.0	74502	2	AC024300 Homo sapi

20	265	18.3	468	6	CQ682719	Sequence
c 21	198	13.7	625	6	AX775051	Sequence
c 22	163	11.2	611	6	AX775052	Sequence
23	142	9.8	1446	9	AY426336	Macaca fa
24	91	6.3	809	11	BV166047	C3AR1 491
25	60	4.1	60	6	CQ545227	Sequence
26	49	3.4	2093	10	RNU86379	U86379 Rattus norv
27	49	3.4	240641	2	AC098537	Rattus no
28	47	3.2	200	6	AX392846	Sequence
29	47	3.2	1431	10	MMU97537	U97537 Mus musculu
30	47	3.2	1701	10	BC003728	Mus muscu
31	47	3.2	2657	6	AX392843	Sequence
32	47	3.2	2657	10	MMU77461	U77461 Mus musculu
33	47	3.2	3329	6	AX080444	Sequence
34	47	3.2	3329	10	MMU77460	U77460 Mus musculu
35	47	3.2	8308	10	AF053757	AF053757 Mus muscu
36	47	3.2	193712	10	AC123874	AC123874 Mus muscu
37	40	2.8	1428	10	CPAJ6402	AJ06402 Cavia por
38	40	2.8	2220	10	CPU86378	U86378 Cavia porce
c 39	28	1.9	37	6	AX280413	Sequence
40	25	1.7	25	6	CQ880091	Sequence
41	25	1.7	7449	6	AX345178	Sequence
c 42	24	1.7	7449	6	AX345179	Sequence
43	22	1.5	40	6	AX280606	Sequence
c 44	22	1.5	40	6	AX280607	Sequence
45	22	1.5	65	6	CQ557637	Sequence
46	22	1.5	163057	10	AL928891	AL928891 Mouse DNA
47	22	1.5	215158	5	BX539313	BX539313 Zebrafish
48	22	1.5	231853	2	AC093352	Mus muscu
49	22	1.5	239522	2	AC095395	Rattus no
c 50	22	1.5	276186	2	AC120756	Rattus no
51	21	1.4	21	6	CQ880089	Sequence
52	21	1.4	928	8	AK121986	AK121986 Oryza sat
53	21	1.4	1071	6	AR308731	Sequence
54	21	1.4	1071	6	AR308750	Sequence
55	21	1.4	1071	6	AX549198	Sequence
56	21	1.4	1071	9	BC067453	Homo sapi
57	21	1.4	1071	9	BC067454	Homo sapi
58	21	1.4	1797	9	AF045764	Homo sapi
59	21	1.4	12606	1	AE001077	Archaeogl
60	21	1.4	25381	2	AC017495	Drosophil
c 61	21	1.4	61453	2	AC115048	Mus muscu
62	21	1.4	78507	9	AC110743	Homo sapi
63	21	1.4	122461	10	AL645684	Mouse DNA
c 64	21	1.4	133651	9	AC092791	Homo sapi
c 65	21	1.4	147695	2	EX908793	Danio rer
66	21	1.4	152272	8	AC137589	Oryza sat
67	21	1.4	152272	8	AC144558	Oryza sat
c 68	21	1.4	163703	2	CR790365	Danio rer
c 69	21	1.4	164820	9	AL627443	Human DNA
70	21	1.4	166439	9	AC010325	Homo sapi
c 71	21	1.4	166695	5	EX005440	Zebrafish
72	21	1.4	184671	2	AC112648	Homo sapi
73	21	1.4	188807	2	AC036199	Homo sapi
74	21	1.4	189254	3	AC009391	Drosophil
c 75	21	1.4	193178	10	AL831706	Mouse DNA
c 76	21	1.4	193735	2	AC148501	Callithri
c 77	21	1.4	198294	10	AC135104	Mus muscu
c 78	21	1.4	206737	2	AC148551	Callithri
79	21	1.4	210003	2	CR388095	Danio rer
80	21	1.4	212991	2	CR759907	Danio rer
c 81	21	1.4	245648	2	AC138762	Homo sapi
c 82	21	1.4	245795	2	AC096419	Rattus no
83	21	1.4	246007	2	EX914205	Danio rer
c 84	21	1.4	253189	3	AB003780	Drosophil
c 85	21	1.4	254057	2	AC094747	Rattus no
86	21	1.4	315463	2	AC122070	Rattus no
c 87	20	1.4	20	6	CQ880090	Sequence
c 88	20	1.4	752	1	AB022638	Unculture
c 89	20	1.4	888	8	NTGRPR	X74106 N.tabacum g
c 90	20	1.4	1088	8	AK104555	Oryza sat
c 91	20	1.4	1093	8	AK104820	Oryza sat
c 92	20	1.4	1220	8	AK060132	Oryza sat

93	20	1.4	1379	9	HS802049	AL137362 Homo sapi	166	20	1.4	257992	2	AC112363	AC112363 Rattus no	
c 94	20	1.4	1392	8	AK0711375	AK0711375 Oryza sat	c 167	20	1.4	263038	2	AC110337	AC110337 Rattus no	
95	20	1.4	1579	6	AX118599	AX118599 Sequence	168	20	1.4	270268	2	AC130516	AC130516 Rattus no	
96	20	1.4	1733	9	BC009676	BC009676 Homo sapi	169	20	1.4	270854	10	AC108409	AC108409 Mus muscu	
97	20	1.4	1755	6	AX705307	AX705307 Sequence	170	19	1.3	32	32	6	AX280412	AX280412 Sequence
98	20	1.4	1755	9	AK025890	AK025890 Homo sapi	171	19	1.3	200	6	AX192845	AX192845 Sequence	
99	20	1.4	1764	9	AK025426	AK025426 Homo sapi	172	19	1.3	299	3	AY261265	AY261265 Echinosmet	
100	20	1.4	2073	9	HSDOC201	U41096 Human non-c	173	19	1.3	338	4	AY194233	AY194233 Bos tauru	
101	20	1.4	2156	8	AB087677	AB087677 Nicotiana	174	19	1.3	373	10	S63503S1	S63503 Integrin be	
c 102	20	1.4	2177	10	BC0118484	BC0118484 Mus muscu	c 175	19	1.3	400	11	G16803	G16803 human STS S	
c 103	20	1.4	2272	8	AK066986	AK066986 Oryza sat	c 176	19	1.3	400	11	G28471	G28471 SHGC-23817	
c 104	20	1.4	2965	10	BC058952	BC058952 Mus muscu	c 177	19	1.3	412	11	G34518	G34518 human STS S	
c 105	20	1.4	3061	10	AY281291	AY281291 Mus muscu	c 178	19	1.3	412	11	G03758	G03758 human STS W	
c 106	20	1.4	3095	10	AY281290	AY281290 Mus muscu	179	19	1.3	487	6	CQ069635	CQ069635 Sequence	
c 107	20	1.4	3160	9	AB052134	AB052134 Nacaca fa	180	19	1.3	487	6	CQ096746	CQ096746 Sequence	
c 108	20	1.4	3971	8	AK1211129	AK1211129 Oryza sat	181	19	1.3	487	6	CQ135543	CQ135543 Sequence	
c 109	20	1.4	4251	10	BC066027	BC066027 Mus muscu	182	19	1.3	487	6	CQ173977	CQ173977 Sequence	
110	20	1.4	34029	9	AF218839S2	AF205890 Homo sapi	183	19	1.3	487	6	CQ218837	CQ218837 Sequence	
111	20	1.4	60173	10	AX005281	AX005281 Mouse DNA	184	19	1.3	487	6	CQ257418	CQ257418 Sequence	
112	20	1.4	92740	9	AC008946	AC008946 Homo sapi	185	19	1.3	487	6	CQ294643	CQ294643 Sequence	
c 113	20	1.4	100815	8	ATF12A12	AL133314 Arabidops	186	19	1.3	487	6	CQ331306	CQ331306 Sequence	
c 114	20	1.4	105517	3	AC139125	AC139125 Leishmani	187	19	1.3	513	10	AF521561	AF521561 Rattus no	
115	20	1.4	117406	2	OSGN00211	AL663010 Oryza sat	188	19	1.3	563	11	BV045320	BV045320 S212P6618	
c 116	20	1.4	123203	9	AC003036	AC003036 Homo sapi	c 189	19	1.3	594	11	BV092550	BV092550 RPAMMSEQ0	
c 117	20	1.4	127287	2	AC069179	AC069179 Homo sapi	c 190	19	1.3	594	11	BV155634	BV155634 RPAMMSEQ0	
c 118	20	1.4	128795	10	AL807806	AL807806 Mouse DNA	c 191	19	1.3	614	6	CQ518123	CQ518123 Sequence	
c 119	20	1.4	133862	9	AC008916	AC008916 Homo sapi	192	19	1.3	749	8	AF098768	AF098768 Gracilari	
c 120	20	1.4	144644	8	AP002818	AP002818 Oryza sat	193	19	1.3	759	8	AK121505	AK121505 Oryza sat	
c 121	20	1.4	151341	10	AC115236	AC115236 Rattus no	194	19	1.3	771	3	AY617447	AY617447 Sterkiell	
c 122	20	1.4	154329	2	AC115830	AC115830 Mus muscu	c 195	19	1.3	792	5	AF137229	AF137229 Oncorhync	
c 123	20	1.4	155151	10	AL596062	AL596062 Mouse DNA	196	19	1.3	814	11	BMU937031	BMU937031 Mus musculu	
c 124	20	1.4	156002	2	AC036110	AC036110 Homo sapi	c 197	19	1.3	815	11	BV013277	BV013277 S212P6840	
125	20	1.4	156850	8	AP002901	AP002901 Oryza sat	198	19	1.3	909	5	AF071234	AF071234 Petromyzo	
c 126	20	1.4	159691	2	AC132764	AC132764 Rattus no	199	19	1.3	1083	10	AY471575	AY471575 Rattus no	
127	20	1.4	161071	9	AC093010	AC093010 Homo sapi	200	19	1.3	1093	10	RNU1173	RNU1173 Rat UI RNA	
c 128	20	1.4	162083	2	AC021845	AC021845 Homo sapi	c 201	19	1.3	1141	14	HPCNS5002	HPCNS5002 Hepatitis C	
c 129	20	1.4	163822	2	AC151370	AC151370 Aotus nan	c 202	19	1.3	1155	9	HS77N191	HS77N191 Human gen	
c 130	20	1.4	165890	10	AC121891	AC121891 Mus muscu	c 203	19	1.3	1171	10	AF054507	AF054507 Mus muscu	
c 131	20	1.4	166000	9	AC090509	AC090509 Homo sapi	c 204	19	1.3	1237	9	HS77N191	HS77N191 Human gen	
c 132	20	1.4	167348	2	AC104201	AC104201 Mus muscu	c 205	19	1.3	1297	10	AY228550	AY228550 Rattus no	
c 133	20	1.4	173706	2	AC022694	AC022694 Homo sapi	c 206	19	1.3	1380	10	RNU166A	RNU166A Rat UI RNA	
c 134	20	1.4	177626	9	AC090005	AC090005 Homo sapi	c 207	19	1.3	1406	9	HSTULP1S02	HSTULP1S02 Homo sapi	
c 135	20	1.4	177717	9	AC060788	AC060788 Homo sapi	c 208	19	1.3	1870	5	BC065657	BC065657 Danio rer	
c 136	20	1.4	180177	10	AC129590	AC129590 Mus muscu	c 209	19	1.3	1995	6	CQ714164	CQ714164 Sequence	
c 137	20	1.4	181394	9	AC090951	AC090951 Homo sapi	c 210	19	1.3	2188	6	FSU61842	FSU61842 Fusarium so	
c 138	20	1.4	182340	2	AC024417	AC024417 Homo sapi	c 211	19	1.3	2204	6	BD211234	BD211234 Endometri	
c 139	20	1.4	183607	9	AC066597	AC066597 Homo sapi	c 212	19	1.3	2204	6	AR350652	AR350652 Sequence	
c 140	20	1.4	184013	2	BX511087	BX511087 Danio rer	c 213	19	1.3	2204	6	AX009356	AX009356 Sequence	
c 141	20	1.4	184759	9	AC022695	AC022695 Homo sapi	c 214	19	1.3	2288	6	BD211235	BD211235 Endometri	
c 142	20	1.4	184840	2	AC148136	AC148136 Callicebu	c 215	19	1.3	2288	6	AR350653	AR350653 Sequence	
c 143	20	1.4	185989	2	CR407587	CR407587 Danio rer	c 216	19	1.3	2288	6	AX009358	AX009358 Sequence	
c 144	20	1.4	187126	2	AP002395	AP002395 Homo sapi	c 217	19	1.3	2633	9	AF175409	AF175409 Homo sapi	
c 145	20	1.4	193773	2	AC133652	AC133652 Mus muscu	c 218	19	1.3	2644	10	AB109092	AB109092 Mus muscu	
c 146	20	1.4	196832	2	AC027054	AC027054 Homo sapi	c 219	19	1.3	2910	9	AY282806	AY282806 Homo sapi	
c 147	20	1.4	202444	10	AC093474	AC093474 Mus muscu	c 220	19	1.3	3574	6	CQ849657	CQ849657 Sequence	
c 148	20	1.4	204235	9	AL590426	AL590426 Human DNA	c 221	19	1.3	3574	6	AK126688	AK126688 Homo sapi	
c 149	20	1.4	208989	9	AC027124	AC027124 Homo sapi	c 222	19	1.3	4236	6	BD062570	BD062570 C1TA-int	
c 150	20	1.4	209705	10	AC101931	AC101931 Mus muscu	c 223	19	1.3	6698	9	AB002344	AB002344 Human mRN	
c 151	20	1.4	210833	2	AC018566	AC018566 Homo sapi	c 224	19	1.3	10164	1	AE011812	AE011812 Xanthomon	
c 152	20	1.4	210949	2	AC146885	AC146885 Callithri	c 225	19	1.3	10900	8	AP002056	AP002056 Arabidops	
c 153	20	1.4	217456	9	AC068319	AC068319 Homo sapi	c 226	19	1.3	16934	10	AB109091	AB109091 Mus muscu	
c 154	20	1.4	218636	2	AC021476	AC021476 Mus muscu	c 227	19	1.3	18174	3	AC006619	AC006619 Caenorhab	
c 155	20	1.4	220761	2	AC101700	AC101700 Mus muscu	c 228	19	1.3	21392	10	BX321895	BX321895 Mouse DNA	
c 156	20	1.4	222361	2	AC110091	AC110091 Mus muscu	c 229	19	1.3	25003	3	U88181	U88181 Caenorhabdi	
c 157	20	1.4	227648	10	AC121286	AC121286 Mus muscu	c 230	19	1.3	29612	5	AF464190	AF464190 Petromyzo	
c 158	20	1.4	230323	5	AL935285	AL935285 Zebrafish	c 231	19	1.3	34337	6	AX398707	AX398707 Sequence	
c 159	20	1.4	230827	2	AC111260	AC111260 Rattus no	c 232	19	1.3	35294	2	AC151931	AC151931 Phaeodact	
c 160	20	1.4	237814	10	AC091464	AC091464 Mus muscu	c 233	19	1.3	36328	3	LMFL5213	LMFL5213 Leishmani	
c 161	20	1.4	238466	2	AC097567	AC097567 Rattus no	c 234	19	1.3	43152	2	AC013679	AC013679 Homo sapi	
c 162	20	1.4	239772	2	AC125647	AC125647 Rattus no	c 235	19	1.3	43323	2	AC114797	AC114797 Homo sapi	
c 163	20	1.4	242997	2	AC129340	AC129340 Rattus no	c 236	19	1.3	55093	2	AC114909	AC114909 Homo sapi	
c 164	20	1.4	250505	2	AC112048	AC112048 Rattus no	c 237	19	1.3	56804	9	HS77N19	HS77N19 Human DNA	
c 165	20	1.4	251341	2	AC131346	AC131346 Rattus no	c 238	19	1.3					

C 239	19	1.3	56944	2	AC100526	AC100526 Mus muscu	C 312	19	1.3	149316	10	AC123791	AC123791 Mus muscu
C 240	19	1.3	57000	6	AC078862	AC078862 Homo sapi	C 313	19	1.3	149805	2	AC118312	AC118312 Rattus no
C 241	19	1.3	57000	6	ES4646	ES4646 Bae sequen	C 314	19	1.3	150362	10	AC123085	AC123085 Mus muscu
C 242	19	1.3	58343	2	AC130344	AC130344 Homo sapi	C 315	19	1.3	151057	2	AC019198	AC019198 Homo sapi
C 243	19	1.3	61470	9	BX664725	BX664725 Human DNA	C 316	19	1.3	151479	2	AC012278	AC012278 Homo sapi
C 244	19	1.3	63416	2	AC136323	AC136323 Homo sapi	C 317	19	1.3	151980	2	AC084209	AC084209 Homo sapi
C 245	19	1.3	69837	2	AC136367	AC136367 Homo sapi	C 318	19	1.3	151983	2	AC027178	AC027178 Homo sapi
C 246	19	1.3	71512	10	AF234171	AF234171 Mus muscu	C 319	19	1.3	152345	9	AP000009	AP000009 Homo sapi
C 247	19	1.3	73899	2	AC133289	AC133289 Homo sapi	C 320	19	1.3	152816	2	AC097939	AC097939 Homo sapi
C 248	19	1.3	74796	2	AC023344	AC023344 Homo sapi	C 321	19	1.3	153861	2	AC092061	AC092061 Homo sapi
C 249	19	1.3	75425	2	AC135034	AC135034 Homo sapi	C 322	19	1.3	154698	2	AC026747	AC026747 Homo sapi
C 250	19	1.3	76072	8	NCB1D1	AL355927 Neurospor	C 323	19	1.3	154986	2	AC141766	AC141766 Apis mell
C 251	19	1.3	76336	9	AL445529	AL445529 Human DNA	C 324	19	1.3	155150	9	AP005121	AP005121 Homo sapi
C 252	19	1.3	77564	9	AL391385	AL391385 Human DNA	C 325	19	1.3	155630	9	AC009724	AC009724 Homo sapi
C 253	19	1.3	78529	8	AB028609	AB028609 Arabidops	C 326	19	1.3	156168	2	BX927212	BX927212 Danio rer
C 254	19	1.3	82212	8	AC004484	AC004484 Arabidops	C 327	19	1.3	156180	9	AC092798	AC092798 Homo sapi
C 255	19	1.3	83122	8	ATT20010	AL163816 Arabidops	C 328	19	1.3	156180	9	AL161439	AL161439 Human DNA
C 256	19	1.3	85556	2	AC069589	AC069589 Homo sapi	C 329	19	1.3	156899	2	AC103884	AC103884 Homo sapi
C 257	19	1.3	85691	9	AP001429	AP001429 Homo sapi	C 330	19	1.3	157241	2	AC046194	AC046194 Homo sapi
C 258	19	1.3	87080	8	AC004747	AC004747 Arabidops	C 331	19	1.3	157571	2	AC068255	AC068255 Homo sapi
C 259	19	1.3	87849	3	AC084453	AC084453 Caenorhab	C 332	19	1.3	159128	10	AL928557	AL928557 Mouse DNA
C 260	19	1.3	89840	8	AC004705	AC004705 Arabidops	C 333	19	1.3	160402	2	AC067775	AC067775 Homo sapi
C 261	19	1.3	93824	9	AP006565	AP006565 Homo sapi	C 334	19	1.3	160681	10	AL844140	AL844140 Mouse DNA
C 262	19	1.3	94147	9	AC016604	AC016604 Homo sapi	C 335	19	1.3	160705	2	AC130060	AC130060 Rattus no
C 263	19	1.3	95576	2	AC114931	AC114931 Homo sapi	C 336	19	1.3	161277	8	AP002972	AP002972 Oryza sat
C 264	19	1.3	98758	9	HS2233H9	AL008562 Human DNA	C 337	19	1.3	161505	9	AP001888	AP001888 Homo sapi
C 265	19	1.3	100000	9	AP000150	AP000150 Homo sapi	C 338	19	1.3	162254	2	CR388125	CR388125 Danio rer
C 266	19	1.3	102748	9	AC128708	AC128708 Homo sapi	C 339	19	1.3	162545	8	AP004274	AP004274 Oryza sat
C 267	19	1.3	105951	8	AC141106	AC141106 Medicago	C 340	19	1.3	162659	2	AC138875	AC138875 Homo sapi
C 268	19	1.3	107482	8	BX908789	BX908789 Neurospor	C 341	19	1.3	163404	2	AL355308	AL355308 Homo sapi
C 269	19	1.3	108847	8	AP002109	AP002109 Arabidops	C 342	19	1.3	163463	2	AC102732	AC102732 Mus muscu
C 270	19	1.3	110000	2	AC013623_2	Continuation (3 of	C 343	19	1.3	163536	9	AC016635	AC016635 Homo sapi
C 271	19	1.3	110000	2	AC109085_0	AC109085 Rattus no	C 344	19	1.3	163648	2	AC142370	AC142370 Rattus no
C 272	19	1.3	110000	2	AC021632_1	Continuation (2 of	C 345	19	1.3	163772	2	AC010381	AC010381 Homo sapi
C 273	19	1.3	110000	2	LMFLCHR15_3	Continuation (4 of	C 346	19	1.3	164514	2	AC090715	AC090715 Homo sapi
C 274	19	1.3	110000	2	LMFLCHR31_16	Continuation (17 of	C 347	19	1.3	164629	10	AC121094	AC121094 Mus muscu
C 275	19	1.3	110174	9	D83253	D83253 Homo sapien	C 348	19	1.3	165221	9	AC098976	AC098976 Homo sapi
C 276	19	1.3	111284	2	AC138233	AC138233 Homo sapi	C 349	19	1.3	165328	9	AC022929	AC022929 Homo sapi
C 277	19	1.3	111648	9	HS16C2	AL049911 Homo sapi	C 350	19	1.3	165682	2	AC140892	AC140892 Homo sapi
C 278	19	1.3	111704	2	AC146847	AC146847 Ornithorh	C 351	19	1.3	165870	9	AC138919	AC138919 Homo sapi
C 279	19	1.3	111764	9	AL133379	AL133379 Human DNA	C 352	19	1.3	165969	10	AL626806	AL626806 Mouse DNA
C 280	19	1.3	112222	9	AC099313	AC099313 Homo sapi	C 353	19	1.3	166256	9	AC018922	AC018922 Homo sapi
C 281	19	1.3	114314	9	AL359494	AL359494 Human DNA	C 354	19	1.3	166602	2	AC022899	AC022899 Homo sapi
C 282	19	1.3	115626	9	AC103792	AC103792 Homo sapi	C 355	19	1.3	167071	9	AC128649	AC128649 Homo sapi
C 283	19	1.3	115793	9	AC025166	AC025166 Homo sapi	C 356	19	1.3	167322	2	AC016788	AC016788 Homo sapi
C 284	19	1.3	117963	9	AC016651	AC016651 Homo sapi	C 357	19	1.3	167331	9	AC073115	AC073115 Homo sapi
C 285	19	1.3	119182	9	HSB62120	AL050302 Homo sapi	C 358	19	1.3	167421	9	AC084773	AC084773 Homo sapi
C 286	19	1.3	119451	2	AP003958	AP003958 Oryza sat	C 359	19	1.3	167705	2	AC074252	AC074252 Homo sapi
C 287	19	1.3	119956	9	AC090741	AC090741 Homo sapi	C 360	19	1.3	168136	10	AC117803	AC117803 Mus muscu
C 288	19	1.3	120538	9	AC004815	AC004815 Homo sapi	C 361	19	1.3	168216	2	AC013398	AC013398 Homo sapi
C 289	19	1.3	122458	2	AC010391	AC010391 Homo sapi	C 362	19	1.3	168665	5	AC146870	AC146870 Xenopus t
C 290	19	1.3	123129	8	AP004743	AP004743 Oryza sat	C 363	19	1.3	169079	2	AC140018	AC140018 Homo sapi
C 291	19	1.3	123551	9	AC026361	AC026361 Homo sapi	C 364	19	1.3	169998	6	AR225961	AR225961 Sequence
C 292	19	1.3	127646	9	AC008171	AC008171 Homo sapi	C 365	19	1.3	170776	2	AC138929	AC138929 Homo sapi
C 293	19	1.3	129311	8	AP003218	AP003218 Oryza sat	C 366	19	1.3	171428	9	AC013407	AC013407 Homo sapi
C 294	19	1.3	130361	10	AL929546	AL929546 Mouse DNA	C 367	19	1.3	171507	5	BX469935	BX469935 Zebrafish
C 295	19	1.3	131275	10	AL669860	AL669860 Mouse DNA	C 368	19	1.3	171690	2	AC090539	AC090539 Homo sapi
C 296	19	1.3	133373	8	AC105734	AC105734 Oryza sat	C 369	19	1.3	172024	2	AC140907	AC140907 Homo sapi
C 297	19	1.3	134605	2	AC147872	AC147872 Monodelph	C 370	19	1.3	172228	10	AC114671	AC114671 Mus muscu
C 298	19	1.3	135513	9	AC008454	AC008454 Homo sapi	C 371	19	1.3	172331	9	AC127459	AC127459 Homo sapi
C 299	19	1.3	138317	9	AP003481	AP003481 Homo sapi	C 372	19	1.3	172845	9	AL160053	AL160053 Human DNA
C 300	19	1.3	138860	2	AC055703	AC055703 Mus muscu	C 373	19	1.3	173550	2	AC151434	AC151434 Callithri
C 301	19	1.3	138989	2	AC027186	AC027186 Homo sapi	C 374	19	1.3	173558	5	BX322795	BX322795 Zebrafish
C 302	19	1.3	139145	8	AP004125	AP004125 Oryza sat	C 375	19	1.3	174099	2	AC143333	AC143333 Homo sapi
C 303	19	1.3	141578	4	AC092728	AC092728 Canis fam	C 376	19	1.3	174412	9	AC009413	AC009413 Homo sapi
C 304	19	1.3	141771	9	AC091821	AC091821 Homo sapi	C 377	19	1.3	174440	2	AC140010	AC140010 Homo sapi
C 305	19	1.3	142174	10	AL772333	AL772333 Mouse DNA	C 378	19	1.3	174600	2	AC139471	AC139471 Homo sapi
C 306	19	1.3	143463	9	AL359312	AL359312 Human DNA	C 379	19	1.3	174985	2	AC142713	AC142713 Macaca mu
C 307	19	1.3	143538	2	AC026555	AC026555 Homo sapi	C 380	19	1.3	175299	2	AC116822	AC116822 Mus muscu
C 308	19	1.3	144118	2	AC141995	AC141995 Rattus no	C 381	19	1.3	175368	9	CNS01DWF	AL137164 Human chr
C 309	19	1.3	144239	9	AC004015	AC004015 Homo sapi	C 382	19	1.3	175582	2	AC112427	AC112427 Rattus no
C 310	19	1.3	145014	2	AC118321	AC118321 Rattus no	C 383	19	1.3	175763	9	AC104758	AC104758 Homo sapi
C 311	19	1.3	147259	2	AC019248	AC019248 Homo sapi	C 384	19	1.3	176278	9	AC024028	AC024028 Homo sapi

C 531	19	1.3	248901	2	AC118087	18	1.2	482	11	G63164	SHGC-140966
C 532	19	1.3	249404	2	AC122042	18	1.2	484	6	AR501495	Sequence
C 533	19	1.3	251141	2	AC116235	18	1.2	484	6	AR516777	Sequence
C 534	19	1.3	252473	2	AC093972	18	1.2	490	6	AR317247	Sequence
C 535	19	1.3	253417	2	AC134219	18	1.2	493	6	AR317249	Sequence
C 536	19	1.3	253649	2	AC106142	18	1.2	496	6	AR317248	Sequence
C 537	19	1.3	253751	2	AC051621	18	1.2	499	6	AR317246	Sequence
C 538	19	1.3	254538	2	AC097032	18	1.2	534	10	MUSTRERB	M23894 Mus musculus
C 539	19	1.3	254733	3	AC117075	18	1.2	534	10	MUSTRERB	M23894 Mus musculus
C 540	19	1.3	255590	2	AC097958	18	1.2	549	9	HUMHBV2	M15771 Human DNA/e
C 541	19	1.3	255782	2	AC106301	18	1.2	555	8	ATH520578	Arabidops
C 542	19	1.3	256873	2	AC125949	18	1.2	565	14	AV315183	AV315183 Fowl aden
C 543	19	1.3	257313	2	AC108696	18	1.2	569	6	CQ104053	CQ104053 Sequence
C 544	19	1.3	258065	2	AC135492	18	1.2	569	6	CQ142815	CQ142815 Sequence
C 545	19	1.3	259074	2	AC126723	18	1.2	569	6	CQ226046	CQ226046 Sequence
C 546	19	1.3	259291	2	AC114186	18	1.2	569	6	CQ264125	CQ264125 Sequence
C 547	19	1.3	259358	2	AC111788	18	1.2	569	6	CQ301215	CQ301215 Sequence
C 548	19	1.3	259575	2	AC126259	18	1.2	569	6	CQ338462	CQ338462 Sequence
C 549	19	1.3	261124	2	AC098233	18	1.2	580	6	CQ070974	CQ070974 Sequence
C 550	19	1.3	262697	2	AC108642	18	1.2	580	6	CQ100372	CQ100372 Sequence
C 551	19	1.3	263283	2	AC109389	18	1.2	580	6	CQ139364	CQ139364 Sequence
C 552	19	1.3	263776	2	AC087335	18	1.2	580	6	CQ175826	CQ175826 Sequence
C 553	19	1.3	268836	3	AE003824	18	1.2	580	6	CQ222743	CQ222743 Sequence
C 554	19	1.3	270120	2	AC128627	18	1.2	580	6	CQ260700	CQ260700 Sequence
C 555	19	1.3	270662	2	AC132962	18	1.2	580	6	CQ298258	CQ298258 Sequence
C 556	19	1.3	270873	2	AC118304	18	1.2	580	6	CQ334835	CQ334835 Sequence
C 557	19	1.3	271368	2	AC134642	18	1.2	582	6	AX240803	CQ240803 Sequence
C 558	19	1.3	271961	2	AC107572	18	1.2	582	6	AX488729	AX488729 Sequence
C 559	19	1.3	275989	2	AC105503	18	1.2	610	14	AV315184	AV315184 Fowl aden
C 560	19	1.3	290179	2	AC134072	18	1.2	617	11	G99775	G99775 S209P6330RD
C 561	19	1.3	298672	2	AC108330	18	1.2	633	6	AR546236	AR546236 Sequence
C 562	19	1.3	303425	2	AC111410	18	1.2	662	10	AY170508	AY170508 Mus muscu
C 563	19	1.3	307991	2	AC129728	18	1.2	669	14	AY315185	AY315185 Fowl aden
C 564	19	1.3	315475	2	AC136606	18	1.2	673	10	MUSMHTPE21	J00407 Mouse MHC c
C 565	19	1.3	326899	2	AC114071	18	1.2	676	8	TOBCELPE	L13443 N tabacum c
C 566	19	1.3	340000	9	AP001727	18	1.2	690	9	HSR332072	HSR332072
C 567	19	1.3	340000	9	HS21C003	18	1.2	699	11	BV034714	BV034714 S212P6315
C 568											

677	1.2	1157	6	CQ730523	Sequence	750	1.2	18	1.2	2218	6	AX332575	AX332575 Sequence
678	1.2	1157	6	AX549250	Sequence	751	1.2	18	1.2	2218	6	AX333214	AX333214 Sequence
679	1.2	1157	6	AF073799	Homo sapi	752	1.2	18	1.2	2218	6	HUMGLT015	Human gluco
680	1.2	1158	9	AX654289	Sequence	753	1.2	18	1.2	2219	6	CQ720131	Sequence
681	1.2	1158	9	AB041639	Bombyx mo	c 754	1.2	18	1.2	2250	6	AR528023	Sequence
682	1.2	1196	3	BC034017	Homo sapi	755	1.2	18	1.2	2250	6	BD135449	Galanin r
683	1.2	1233	9	MUSMKB	Mus muscu	756	1.2	18	1.2	2263	6	AR278021	Sequence
684	1.2	1235	10	MUSMHB	Mus muscu	c 757	1.2	18	1.2	2324	10	MMHCQ2K	MMHCQ2K
685	1.2	1252	10	MUSMHB2DA	Mus muscu	758	1.2	18	1.2	2378	9	HUMIGCAA	Human alpha
686	1.2	1275	6	AR475985	Mouse class	c 759	1.2	18	1.2	2427	5	CGA012647	CGA012647
687	1.2	1318	10	MUSMHTLB	Mus muscu	760	1.2	18	1.2	2464	6	AX646279	AX646279
688	1.2	1335	6	BD247557	Methods f	761	1.2	18	1.2	2464	6	AB065934	AB065934
689	1.2	1345	10	BC011306	Mus muscu	762	1.2	18	1.2	2593	8	ASNNUCS	ASNNUCS
690	1.2	1379	10	MUSMRNAC	Mus muscu	763	1.2	18	1.2	2637	10	MUSMHC2K	MUSMHC2K
691	1.2	1412	10	MUSMHC1H2D	Mus muscu	764	1.2	18	1.2	2637	10	MUSMHC2K	MUSMHC2K
692	1.2	1415	10	MUSMHC2DR	Mus muscu	765	1.2	18	1.2	2818	5	BC080992	BC080992
693	1.2	1415	10	MUSMHC2DS	Mus muscu	c 766	1.2	18	1.2	2865	3	AY060699	AY060699
694	1.2	1415	10	MUSMRNAA	Mus muscu	c 767	1.2	18	1.2	2872	9	GGIGA1CR	GGIGA1CR
695	1.2	1417	6	AR168030	Mus muscu	768	1.2	18	1.2	2916	14	FAD459805	FAD459805
696	1.2	1417	6	AR204801	Sequence	c 769	1.2	18	1.2	2920	3	MOTGABANT	MOTGABANT
697	1.2	1424	10	MUSMRNAB	Mus muscu	770	1.2	18	1.2	2934	6	AX660154	AX660154
698	1.2	1426	10	MUSMHC2DA	Mus muscu	c 771	1.2	18	1.2	2964	9	GGIGA2C	GGIGA2C
699	1.2	1431	10	MMQ7BANR	Mus muscu	772	1.2	18	1.2	2992	10	MUSHQ2K1K	MUSHQ2K1K
700	1.2	1432	9	AB032158S4	AB032158	773	1.2	18	1.2	3073	10	MMG37	MMG37
701	1.2	1435	10	MUSMHCQO	Mus muscu	774	1.2	18	1.2	3077	8	AF530594	AF530594
702	1.2	1442	10	MUSLW16A3A	Mus muscu	775	1.2	18	1.2	3165	9	HUGLUT6	HUGLUT6
703	1.2	1442	10	MUSMHC2KI	Mus muscu	776	1.2	18	1.2	3210	8	SCYOR034C	SCYOR034C
704	1.2	1443	10	MUSMHC2A	Mus muscu	777	1.2	18	1.2	3241	3	BMPTTHKS	BMPTTHKS
705	1.2	1450	10	MUSMHC2A	Mus muscu	778	1.2	18	1.2	3289	3	BMPTTHK	BMPTTHK
706	1.2	1452	10	MUSMHC2A	Mus muscu	779	1.2	18	1.2	3293	8	AK100082	AK100082
707	1.2	1457	10	MUSMHC2A	Mus muscu	780	1.2	18	1.2	3300	14	FAD431719	FAD431719
708	1.2	1462	10	MUSMHC2A	Mus muscu	c 781	1.2	18	1.2	3417	9	HSU41483	HSU41483
709	1.2	1462	10	MUSMHC2A	Mus muscu	c 782	1.2	18	1.2	3652	3	AK112758	AK112758
710	1.2	1462	10	MUSMHC2A	Mus muscu	c 783	1.2	18	1.2	3688	10	RNO7628	RNO7628
711	1.2	1462	10	MUSMHC2A	Mus muscu	784	1.2	18	1.2	3709	10	BC059854	BC059854
712	1.2	1462	10	MUSMHC2A	Mus muscu	c 785	1.2	18	1.2	3736	6	AR179196	AR179196
713	1.2	1462	10	MUSMHC2A	Mus muscu	c 786	1.2	18	1.2	3736	10	AB022699	AB022699
714	1.2	1462	10	MUSMHC2A	Mus muscu	787	1.2	18	1.2	3857	6	BD170434	BD170434
715	1.2	1462	10	MUSMHC2A	Mus muscu	788	1.2	18	1.2	3912	10	MUSMHC2K	MUSMHC2K
716	1.2	1473	10	MUSMHC2A	Mus muscu	789	1.2	18	1.2	3947	10	AF088905	AF088905
717	1.2	1477	10	MUSMHC2A	Mus muscu	790	1.2	18	1.2	3969	10	MUSMHC2K	MUSMHC2K
718	1.2	1483	10	MUSMHC2A	Mus muscu	c 791	1.2	18	1.2	3994	10	EX511043	EX511043
719	1.2	1504	10	MUSMHC2A	Mus muscu	792	1.2	18	1.2	4180	8	ATH510210	ATH510210
720	1.2	1517	10	BC023409	BC023409	c 793	1.2	18	1.2	4213	9	HS237948	HS237948
721	1.2	1540	10	MMU47329	MMU47329	c 794	1.2	18	1.2	4500	5	CHKAGRPR1A	CHKAGRPR1A
722	1.2	1541	10	MMU47329	MMU47329	c 795	1.2	18	1.2	4550	5	CHKAGRPR1A	CHKAGRPR1A
723	1.2	1544	10	BC054430	BC054430	796	1.2	18	1.2	4693	10	MUSMHC2K	MUSMHC2K
724	1.2	1560	10	MUSMHC2A	Mus muscu	797	1.2	18	1.2	4707	10	MUSMHC2K	MUSMHC2K
725	1.2	1564	10	MMU47328	MMU47328	798	1.2	18	1.2	4731	10	MUSMHC2K	MUSMHC2K
726	1.2	1567	10	MMU47325	MMU47325	799	1.2	18	1.2	4763	10	MUSMHC2K	MUSMHC2K
727	1.2	1567	10	MMU47327	MMU47327	800	1.2	18	1.2	4968	10	MUSMHC2K	MUSMHC2K
728	1.2	1598	10	BC018402	BC018402	801	1.2	18	1.2	5141	10	MMANT12	MMANT12
729	1.2	1611	6	CQ805724	CQ805724	802	1.2	18	1.2	5164	10	AK129330	AK129330
730	1.2	1630	10	BC080756	BC080756	803	1.2	18	1.2	5221	10	MUSMHC2K	MUSMHC2K
731	1.2	1666	10	MMH2L3	MMH2L3	804	1.2	18	1.2	5273	10	MMQ1K5	MMQ1K5
732	1.2	1666	10	MUSMHC2A	Mus muscu	c 805	1.2	18	1.2	5280	3	TER318886	TER318886
733	1.2	1673	10	BC010602	BC010602	806	1.2	18	1.2	5373	9	HSM803141	HSM803141
734	1.2	1745	8	BT002790	BT002790	c 807	1.2	18	1.2	5464	6	CQ588569	CQ588569
735	1.2	1810	5	DLA419594	DLA419594	808	1.2	18	1.2	5479	10	MMH2KK	MMH2KK
736	1.2	1813	5	AP218841	AP218841	809	1.2	18	1.2	5703	10	BC054080	BC054080
737	1.2	1814	10	MMHQ7G2	MMHQ7G2	810	1.2	18	1.2	5709	10	MMH2KB	MMH2KB
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741	1.2	1947	8	AY341855	AY341855	814	1.2	18	1.2	6447	6	CQ592310	CQ592310
742	1.2	2000	6	AX508666	AX508666	c 815	1.2	18	1.2	7330	9	HSK308545	HSK308545
743	1.2	2005	8	AX121093	AX121093	c 816	1.2	18	1.2	8025	5	CHKAGRIN	CHKAGRIN
744	1.2	2011	3	AB092510	AB092510	c 817	1.2	18	1.2	8205	5	HSK308545	HSK308545
745	1.2	2014	10	MMH2DQ3	MMH2DQ3	c 818	1.2	18	1.2	8410	8	CVU39931	CVU39931
746	1.2	2014	10	MMH2LQ3	MMH2LQ3	c 819	1.2	18	1.2	9488	8	CNS08CBX	CNS08CBX
747	1.2	2018	10	AB013890	AB013890	820	1.2	18	1.2	9906	6	AX957039	AX957039
748	1.2	2213	9	BC001692	BC001692	821	1.2	18	1.2	9917	6	AX957038	AX957038
749	1.2	2213	9	BC001820	BC001820	822	1.2	18	1.2	9999	1	AE001942	AE001942

C 823	18	1.2	10002	1	AE008950	Agrobacte	C 896	18	1.2	74822	9	HSJ797M17	AL049798	Human DNA
C 824	18	1.2	10115	1	AE007897	Agrobacte	C 897	18	1.2	74965	9	AC092607	AC092607	Homo sapi
C 825	18	1.2	10351	1	AE013038	Thermoana	C 898	18	1.2	74999	9	AC008960	AC008960	Homo sapi
C 826	18	1.2	10359	1	AE007591	AE007591	C 899	18	1.2	75323	10	AC076971	AC076971	Homo sapi
C 827	18	1.2	10485	1	AE002424	Neisseria	C 900	18	1.2	76465	9	AL607129	AL607129	Mouse DNA
C 828	18	1.2	10591	1	AE005819	Caulobact	C 901	18	1.2	77366	10	AC087217	AC087217	Mus muscu
C 829	18	1.2	14050	1	AE000731	Aquifex a	C 902	18	1.2	77427	2	AC027159	AC027159	Homo sapi
C 830	18	1.2	15698	10	RNO292748	Au292748	C 903	18	1.2	79173	9	AC114958	AC114958	Homo sapi
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C 837	18	1.2	20462	9	AP000325	Homo sapi	C 910	18	1.2	81169	2	AL357292	AL357292	Homo sapi
C 838	18	1.2	21111	9	AL592526	Human DNA	C 911	18	1.2	81784	8	AC078893	AC078893	Oryza sat
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C 843	18	1.2	27400	3	CFP28H7	Z72508	C 916	18	1.2	86620	2	AC084124	AC084124	Homo sapi
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C 845	18	1.2	31433	3	U88165	U88165	C 918	18	1.2	87551	2	AC021944	AC021944	Homo sapi
C 846	18	1.2	32239	10	AB034241	Rattus no	C 919	18	1.2	88543	8	AC004680	AC004680	Arabisops
C 847	18	1.2	36558	2	AC135099	AC135099	C 920	18	1.2	88940	2	AC138602	AC138602	Mus muscu
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C 867	18	1.2	44562	2	AC151590	AC151590	C 940	18	1.2	101218	8	AC118284	AC118284	Oryza sat
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C 877	18	1.2	60286	9	AL163544	AL163544	C 950	18	1.2	106635	2	AY555279	AY555279	Mus muscu
C 878	18	1.2	60869	9	AL590136	AL590136	C 951	18	1.2	107714	2	AL356306	AL356306	Homo sapi
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C 881	18	1.2	61187	9	HS83L6	Z99130	C 954	18	1.2	110000	2	AC013623	AC013623	Continuation (3 of
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C 886	18	1.2	65229	9	AL672108	AL672108	C 959	18	1.2	110000	2	AC109940	AC109940	Continuation (3 of
C 887	18	1.2	68780	2	AC111118	AC111118	C 960	18	1.2	110000	2	AC110355	AC110355	Rattus no
C 888	18	1.2	69663	9	AL133377	AL133377	C 961	18	1.2	110000	2	AC114055	AC114055	Continuation (4 of
C 889	18	1.2	70194	2	AC133888	AC133888	C 962	18	1.2	110000	2	AC117310	AC117310	Continuation (2 of
C 890	18	1.2	71823	2	AC104962	AC104962	C 963	18	1.2	110000	2	AC118144	AC118144	Rattus no
C 891	18	1.2	72322	6	AX695443	AX695443	C 964	18	1.2	110000	2	AC126295	AC126295	Continuation (4 of
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C 893	18	1.2	73947	9	AL591968	AL591968	C 966	18	1.2	110000	2	AX842678	AX842678	Continuation (2 of
C 894	18	1.2	74029	9	AL356512	AL356512	C 967	18	1.2	110000	8	CR382135	CR382135	Continuation (15 of
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RESULT 2
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DEFINITION Sequence 1 from Patent WO2004082566.
ACCESSION CQ880087
VERSION CQ880087.1 GI:54033865
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Golz, S., Brueggemeier, U. and Summer, H.
TITLE Diagnostics and therapeutics for diseases associated with
complement component 3a receptor 1 (c3arl)
JOURNAL Patent: WO 2004082566-A 1 30-SEP-2004;
Bayer Healthcare AG (DE)
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REFERENCE

<p>AUTHORS Brown, J.P., Burmer, G.C., Roush, C.L., and Morningstar, D.A. TITLE Diagnostic and therapeutic compositions and methods related to anaphylatoxin c3a receptor JOURNAL Patent: WO 0244737-A 1 06-JUN-2002; Lifespan Biosciences, Inc. (US) FEATURES Location/Qualifiers source 1..1449 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"</p>	
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QY	61	CCCCAGTAAATCTCTCCATGTCATCTTCAGCCCTACTTTTAACTGGGATGTCAGGC	120		
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QY	1381	GAGCTCACAGTTCACCCCTGCTCCCTCAACCAATGTCTTTCAGAAAGAAATAGTACA	1440		
DB	1381	GAGCTCACAGTTCACCCCTGCTCCCTCAACCAATGTCTTTCAGAAAGAAATAGTACA	1440		
QY	1441	ACTGTGTGA 1449			
DB	1441	ACTGTGTGA 1449			
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LOCUS		complete cds.			
ACCESSION		AY268431			
VERSION		AY268431.1 GI:30385605			
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SOURCE		Homo sapiens			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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AUTHORS		Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.			
TITLE		Isolation of complete coding sequence for complement component 3a receptor 1 (C3AR1)			
JOURNAL		Unpublished			
REFERENCE		2 (bases 1 to 1449)			
AUTHORS		Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.			
TITLE		Direct Submission			
JOURNAL		Submitted (01-APR-2003) Guthrie cDNA Resource Center, Guthrie Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA			
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DEFINITION H.sapiens mRNA for C3a anaphylatoxin receptor.
ACCESSION Z73157
VERSION Z73157.1 GI:2826756
KEYWORDS C3a anaphylatoxin receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1449)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Expression cloning of the human C3a anaphylatoxin receptor (C3aR)
JOURNAL from differentiated U-937 cells
MEDLINE Eur. J. Immunol. 26 (8), 1944-1950 (1996)
PUBMED 96350520
REFERENCE 2
AUTHORS Bautsch, W.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1996) Crass T., Hannover Medical School,
Institute of Medical Microbiology, Carl-Neuberg-Str. 1, Hannover,
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Germany, 30625
 Revised by [3]
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 Bautsch, W.
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 Submitted (28-JAN-1998) Bautsch W., Hannover Medical School,
 Institute of Medical Microbiology, Konstanty-Gutschow-Str. 8,
 Hannover, Germany, 30625
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ORIGIN

Query Match 100.0%; Score 1449; DB 9; Length 1449;
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DEFINITION Sequence 661 from Patent EP1270724.
ACCESSION AX646469
VERSION AX646469.1 GI:28798850
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Suwa, M., Arai, K., Akiyama, Y. and Aburatani, H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 661 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology Incubation, Ltd.
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RESULT 9
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LOCUS AB065870 1849 bp DNA linear PRI 23-JUL-2002

DEFINITION Homo sapiens gene for seven transmembrane helix receptor, complete
 cds, isolate:CBRC7TM_433.

ACCESSION AB065870
 VERSION AB065870.1 GI:21929004

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Suwa,M.; Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
 Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.

TITLE Genome-wide discovery and analysis of human seven transmembrane
 helix receptor genes

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1849)

AUTHORS Suwa,M.
 TITLE Direct Submission

JOURNAL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
 Center (CBRC), National Institute of Advanced Industrial Science
 and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
 (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
 Tel.81-3-3599-8080, Fax:81-3-3599-8081)

COMMENT This sequence is a seven transmembrane helix receptor candidate
 predicted from the whole human genome sequences using our automated
 system that contains programs of gene
 finding (GeneDecoder), sequence search, motif-domain assignment and
 transmembrane helix prediction.

And the sequence is submitted by the collaborative project between
 (Computational Biology Research Center (CBRC), National Institute
 of Advanced Industrial Science and Technology (AIST)) and [Genome
 Science Division, Research Center for Advanced Science and
 Technology (RCAT), University of Tokyo].

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 Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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 DEFINITION Homo sapiens complement component 3a receptor 1, mRNA (CDNA clone
 MGC:22570 IMAGE:4690283), complete cds.

ACCESSION BC020742
 VERSION BC020742.1 GI:18088764
 KEYWORDS MGC
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1985)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Altschuler, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
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 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 1985)
 Strausberg, R.
 Direct Submission
 Submitted (03-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

TITLE
 JOURNAL
 PUBLISHED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT

NIH-MGC Project URL: <http://mgi.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil1.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAL Plate: 36 Row: 1 Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 21314629.

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 Best Local Similarity 100.0%; Pred. No. 0;
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 Qy 121 AATGGCTGGTCTGCTGGTGGCTGGCTGAGATGACGGGACAGTGAACACAATTTGG 180
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 VERSION AY455929.1 GI:38201494
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (Bases 1 to 12053)
 AUTHORS Rieder,M.J., Daniels,R.L., da Ponte,S.H., Hastings,N.C.,
 Ahearn,M.O., Rajkumar,N., Yi,Q. and Nickerson,D.A.
 TITLE Direct Submission
 JOURNAL Submitted (31-OCT-2003) Genome Sciences, University of Washington,
 1705 NE Pacific, Seattle, WA 98195, USA
 COMMENT To cite this work please use: SeattleSNPs, NHLBI HL66682 Program
 for Genomic Applications, UW-PHCRC, Seattle, WA (URL:
 http://pga.gs.washington.edu).
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Qy  121  AATGGCTGGTGTGGTGGTGGCTGAGATGACGGGACAGTGAACACAAATTTGG 180
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 Human BAC Library) complete sequence.

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 ORGANISM Homo sapiens

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 AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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 Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
 Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
 Submitted (29-APR-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
 Submitted (30-APR-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
 Submitted (01-SEP-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 6 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
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 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 7 (bases 1 to 186321)
 Worley,K.C.
 Direct Submission
 Submitted (03-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 8 (bases 1 to 186321)
 Worley,K.C.

TITLE
JOURNAL

Direct Submission
Submitted (31-DEC-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 29, 1999 this sequence version replaced gi:4309839.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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 REFERENCE 1 (bases 1 to 1956)
 AUTHORS Roglic,A., Prossnitz,E.R., Cavanagh,S.L., Pan,Z., Zou,A. and
 Ye,R.D.
 TITLE cDNA cloning of a novel G protein-coupled receptor with a large
 extracellular loop structure
 JOURNAL Biochim. Biophys. Acta 1305 (1-2), 39-43 (1996)
 MEDLINE 96180983
 PUBMED 8605247
 REFERENCE 2 (bases 1 to 1956)
 AUTHORS Ye,R.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-1995) Richard D. Ye, Immunology, IMM-25, Scripps
 Research Institute, 10666 N. Torrey Pines Road, La Jolla, CA 92037,
 USA

FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:52:00 ; Search time 267 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 81813359 residues

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SUMMARIES

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9	21	1.4	28493	4	US-09-502-540-1241
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C 23	19	1.3	197496	4	US-09-877-177A-10
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32	18	1.2	493	4	US-09-430-470-9	Sequence 9, Appli
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34	18	1.2	499	4	US-09-430-470-3	Sequence 3, Appli
C 35	18	1.2	582	4	US-09-792-024-41	Sequence 41, Appli
36	18	1.2	601	4	US-09-949-016-19180	Sequence 19180, A
37	18	1.2	601	4	US-09-949-016-19181	Sequence 19181, A
38	18	1.2	601	4	US-09-949-016-19182	Sequence 19182, A
39	18	1.2	601	4	US-09-949-016-23333	Sequence 23333, A
40	18	1.2	601	4	US-09-949-016-45600	Sequence 45600, A
C 41	18	1.2	601	4	US-09-949-016-75741	Sequence 75741, A
C 42	18	1.2	601	4	US-09-949-016-75742	Sequence 75742, A
C 43	18	1.2	601	4	US-09-949-016-75743	Sequence 75743, A
44	18	1.2	601	4	US-09-949-016-130449	Sequence 130449, A
45	18	1.2	601	4	US-09-949-016-130450	Sequence 130450, A
46	18	1.2	601	4	US-09-949-016-130451	Sequence 130451, A
C 47	18	1.2	633	4	US-09-248-796A-1367	Sequence 1367, Ap
48	18	1.2	941	3	US-08-829-613-1	Sequence 1, Appli
49	18	1.2	1107	4	US-09-595-549-3	Sequence 3, Appli
50	18	1.2	1275	4	US-08-916-247A-3	Sequence 3, Appli
51	18	1.2	1417	3	US-09-199-737-3	Sequence 3, Appli
52	18	1.2	1417	3	US-09-058-333A-3	Sequence 3, Appli
53	18	1.2	1427	4	US-09-500-495A-3	Sequence 3, Appli
C 54	18	1.2	2250	4	US-09-614-221A-326	Sequence 326, App
55	18	1.2	2263	4	US-09-595-549-1	Sequence 1, Appli
C 56	18	1.2	3513	4	US-09-815-923-13	Sequence 13, Appli
C 57	18	1.2	3736	3	US-09-600-776-10	Sequence 10, Appli
C 58	18	1.2	3736	4	US-09-965-830-10	Sequence 10, Appli
C 59	18	1.2	8671	4	US-09-949-016-15455	Sequence 15455, A
60	18	1.2	11667	4	US-09-949-016-13934	Sequence 13934, A
C 61	18	1.2	23276	4	US-09-949-016-15461	Sequence 15461, A
62	18	1.2	26075	4	US-09-949-016-12004	Sequence 12004, A
C 63	18	1.2	28076	4	US-09-949-016-13041	Sequence 13041, A
C 64	18	1.2	28845	4	US-09-949-016-11815	Sequence 11815, A
C 65	18	1.2	27132	4	US-09-949-016-15424	Sequence 15424, A
C 66	18	1.2	34199	4	US-09-902-540-1255	Sequence 1255, Ap
67	18	1.2	36661	4	US-09-949-016-16102	Sequence 16102, A
68	18	1.2	49212	4	US-09-949-016-12494	Sequence 12494, A
69	18	1.2	49220	4	US-09-949-016-14726	Sequence 14726, A
70	18	1.2	87562	4	US-09-949-016-13685	Sequence 13685, A
71	18	1.2	102409	4	US-09-949-016-15148	Sequence 15148, A
C 72	18	1.2	112112	4	US-09-949-016-15639	Sequence 15639, A
73	18	1.2	116652	4	US-09-949-016-13413	Sequence 13413, A
C 74	18	1.2	152582	4	US-09-949-016-12086	Sequence 12086, A
C 75	18	1.2	152583	4	US-09-949-016-17390	Sequence 17390, A
C 76	18	1.2	152583	4	US-09-949-016-17391	Sequence 17391, A
C 77	18	1.2	227390	4	US-09-949-016-12201	Sequence 12201, A
C 78	18	1.2	227391	4	US-09-949-016-13365	Sequence 13365, A
79	18	1.2	236341	4	US-09-949-016-13978	Sequence 13978, A
80	18	1.2	670689	4	US-09-949-016-12505	Sequence 12505, A
81	18	1.2	670690	4	US-09-949-016-14207	Sequence 14207, A
C 82	17	1.2	30	2	US-08-467-948A-14	Sequence 14, Appli
C 83	17	1.2	30	3	US-08-467-947A-14	Sequence 7, Appli
C 84	17	1.2	153	5	PCT-US91-06418-7	Sequence 1072, Ap
85	17	1.2	183	4	US-09-134-000C-1072	Sequence 1072, Ap
86	17	1.2	240	3	US-09-476-124-7	Sequence 7, Appli
87	17	1.2	240	3	US-09-476-124-42	Sequence 42, Appli
88	17	1.2	240	3	US-09-270-542-105	Sequence 105, App
89	17	1.2	241	3	US-09-476-124-6	Sequence 6, Appli
C 90	17	1.2	305	4	US-09-513-999C-2219	Sequence 2219, Ap
C 91	17	1.2	319	4	US-09-513-999C-11852	Sequence 11852, A
92	17	1.2	340	4	US-09-621-976-1395	Sequence 1395, Ap
93	17	1.2	369	3	US-09-270-542-121	Sequence 121, App
94	17	1.2	369	3	US-09-389-681-236	Sequence 236, App
C 95	17	1.2	441	4	US-09-620-405B-236	Sequence 236, App
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C 100	17	1.2	441	4	US-09-834-759-236	Sequence 236, App

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C 102	17	1.2	441	4	US-09-551-621-236	Sequence 236, App	175	17	1.2	1699	2	US-08-484-158B-3	Sequence 3, Appli
C 103	17	1.2	472	1	US-08-361-467B-2	Sequence 2, Appli	176	17	1.2	1699	2	US-08-484-596A-3	Sequence 3, Appli
C 104	17	1.2	472	1	US-08-484-332C-2	Sequence 16397, A	177	17	1.2	1699	2	US-08-480-150A-3	Sequence 3, Appli
C 105	17	1.2	472	1	US-09-621-976-16397	Sequence 1463, A	178	17	1.2	1699	3	US-08-458-731-3	Sequence 3, Appli
C 106	17	1.2	472	4	US-09-702-705-1463	Sequence 1463, A	179	17	1.2	1699	3	US-08-149-223A-3	Sequence 3, Appli
C 107	17	1.2	502	4	US-09-736-457-1463	Sequence 1463, A	180	17	1.2	1770	4	US-09-908-540-345	Sequence 345, App
C 108	17	1.2	502	4	US-09-614-124B-1463	Sequence 1463, A	181	17	1.2	1820	4	US-09-270-542-129	Sequence 129, App
C 109	17	1.2	502	4	US-09-671-325-1463	Sequence 1463, A	182	17	1.2	1820	4	US-09-023-655-1031	Sequence 1031, App
C 110	17	1.2	502	4	US-09-588-824-1463	Sequence 1463, A	183	17	1.2	1870	3	US-09-476-124-9	Sequence 9, Appli
C 111	17	1.2	537	4	US-09-270-767-3199	Sequence 3199, App	184	17	1.2	1870	3	US-09-270-542-128	Sequence 128, App
C 112	17	1.2	537	4	US-09-270-767-18481	Sequence 18481, A	185	17	1.2	1908	4	US-09-248-796A-2841	Sequence 2841, App
C 113	17	1.2	601	4	US-09-949-016-22271	Sequence 22271, A	186	17	1.2	1941	4	US-09-205-258-191	Sequence 191, App
C 114	17	1.2	601	4	US-09-949-016-25973	Sequence 25973, A	187	17	1.2	1942	3	US-09-270-542-127	Sequence 127, App
C 115	17	1.2	601	4	US-09-949-016-27447	Sequence 27447, A	188	17	1.2	1942	4	US-09-016-434-1191	Sequence 1191, App
C 116	17	1.2	601	4	US-09-949-016-27448	Sequence 27448, A	189	17	1.2	1954	3	US-08-922-635-2	Sequence 2, Appli
C 117	17	1.2	601	4	US-09-949-016-27448	Sequence 27448, A	190	17	1.2	1986	3	US-09-221-017B-150	Sequence 150, App
C 118	17	1.2	601	4	US-09-949-016-29426	Sequence 29426, A	191	17	1.2	2001	4	US-09-841-683-3	Sequence 1, Appli
C 119	17	1.2	601	4	US-09-949-016-33982	Sequence 33982, A	192	17	1.2	2024	2	US-08-458-970A-1	Sequence 1, Appli
C 120	17	1.2	601	4	US-09-949-016-64813	Sequence 64813, A	193	17	1.2	2105	4	US-09-949-016-195	Sequence 195, App
C 121	17	1.2	601	4	US-09-949-016-85389	Sequence 85389, A	194	17	1.2	2132	3	US-09-159-385-3	Sequence 3, Appli
C 122	17	1.2	601	4	US-09-949-016-85476	Sequence 85476, A	195	17	1.2	2132	3	US-09-186-277-3	Sequence 3, Appli
C 123	17	1.2	601	4	US-09-949-016-92665	Sequence 92665, A	196	17	1.2	2157	4	US-09-949-016-1966	Sequence 1966, App
C 124	17	1.2	601	4	US-09-949-016-94440	Sequence 94440, A	197	17	1.2	2216	3	US-09-270-542-126	Sequence 126, App
C 125	17	1.2	601	4	US-09-949-016-96287	Sequence 96287, A	198	17	1.2	2340	4	US-09-023-655-359	Sequence 359, App
C 126	17	1.2	601	4	US-09-949-016-116885	Sequence 116885, A	199	17	1.2	2389	3	US-08-691-563C-52	Sequence 52, Appli
C 127	17	1.2	601	4	US-09-949-016-116886	Sequence 116886, A	200	17	1.2	2389	4	US-08-374-766-52	Sequence 52, Appli
C 128	17	1.2	601	4	US-09-949-016-121072	Sequence 121072, A	201	17	1.2	2389	4	US-08-979-847B-48	Sequence 48, Appli
C 129	17	1.2	601	4	US-09-949-016-140277	Sequence 140277, A	202	17	1.2	2487	4	US-09-949-016-2924	Sequence 2924, App
C 130	17	1.2	601	4	US-09-949-016-140278	Sequence 140278, A	203	17	1.2	2488	1	US-08-279-270A-2	Sequence 2, Appli
C 131	17	1.2	601	4	US-09-949-016-148472	Sequence 148472, A	204	17	1.2	2488	4	US-09-949-016-634	Sequence 634, App
C 132	17	1.2	601	4	US-09-949-016-148473	Sequence 148473, A	205	17	1.2	2499	4	US-09-949-016-2925	Sequence 2925, App
C 133	17	1.2	601	4	US-09-949-016-148474	Sequence 148474, A	206	17	1.2	2525	4	US-08-205-258-121	Sequence 121, App
C 134	17	1.2	601	4	US-09-949-016-152652	Sequence 152652, A	207	17	1.2	2635	4	US-09-949-016-5032	Sequence 5032, App
C 135	17	1.2	601	4	US-09-949-016-175603	Sequence 175603, A	208	17	1.2	2677	3	US-07-945-295-3	Sequence 3, Appli
C 136	17	1.2	601	4	US-09-949-016-175634	Sequence 175634, A	209	17	1.2	2739	4	US-08-693-174-5	Sequence 5, Appli
C 137	17	1.2	601	4	US-09-949-016-176535	Sequence 176535, A	210	17	1.2	3157	2	US-09-253-738-5	Sequence 5, Appli
C 138	17	1.2	601	4	US-09-949-016-176536	Sequence 176536, A	211	17	1.2	3157	3	US-08-650-766-3	Sequence 3, Appli
C 139	17	1.2	601	4	US-09-949-016-190125	Sequence 190125, A	212	17	1.2	3318	3	US-08-922-635-3	Sequence 3, Appli
C 140	17	1.2	601	4	US-09-949-016-192460	Sequence 192460, A	213	17	1.2	3318	3	US-08-389-487-3	Sequence 3, Appli
C 141	17	1.2	601	4	US-09-949-016-192461	Sequence 192461, A	214	17	1.2	3385	4	US-08-650-766-1	Sequence 1, Appli
C 142	17	1.2	601	4	US-09-949-016-196977	Sequence 196977, A	215	17	1.2	3385	3	US-08-922-635-1	Sequence 1, Appli
C 143	17	1.2	601	4	US-09-949-016-199631	Sequence 199631, A	216	17	1.2	3385	4	US-09-389-487-1	Sequence 1, Appli
C 144	17	1.2	601	4	US-09-949-016-204396	Sequence 204396, A	217	17	1.2	3694	3	US-09-232-200-46	Sequence 46, Appli
C 145	17	1.2	699	4	US-09-949-016-5374	Sequence 5374, App	218	17	1.2	3694	3	US-09-232-197-46	Sequence 46, Appli
C 146	17	1.2	837	4	US-09-502-540-6253	Sequence 6253, App	219	17	1.2	3694	3	US-09-232-200-24	Sequence 24, Appli
C 147	17	1.2	927	4	US-09-248-796A-7190	Sequence 7190, App	220	17	1.2	3704	3	US-09-232-201-24	Sequence 24, Appli
C 148	17	1.2	1068	4	US-09-252-991A-13963	Sequence 13963, A	221	17	1.2	3704	3	US-09-232-195-24	Sequence 24, Appli
C 149	17	1.2	1068	4	US-09-170-496D-1	Sequence 1, Appli	222	17	1.2	3930	3	US-09-162-373-2	Sequence 2, Appli
C 150	17	1.2	1086	4	US-09-252-991A-13855	Sequence 13855, A	223	17	1.2	3930	3	US-09-467-346-2	Sequence 2, Appli
C 151	17	1.2	1128	2	US-08-446-875-7	Sequence 7, Appli	224	17	1.2	3975	4	US-09-949-016-4064	Sequence 4064, App
C 152	17	1.2	1128	2	US-08-102-385G-7	Sequence 3, Appli	225	17	1.2	4338	4	US-09-360-237-4	Sequence 3, Appli
C 153	17	1.2	1134	4	US-09-248-796A-6124	Sequence 6124, App	226	17	1.2	4338	4	US-09-891-711-3	Sequence 3, Appli
C 154	17	1.2	1222	1	US-08-195-744-3	Sequence 3, Appli	227	17	1.2	4338	4	US-09-949-016-542	Sequence 542, App
C 155	17	1.2	1222	2	US-08-788-279-3	Sequence 3, Appli	228	17	1.2	4338	4	US-09-949-016-4816	Sequence 4816, App
C 156	17	1.2	1239	4	US-09-949-016-5617	Sequence 5617, App	229	17	1.2	4755	4	US-09-799-451-377	Sequence 377, App
C 157	17	1.2	1328	4	US-09-799-451-396	Sequence 396, App	230	17	1.2	4836	4	US-09-799-451-376	Sequence 376, App
C 158	17	1.2	1365	4	US-09-252-991A-13593	Sequence 13593, A	231	17	1.2	5128	4	US-09-364-206-1	Sequence 1, Appli
C 159	17	1.2	1406	4	US-09-248-796A-5081	Sequence 5081, A	232	17	1.2	5175	2	US-08-643-530B-3	Sequence 3, Appli
C 160	17	1.2	1477	4	US-09-949-016-5325	Sequence 5325, App	233	17	1.2	5175	2	US-09-636-728-3	Sequence 3, Appli
C 161	17	1.2	1438	4	US-09-016-434-1426	Sequence 1426, App	234	17	1.2	5697	2	US-08-843-530B-5	Sequence 5, Appli
C 162	17	1.2	1533	4	US-09-543-681A-1482	Sequence 1482, App	235	17	1.2	5697	2	US-08-636-728-4	Sequence 4, Appli
C 163	17	1.2	1545	4	US-09-841-683-1	Sequence 1, Appli	236	17	1.2	6063	1	US-08-195-744-4	Sequence 4, Appli
C 164	17	1.2	1560	4	US-08-248-796A-5085	Sequence 5085, App	237	17	1.2	6063	2	US-08-788-279-4	Sequence 4, Appli
C 165	17	1.2	1645	4	US-09-949-016-3832	Sequence 3832, App	238	17	1.2	6545	2	US-08-843-530B-1	Sequence 1, Appli
C 166	17	1.2	1647	3	US-09-270-542-120	Sequence 120, App	239	17	1.2	6545	4	US-09-636-728-1	Sequence 1, Appli
C 167	17	1.2	1673	1	US-08-476-008-4	Sequence 4, Appli	240	17	1.2	9377	4	US-09-801-874-3	Sequence 3, Appli
C 168	17	1.2	1673	1	US-08-306-063-4	Sequence 4, Appli	241	17	1.2	10634	4	US-09-949-016-15253	Sequence 15253, A
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C 170	17	1.2	1673	3	US-09-137-440-4	Sequence 4, Appli	243	17	1.2				
C 171	17	1.2	1673	5	PCT-US91-06148A-4	Sequence 2, Appli	244	17	1.2				
C 172	17	1.2	1678	3	US-08-650-766-2	Sequence 2, Appli	245	17	1.2				
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c 256	1.2	16221	4	US-09-949-016-13708	Sequence 13708, A	329	17	1.2	155019	3	US-09-949-016-16029	Sequence 16029, A
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c 258	1.2	16740	4	US-09-949-016-17516	Sequence 17516, A	331	17	1.2	176737	3	US-09-128-155-17	Sequence 17, Appl
c 259	1.2	17146	4	US-09-949-016-16774	Sequence 16774, A	332	17	1.2	187136	4	US-09-949-016-17231	Sequence 17231, A
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c 263	1.2	20063	4	US-09-949-016-14176	Sequence 14176, A	c 336	17	1.2	312470	4	US-09-949-016-14043	Sequence 14043, A
c 264	1.2	20520	4	US-09-949-016-14394	Sequence 14394, A	c 337	17	1.2	325034	4	US-09-949-016-14957	Sequence 14957, A
c 265	1.2	20852	4	US-09-949-016-14974	Sequence 14974, A	c 338	17	1.2	330024	4	US-09-949-016-12373	Sequence 12373, A
c 266	1.2	22123	4	US-09-949-016-12376	Sequence 12376, A	c 339	17	1.2	340380	4	US-09-949-016-14179	Sequence 14179, A
c 267	1.2	22124	4	US-09-949-016-14666	Sequence 14666, A	340	17	1.2	373182	4	US-09-949-016-17371	Sequence 17371, A
c 268	1.2	22131	4	US-09-949-016-15391	Sequence 15391, A	341	17	1.2	373694	4	US-09-949-016-12062	Sequence 12062, A
c 269	1.2	22131	4	US-09-949-016-15392	Sequence 15392, A	342	17	1.2	387902	4	US-09-949-016-14543	Sequence 14543, A
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c 272	1.2	26016	4	US-09-326-480A-1	Sequence 1, Appl	345	17	1.2	480073	3	US-08-545-528D-1	Sequence 1, Appl
c 273	1.2	26884	4	US-09-949-016-15109	Sequence 15109, A	c 346	17	1.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
c 274	1.2	26884	4	US-09-949-016-15110	Sequence 15110, A	c 347	17	1.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl
c 275	1.2	26684	4	US-09-949-016-17409	Sequence 17409, A	c 348	16	1.1	20	3	US-09-428-696-49	Sequence 49, Appl
c 276	1.2	26684	4	US-09-949-016-17410	Sequence 17410, A	349	16	1.1	43	4	US-10-043-142-4	Sequence 4, Appl
c 277	1.2	27180	4	US-09-949-016-14586	Sequence 14586, A	350	16	1.1	43	4	US-09-806-399-4	Sequence 4, Appl
c 278	1.2	27180	4	US-09-949-016-1587	Sequence 1587, A	c 351	16	1.1	138	4	US-09-621-976-9587	Sequence 9587, Ap
c 279	1.2	28819	4	US-09-949-016-15806	Sequence 15806, A	c 352	16	1.1	171	4	US-09-513-999C-22899	Sequence 22899, A
c 280	1.2	28843	4	US-09-949-016-17325	Sequence 17325, A	c 353	16	1.1	172	4	US-09-513-999C-26355	Sequence 26355, A
c 281	1.2	29965	4	US-09-949-016-11953	Sequence 11953, A	c 354	16	1.1	173	4	US-09-513-999C-23108	Sequence 23108, A
c 282	1.2	29966	4	US-09-949-016-16728	Sequence 16728, A	c 355	16	1.1	195	4	US-09-248-796A-10922	Sequence 10922, A
c 283	1.2	31407	4	US-09-949-016-17359	Sequence 17359, A	c 356	16	1.1	195	4	US-09-513-999C-433	Sequence 433, App
c 284	1.2	35417	4	US-09-949-016-16129	Sequence 16129, A	c 357	16	1.1	198	4	US-09-248-796A-9882	Sequence 9882, Ap
c 285	1.2	36577	4	US-09-949-016-13176	Sequence 13176, A	c 358	16	1.1	241	4	US-09-471-276-611	Sequence 611, App
c 286	1.2	37622	4	US-09-949-016-12294	Sequence 12294, A	c 359	16	1.1	260	4	US-09-313-294A-2528	Sequence 2528, Ap
c 287	1.2	37622	4	US-09-949-016-15726	Sequence 15726, A	c 360	16	1.1	261	4	US-09-621-976-15510	Sequence 15510, A
c 288	1.2	38961	4	US-09-949-016-12143	Sequence 12143, A	c 361	16	1.1	276	4	US-09-513-999C-11063	Sequence 11063, A
c 289	1.2	38961	4	US-09-949-016-14474	Sequence 14474, A	c 362	16	1.1	288	4	US-09-543-681A-926	Sequence 926, App
c 290	1.2	42404	4	US-09-949-016-16415	Sequence 16415, A	c 363	16	1.1	298	4	US-09-513-999C-24440	Sequence 24440, A
c 291	1.2	42931	4	US-08-311-731A-1281	Sequence 129, App	c 364	16	1.1	305	4	US-09-513-999C-2372	Sequence 2372, Ap
c 292	1.2	43717	4	US-09-949-016-16821	Sequence 16821, A	c 365	16	1.1	312	4	US-09-270-767-26747	Sequence 26747, A
c 293	1.2	47471	4	US-09-949-016-12271	Sequence 12271, A	c 366	16	1.1	343	2	US-08-473-020A-5	Sequence 5, Appl
c 294	1.2	47787	4	US-09-949-016-11969	Sequence 11969, A	c 367	16	1.1	348	3	US-09-423-233-15	Sequence 15, Appl
c 295	1.2	49052	4	US-09-949-016-12203	Sequence 12203, A	c 368	16	1.1	349	3	US-09-423-233-16	Sequence 16, Appl
c 296	1.2	49189	4	US-09-949-016-15583	Sequence 15583, A	c 369	16	1.1	356	2	US-08-485-158A-9	Sequence 9, Appl
c 297	1.2	50383	4	US-09-949-016-17600	Sequence 17600, A	c 370	16	1.1	356	4	US-09-147-993A-4	Sequence 4, Appl
c 298	1.2	55703	4	US-09-949-016-12007	Sequence 12007, A	c 371	16	1.1	360	4	US-09-621-976-15509	Sequence 61, Appl
c 299	1.2	55703	4	US-09-949-016-15781	Sequence 15781, A	c 372	16	1.1	366	2	US-08-967-101-61	Sequence 61, Appl
c 300	1.2	57178	4	US-09-949-016-12838	Sequence 12838, A	c 373	16	1.1	366	2	US-08-593-541-61	Sequence 61, Appl
c 301	1.2	57178	4	US-09-949-016-17458	Sequence 17458, A	c 374	16	1.1	366	3	US-09-124-698-61	Sequence 61, Appl
c 302	1.2	61461	4	US-09-949-016-16419	Sequence 16419, A	c 375	16	1.1	366	3	US-09-127-480-61	Sequence 61, Appl
c 303	1.2	65990	4	US-09-949-016-11830	Sequence 11830, A	c 376	16	1.1	366	3	US-08-496-841C-61	Sequence 61, Appl
c 304	1.2	67156	4	US-09-949-016-12284	Sequence 12284, A	c 377	16	1.1	366	3	US-09-124-523-61	Sequence 61, Appl
c 305	1.2	67157	4	US-09-949-016-16558	Sequence 16558, A	c 378	16	1.1	366	4	US-09-636-796A-61	Sequence 61, Appl
c 306	1.2	71879	4	US-09-949-016-17465	Sequence 17465, A	c 379	16	1.1	366	4	US-08-431-048F-61	Sequence 61, Appl
c 307	1.2	81927	4	US-09-949-016-15623	Sequence 15623, A	c 380	16	1.1	371	4	US-09-270-767-2348	Sequence 2348, Ap
c 308	1.2	83462	4	US-09-949-016-13116	Sequence 13116, A	c 381	16	1.1	371	4	US-09-270-767-17630	Sequence 17630, A
c 309	1.2	87552	4	US-09-949-016-16807	Sequence 16807, A	c 382	16	1.1	377	4	US-09-513-999C-31153	Sequence 31153, A
c 310	1.2	88906	4	US-09-949-016-17468	Sequence 17468, A	c 383	16	1.1	378	4	US-09-702-705-889	Sequence 889, App
c 311	1.2	92227	4	US-09-949-016-11929	Sequence 11929, A	c 384	16	1.1	378	4	US-09-736-457-889	Sequence 889, App
c 312	1.2	92525	4	US-09-949-016-15421	Sequence 15421, A	c 385	16	1.1	378	4	US-09-614-124B-889	Sequence 889, App
c 313	1.2	93235	4	US-09-949-016-17067	Sequence 17067, A	c 386	16	1.1	378	4	US-09-671-325-889	Sequence 889, App
c 314	1.2	103447	4	US-09-949-016-16320	Sequence 16320, A	c 387	16	1.1	378	4	US-09-658-824-889	Sequence 889, App
c 315	1.2	106746	4	US-09-326-402C-1	Sequence 1, Appl	c 388	16	1.1	378	4	US-09-513-999C-34941	Sequence 34941, A
c 316	1.2	106746	4	US-09-326-402C-12	Sequence 12, Appl	c 389	16	1.1	383	4	US-09-621-976-15508	Sequence 15508, A
c 317	1.2	112705	4	US-09-949-016-15630	Sequence 15630, A	c 390	16	1.1	400	4	US-09-621-976-15511	Sequence 15511, A
c 318	1.2	113283	4	US-09-949-016-16976	Sequence 16976, A	c 391	16	1.1	401	4	US-09-621-976-15506	Sequence 15506, A
c 319	1.2	113283	4	US-09-949-016-16977	Sequence 16977, A	c 392	16	1.1	406	4	US-09-621-976-19126	Sequence 19126, A

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C 394	16	1.1	417	4	US-09-513-999C-23700	Sequence 23700, A	467	16	1.1	601	4	US-09-949-016-82991	Sequence 82991, A
395	16	1.1	436	4	US-09-513-999C-24290	Sequence 24290, A	468	16	1.1	601	4	US-09-949-016-84087	Sequence 84087, A
396	16	1.1	438	4	US-09-270-767-1026	Sequence 1026, Ap	C 469	16	1.1	601	4	US-09-949-016-85038	Sequence 85038, A
397	16	1.1	441	4	US-09-270-767-16308	Sequence 16308, A	C 470	16	1.1	601	4	US-09-949-016-85638	Sequence 85638, A
398	16	1.1	441	4	US-09-530-880-5	Sequence 5, Appl	C 471	16	1.1	601	4	US-09-949-016-87695	Sequence 87695, A
399	16	1.1	442	4	US-09-621-976-16600	Sequence 16600, A	472	16	1.1	601	4	US-09-949-016-95067	Sequence 95067, A
C 400	16	1.1	444	4	US-09-513-999C-34698	Sequence 34698, A	473	16	1.1	601	4	US-09-949-016-95068	Sequence 95068, A
401	16	1.1	448	4	US-09-621-976-19125	Sequence 19125, A	474	16	1.1	601	4	US-09-949-016-95179	Sequence 95179, A
402	16	1.1	449	2	US-08-967-101-75	Sequence 75, Appl	475	16	1.1	601	4	US-09-949-016-95180	Sequence 95180, A
403	16	1.1	449	2	US-08-592-541-75	Sequence 75, Appl	476	16	1.1	601	4	US-09-949-016-103834	Sequence 103834, A
404	16	1.1	449	3	US-09-124-698-75	Sequence 75, Appl	477	16	1.1	601	4	US-09-949-016-103878	Sequence 103878, A
405	16	1.1	449	3	US-09-127-480-75	Sequence 75, Appl	478	16	1.1	601	4	US-09-949-016-108854	Sequence 108854, A
406	16	1.1	449	3	US-08-496-841C-75	Sequence 75, Appl	479	16	1.1	601	4	US-09-949-016-108855	Sequence 108855, A
407	16	1.1	449	3	US-09-124-523-75	Sequence 75, Appl	480	16	1.1	601	4	US-09-949-016-110727	Sequence 110727, A
408	16	1.1	449	4	US-09-636-796A-75	Sequence 75, Appl	481	16	1.1	601	4	US-09-949-016-110888	Sequence 110888, A
409	16	1.1	449	4	US-08-431-048F-75	Sequence 75, Appl	482	16	1.1	601	4	US-09-949-016-111049	Sequence 111049, A
C 410	16	1.1	454	4	US-09-621-976-15530	Sequence 15530, A	483	16	1.1	601	4	US-09-949-016-112120	Sequence 112120, A
C 411	16	1.1	478	4	US-09-513-999C-35711	Sequence 35711, A	484	16	1.1	601	4	US-09-949-016-112735	Sequence 112735, A
C 412	16	1.1	487	4	US-09-621-976-307	Sequence 307, App	485	16	1.1	601	4	US-09-949-016-112819	Sequence 112819, A
C 413	16	1.1	487	4	US-09-270-767-8603	Sequence 8603, Ap	486	16	1.1	601	4	US-09-949-016-112903	Sequence 112903, A
C 414	16	1.1	487	4	US-09-270-767-23885	Sequence 23885, A	487	16	1.1	601	4	US-09-949-016-112979	Sequence 112979, A
415	16	1.1	494	4	US-09-621-976-1902	Sequence 1902, Ap	488	16	1.1	601	4	US-09-949-016-113065	Sequence 113065, A
416	16	1.1	495	4	US-09-621-976-308	Sequence 308, App	489	16	1.1	601	4	US-09-949-016-113843	Sequence 113843, A
C 417	16	1.1	500	2	US-08-967-101-108	Sequence 108, App	490	16	1.1	601	4	US-09-949-016-114011	Sequence 114011, A
C 418	16	1.1	500	2	US-08-592-541-108	Sequence 108, App	491	16	1.1	601	4	US-09-949-016-114179	Sequence 114179, A
C 419	16	1.1	500	3	US-09-124-698-108	Sequence 108, App	492	16	1.1	601	4	US-09-949-016-114347	Sequence 114347, A
C 420	16	1.1	500	3	US-09-127-480-108	Sequence 108, App	493	16	1.1	601	4	US-09-949-016-114515	Sequence 114515, A
C 421	16	1.1	500	3	US-08-496-841C-108	Sequence 108, App	494	16	1.1	601	4	US-09-949-016-114683	Sequence 114683, A
C 422	16	1.1	500	3	US-09-124-523-108	Sequence 108, App	495	16	1.1	601	4	US-09-949-016-114851	Sequence 114851, A
C 423	16	1.1	500	4	US-08-636-796A-108	Sequence 108, App	496	16	1.1	601	4	US-09-949-016-115019	Sequence 115019, A
C 424	16	1.1	500	4	US-08-431-048F-108	Sequence 108, App	C 497	16	1.1	601	4	US-09-949-016-117884	Sequence 117884, A
C 425	16	1.1	501	4	US-09-248-796A-846	Sequence 846, App	C 498	16	1.1	601	4	US-09-949-016-117936	Sequence 117936, A
426	16	1.1	503	4	US-09-270-767-4335	Sequence 4335, Ap	C 499	16	1.1	601	4	US-09-949-016-117988	Sequence 117988, A
427	16	1.1	503	4	US-09-270-767-13617	Sequence 13617, A	C 500	16	1.1	601	4	US-09-949-016-118040	Sequence 118040, A
428	16	1.1	504	4	US-09-621-976-1314	Sequence 1314, Ap	C 501	16	1.1	601	4	US-09-949-016-125049	Sequence 125049, A
C 429	16	1.1	507	4	US-09-621-976-18901	Sequence 18901, A	C 502	16	1.1	601	4	US-09-949-016-125101	Sequence 125101, A
C 430	16	1.1	508	4	US-09-621-976-860	Sequence 860, App	C 503	16	1.1	601	4	US-09-949-016-125153	Sequence 125153, A
C 431	16	1.1	528	4	US-09-248-796A-552	Sequence 552, App	C 504	16	1.1	601	4	US-09-949-016-125205	Sequence 125205, A
C 432	16	1.1	570	4	US-09-248-796A-659	Sequence 659, App	C 505	16	1.1	601	4	US-09-949-016-126470	Sequence 126470, A
C 433	16	1.1	575	4	US-09-270-767-13506	Sequence 13506, A	506	16	1.1	601	4	US-09-949-016-127356	Sequence 127356, A
C 434	16	1.1	601	4	US-09-949-016-23412	Sequence 23412, A	507	16	1.1	601	4	US-09-949-016-127357	Sequence 127357, A
C 435	16	1.1	601	4	US-09-949-016-23412	Sequence 23412, A	508	16	1.1	601	4	US-09-949-016-127358	Sequence 127358, A
C 436	16	1.1	601	4	US-09-949-016-26253	Sequence 26253, A	C 509	16	1.1	601	4	US-09-949-016-135757	Sequence 135757, A
C 437	16	1.1	601	4	US-09-949-016-35043	Sequence 35043, A	C 510	16	1.1	601	4	US-09-949-016-136776	Sequence 136776, A
438	16	1.1	601	4	US-09-949-016-35984	Sequence 35984, A	511	16	1.1	601	4	US-09-949-016-140181	Sequence 140181, A
439	16	1.1	601	4	US-09-949-016-35985	Sequence 35985, A	512	16	1.1	601	4	US-09-949-016-140182	Sequence 140182, A
440	16	1.1	601	4	US-09-949-016-36071	Sequence 36071, A	C 513	16	1.1	601	4	US-09-949-016-141116	Sequence 141116, A
441	16	1.1	601	4	US-09-949-016-36072	Sequence 36072, A	514	16	1.1	601	4	US-09-949-016-141116	Sequence 141116, A
442	16	1.1	601	4	US-09-949-016-37324	Sequence 37324, A	C 515	16	1.1	601	4	US-09-949-016-145982	Sequence 145982, A
443	16	1.1	601	4	US-09-949-016-38333	Sequence 38333, A	C 516	16	1.1	601	4	US-09-949-016-147912	Sequence 147912, A
444	16	1.1	601	4	US-09-949-016-41151	Sequence 41151, A	C 517	16	1.1	601	4	US-09-949-016-150366	Sequence 150366, A
445	16	1.1	601	4	US-09-949-016-41152	Sequence 41152, A	C 518	16	1.1	601	4	US-09-949-016-150367	Sequence 150367, A
446	16	1.1	601	4	US-09-949-016-45222	Sequence 45222, A	519	16	1.1	601	4	US-09-949-016-152459	Sequence 152459, A
447	16	1.1	601	4	US-09-949-016-45223	Sequence 45223, A	520	16	1.1	601	4	US-09-949-016-160245	Sequence 160245, A
448	16	1.1	601	4	US-09-949-016-45224	Sequence 45224, A	521	16	1.1	601	4	US-09-949-016-160289	Sequence 160289, A
C 449	16	1.1	601	4	US-09-949-016-45643	Sequence 45643, A	C 522	16	1.1	601	4	US-09-949-016-164068	Sequence 164068, A
C 450	16	1.1	601	4	US-09-949-016-47533	Sequence 47533, A	523	16	1.1	601	4	US-09-949-016-168174	Sequence 168174, A
C 451	16	1.1	601	4	US-09-949-016-47618	Sequence 47618, A	C 524	16	1.1	601	4	US-09-949-016-169307	Sequence 169307, A
452	16	1.1	601	4	US-09-949-016-49904	Sequence 49904, A	C 525	16	1.1	601	4	US-09-949-016-169890	Sequence 169890, A
C 453	16	1.1	601	4	US-09-949-016-52171	Sequence 52171, A	C 526	16	1.1	601	4	US-09-949-016-175490	Sequence 175490, A
C 454	16	1.1	601	4	US-09-949-016-52769	Sequence 52769, A	C 527	16	1.1	601	4	US-09-949-016-176597	Sequence 176597, A
C 455	16	1.1	601	4	US-09-949-016-66474	Sequence 66474, A	C 528	16	1.1	601	4	US-09-949-016-176598	Sequence 176598, A
C 456	16	1.1	601	4	US-09-949-016-70673	Sequence 70673, A	C 529	16	1.1	601	4	US-09-949-016-176955	Sequence 176955, A
C 457	16	1.1	601	4	US-09-949-016-71524	Sequence 71524, A	530	16	1.1	601	4	US-09-949-016-177078	Sequence 177078, A
C 458	16	1.1	601	4	US-09-949-016-71525	Sequence 71525, A	531	16	1.1	601	4	US-09-949-016-178283	Sequence 178283, A
C 459	16	1.1	601	4	US-09-949-016-71526	Sequence 71526, A	532	16	1.1	601	4	US-09-949-016-178315	Sequence 178315, A
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462	16	1.1	601	4	US-09-949-016-81136	Sequence 81136, A	535	16	1.1	601	4	US-09-949-016-179850	Sequence 179850, A
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464	16	1.1	601	4	US-09-949-016-81138	Sequence 81138, A	537	16	1.1	601	4	US-09-949-016-179852	Sequence 179852, A
465	16	1.1	601	4	US-09-949-016-82620	Sequence 82620, A	538	16	1.1	601	4	US-09-949-016-179853	Sequence 179853, A

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540	16	1.1	601	4	US-09-949-016-181795	Sequence 181795,	613	16	1.1	1296	4	US-09-903-540-7768	Sequence 7768, Ap
541	16	1.1	601	4	US-09-949-016-181913	Sequence 181913,	c 614	16	1.1	1322	4	US-09-634-238-478	Sequence 178, App
542	16	1.1	601	4	US-09-949-016-181914	Sequence 181914,	615	16	1.1	1332	4	US-09-949-016-2081	Sequence 2081, Ap
543	16	1.1	601	4	US-09-949-016-182032	Sequence 182032,	616	16	1.1	1337	4	US-09-270-767-14979	Sequence 14979, A
544	16	1.1	601	4	US-09-949-016-182033	Sequence 182033,	617	16	1.1	1339	4	US-09-023-655-1149	Sequence 1149, Ap
545	16	1.1	601	4	US-09-949-016-186396	Sequence 186396,	618	16	1.1	1339	4	US-09-943-016-722	Sequence 722, App
c 546	16	1.1	601	4	US-09-949-016-186318	Sequence 186318,	619	16	1.1	1340	4	US-09-513-999C-14928	Sequence 14928, A
547	16	1.1	601	4	US-09-949-016-197147	Sequence 197147,	620	16	1.1	1341	4	US-09-903-540-5533	Sequence 5533, Ap
548	16	1.1	601	4	US-09-949-016-197148	Sequence 197148,	621	16	1.1	1350	3	US-09-511-625B-60	Sequence 60, Appl
549	16	1.1	601	4	US-09-949-016-197265	Sequence 197265,	c 622	16	1.1	1392	4	US-09-895-035-13	Sequence 13, Appl
550	16	1.1	601	4	US-09-949-016-197266	Sequence 197266,	c 623	16	1.1	1400	3	US-09-245-281-40	Sequence 40, Appl
551	16	1.1	601	4	US-09-949-016-197383	Sequence 197383,	c 624	16	1.1	1400	3	US-09-207-359B-40	Sequence 40, Appl
552	16	1.1	601	4	US-09-949-016-197384	Sequence 197384,	c 625	16	1.1	1400	4	US-09-340-620A-40	Sequence 40, Appl
553	16	1.1	601	4	US-09-949-016-197501	Sequence 197501,	c 626	16	1.1	1400	4	US-09-023-655-535	Sequence 535, App
554	16	1.1	601	4	US-09-949-016-197502	Sequence 197502,	c 627	16	1.1	1400	4	US-09-865-364-40	Sequence 40, Appl
555	16	1.1	601	4	US-09-949-016-202211	Sequence 202211,	c 628	16	1.1	1404	4	US-09-896-621B-1	Sequence 1, Appl
556	16	1.1	624	4	US-09-248-796A-1369	Sequence 1369, Ap	c 629	16	1.1	1404	4	US-09-896-621B-2	Sequence 2, Appl
557	16	1.1	630	4	US-09-799-451-185	Sequence 185, Ap	c 630	16	1.1	1404	4	US-09-896-621B-3	Sequence 3, Appl
c 558	16	1.1	650	4	US-09-270-767-7616	Sequence 7616, Ap	c 631	16	1.1	1406	4	US-09-943-016-5325	Sequence 5325, Ap
c 559	16	1.1	650	4	US-09-270-767-22898	Sequence 22898, A	c 632	16	1.1	1439	2	US-08-495-695B-27	Sequence 27, Appl
c 560	16	1.1	654	4	US-09-270-767-13556	Sequence 13556, A	633	16	1.1	1439	5	PCT-US94-14436-27	Sequence 27, Appl
c 561	16	1.1	696	3	US-09-280-116-180	Sequence 180, App	c 634	16	1.1	1464	4	US-09-248-796A-3147	Sequence 3147, Ap
c 562	16	1.1	696	4	US-09-902-540-6946	Sequence 6946, Ap	c 635	16	1.1	1484	4	US-09-949-016-1571	Sequence 1571, Ap
c 563	16	1.1	703	3	US-09-280-116-175	Sequence 175, App	c 636	16	1.1	1484	4	US-09-943-016-1572	Sequence 1572, Ap
c 564	16	1.1	737	4	US-09-270-767-8879	Sequence 8879, Ap	c 637	16	1.1	1484	4	US-09-943-016-1573	Sequence 1573, Ap
c 565	16	1.1	737	4	US-09-270-767-24161	Sequence 24161, A	c 638	16	1.1	1485	4	US-09-903-540-9444	Sequence 9444, Ap
566	16	1.1	769	2	US-08-538-711A-9	Sequence 9, Appl	c 639	16	1.1	1488	2	US-08-875-972-3	Sequence 3, Appl
567	16	1.1	769	3	US-08-725-027-9	Sequence 9, Appl	640	16	1.1	1494	1	US-08-318-905-21	Sequence 21, Appl
568	16	1.1	769	4	US-09-542-552-9	Sequence 9, Appl	641	16	1.1	1494	1	US-08-483-232-21	Sequence 21, Appl
c 569	16	1.1	816	4	US-09-270-767-13067	Sequence 13067, A	642	16	1.1	1494	1	US-08-483-140-21	Sequence 21, Appl
570	16	1.1	830	3	US-08-387-707-13	Sequence 13, Appl	643	16	1.1	1494	2	US-08-485-938A-21	Sequence 21, Appl
571	16	1.1	830	3	US-08-405-271A-13	Sequence 13, Appl	644	16	1.1	1494	2	US-08-910-041-21	Sequence 21, Appl
c 572	16	1.1	876	4	US-09-107-532A-2443	Sequence 2443, Ap	645	16	1.1	1494	3	US-09-328-474-21	Sequence 21, Appl
c 573	16	1.1	912	4	US-09-891-641-75	Sequence 75, Appl	646	16	1.1	1494	3	US-09-100-546-21	Sequence 21, Appl
c 574	16	1.1	914	4	US-09-270-767-9986	Sequence 9986, Ap	647	16	1.1	1494	3	US-09-010-715-21	Sequence 21, Appl
c 575	16	1.1	945	3	US-08-888-077A-10	Sequence 10, Appl	648	16	1.1	1494	3	US-09-577-758-21	Sequence 21, Appl
c 576	16	1.1	950	4	US-09-270-767-11073	Sequence 11073, A	c 649	16	1.1	1510	4	US-09-921-099A-20	Sequence 20, Appl
577	16	1.1	966	4	US-09-328-352-3501	Sequence 3501, Ap	c 650	16	1.1	1540	4	US-09-668-097A-3	Sequence 3, Appl
578	16	1.1	972	4	US-09-248-796A-3053	Sequence 3053, Ap	651	16	1.1	1610	3	US-08-889-108-7	Sequence 7, Appl
c 579	16	1.1	992	4	US-09-270-767-11212	Sequence 11212, A	652	16	1.1	1610	5	PCT-US94-10358-7	Sequence 7, Appl
580	16	1.1	1001	3	US-09-641-638-185	Sequence 185, App	c 653	16	1.1	1612	4	US-09-640-211A-2104	Sequence 2104, Ap
581	16	1.1	1001	4	US-10-170-097-185	Sequence 185, App	654	16	1.1	1662	4	US-09-485-473-3	Sequence 3, Appl
582	16	1.1	1029	2	US-08-484-993B-21	Sequence 21, Appl	c 655	16	1.1	1721	4	US-09-919-039-315	Sequence 315, App
583	16	1.1	1029	2	US-08-484-158B-21	Sequence 21, Appl	c 656	16	1.1	1725	4	US-09-668-097A-21	Sequence 21, Appl
584	16	1.1	1029	2	US-08-484-596A-21	Sequence 21, Appl	c 657	16	1.1	1750	3	US-08-670-964-3	Sequence 3, Appl
585	16	1.1	1029	2	US-08-480-150A-21	Sequence 21, Appl	c 658	16	1.1	1762	3	US-08-670-964-1	Sequence 1, Appl
586	16	1.1	1029	3	US-08-458-731-21	Sequence 21, Appl	c 659	16	1.1	1769	3	US-09-428-696-3	Sequence 3, Appl
587	16	1.1	1029	3	US-08-149-223A-21	Sequence 21, Appl	660	16	1.1	1771	4	US-09-943-016-4307	Sequence 4307, Ap
588	16	1.1	1116	4	US-09-620-312D-910	Sequence 910, App	c 661	16	1.1	1814	4	US-09-270-767-3609	Sequence 3609, Ap
589	16	1.1	1122	4	US-09-328-352-2883	Sequence 2883, Ap	c 662	16	1.1	1814	4	US-09-270-767-18891	Sequence 18891, A
590	16	1.1	1165	4	US-09-603-552-2	Sequence 2, Appl	c 663	16	1.1	1854	4	US-09-543-681A-200	Sequence 200, App
591	16	1.1	1170	4	US-09-248-796A-1145	Sequence 1145, Ap	664	16	1.1	1878	4	US-09-252-991A-9765	Sequence 9765, Ap
592	16	1.1	1182	4	US-09-826-509-546	Sequence 546, App	c 665	16	1.1	1895	2	US-08-967-101-165	Sequence 165, App
593	16	1.1	1203	4	US-09-826-509-544	Sequence 544, App	c 666	16	1.1	1895	2	US-08-592-541-165	Sequence 165, App
c 594	16	1.1	1203	3	US-08-872-979-9	Sequence 9, Appl	c 667	16	1.1	1895	3	US-08-888-077A-20	Sequence 20, Appl
c 595	16	1.1	1242	4	US-09-248-796A-1521	Sequence 1521, Ap	c 668	16	1.1	1895	3	US-09-124-698-165	Sequence 165, App
596	16	1.1	1243	4	US-09-620-312D-930	Sequence 930, App	c 669	16	1.1	1895	3	US-09-127-480-165	Sequence 165, App
597	16	1.1	1244	2	US-08-204-288-3	Sequence 3, Appl	c 670	16	1.1	1895	3	US-09-124-523-165	Sequence 165, App
c 598	16	1.1	1250	1	US-08-181-271A-39	Sequence 39, Appl	c 671	16	1.1	1895	4	US-09-636-796A-165	Sequence 165, App
c 599	16	1.1	1250	1	US-08-449-315-39	Sequence 39, Appl	c 672	16	1.1	1914	2	US-08-670-479-24	Sequence 24, Appl
c 600	16	1.1	1250	1	US-08-444-803-39	Sequence 39, Appl	673	16	1.1	1927	4	US-09-949-016-3372	Sequence 3372, Ap
c 601	16	1.1	1250	1	US-08-449-043-39	Sequence 39, Appl	c 674	16	1.1	1929	3	US-09-063-950-3	Sequence 3, Appl
c 602	16	1.1	1250	1	US-08-456-265A-39	Sequence 39, Appl	675	16	1.1	2033	4	US-09-774-528-171	Sequence 171, App
c 603	16	1.1	1250	1	US-08-455-416-39	Sequence 39, Appl	676	16	1.1	2033	4	US-09-949-016-4967	Sequence 4967, Ap
c 604	16	1.1	1250	1	US-08-455-244-39	Sequence 39, Appl	677	16	1.1	2050	3	US-09-891-053-21	Sequence 21, Appl
c 605	16	1.1	1250	1	US-08-454-876-39	Sequence 39, Appl	678	16	1.1	2160	3	US-08-188-275A-1	Sequence 1, Appl
c 606	16	1.1	1250	2	US-08-457-364-39	Sequence 39, Appl	679	16	1.1	2162	3	US-09-351-198-1	Sequence 1, Appl
c 607	16	1.1	1250	2	US-08-456-262-39	Sequence 39, Appl	680	16	1.1	2162	3	US-09-113-426-1	Sequence 1, Appl
c 608	16	1.1	1250	2	US-08-456-240-39	Sequence 39, Appl	681	16	1.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap
c 609	16	1.1	1250	2	US-08-455-736-39	Sequence 39, Appl	682	16	1.1	2162	4	US-09-355-709C-7	Sequence 7, Appl
c 610	16	1.1	1250	2	US-08-971-217-39	Sequence 39, Appl	c 683	16	1.1	2166	4	US-09-248-796A-1004	Sequence 1004, Ap
c 611	16	1.1	1250	3	US-09-350-600-39	Sequence 39, Appl	684	16	1.1	2250	3	US-08-763-938-1	Sequence 1, Appl

685	16	1.1	2250	4	US-09-902-540-4529	Sequence 4529, Ap	C 758	16	1.1	3087	3	US-08-496-841C-5	Sequence 5, Appli
686	16	1.1	2310	3	US-08-556-182-13	Sequence 13, Appl	C 759	16	1.1	3087	3	US-09-124-523-5	Sequence 5, Appli
687	16	1.1	2329	1	US-08-253-785-2	Sequence 2, Appli	C 760	16	1.1	3087	4	US-09-636-796A-5	Sequence 5, Appli
688	16	1.1	2384	4	US-09-894-912A-31	Sequence 31, Appl	C 761	16	1.1	3087	4	US-08-431-048F-5	Sequence 5, Appli
689	16	1.1	2487	1	US-08-261-304-1	Sequence 1, Appli	C 762	16	1.1	3119	4	US-09-949-016-1935	Sequence 1935, Ap
690	16	1.1	2509	2	US-09-014-969-1	Sequence 1, Appli	C 763	16	1.1	3120	4	US-09-169-768-29	Sequence 29, Appl
691	16	1.1	2532	4	US-10-030-330-2	Sequence 2, Appli	C 764	16	1.1	3131	4	US-09-949-016-659	Sequence 659, Appl
692	16	1.1	2555	4	US-09-866-028-68	Sequence 68, Appl	C 765	16	1.1	3200	1	US-08-444-405-1	Sequence 1, Appli
693	16	1.1	2555	4	US-09-866-028-68	Sequence 68, Appl	C 766	16	1.1	3200	1	US-08-384-850-1	Sequence 1, Appli
694	16	1.1	2595	4	US-09-944-457-68	Sequence 1974, Ap	C 767	16	1.1	3375	3	US-09-511-625B-67	Sequence 67, Appl
695	16	1.1	2605	2	US-09-902-540-1974	Sequence 4, Appli	C 768	16	1.1	3580	4	US-09-945-249-9	Sequence 9, Appli
696	16	1.1	2605	4	US-08-680-395-4	Sequence 4, Appli	C 769	16	1.1	3580	4	US-09-041-990-9	Sequence 9, Appli
697	16	1.1	2605	4	US-08-892-695-4	Sequence 4, Appli	C 770	16	1.1	3628	3	US-08-842-306B-47	Sequence 47, Appl
698	16	1.1	2665	4	US-09-949-016-5059	Sequence 5, Appli	C 771	16	1.1	3628	3	US-08-838-973B-47	Sequence 47, Appl
699	16	1.1	2689	2	US-08-885-090-1	Sequence 1, Appli	C 772	16	1.1	3667	3	US-09-511-625B-1	Sequence 1, Appli
700	16	1.1	2699	3	US-09-167-543-1	Sequence 1, Appli	C 773	16	1.1	3698	4	US-09-976-594-1098	Sequence 1098, Ap
701	16	1.1	2699	3	US-09-167-543-1	Sequence 1, Appli	C 774	16	1.1	3894	3	US-09-511-625B-3	Sequence 3, Appli
702	16	1.1	2699	3	US-09-642-855-5	Sequence 5, Appli	C 775	16	1.1	3969	4	US-08-248-796A-5440	Sequence 5440, Ap
703	16	1.1	2705	4	US-09-949-016-839	Sequence 839, App	C 776	16	1.1	4201	3	US-08-945-056-4	Sequence 4, Appli
704	16	1.1	2728	4	US-09-774-528-96	Sequence 96, Appli	C 777	16	1.1	4204	4	US-09-774-528-220	Sequence 220, App
705	16	1.1	2764	3	US-08-923-454A-9	Sequence 27, Appl	C 778	16	1.1	4438	4	US-09-566-921-81	Sequence 81, Appl
706	16	1.1	2764	3	US-08-832-867-2	Sequence 2, Appli	C 779	16	1.1	4526	4	US-09-902-540-772	Sequence 772, App
707	16	1.1	2764	4	US-09-949-016-3302	Sequence 3302, Ap	C 780	16	1.1	4587	4	US-09-902-540-600	Sequence 600, App
708	16	1.1	2764	4	US-09-949-016-3303	Sequence 3303, Ap	C 781	16	1.1	4646	4	US-09-949-016-680	Sequence 680, App
709	16	1.1	2764	4	US-09-949-016-3304	Sequence 3304, Ap	C 782	16	1.1	5056	4	US-09-949-016-1463	Sequence 1463, Ap
710	16	1.1	2765	3	US-08-888-077A-1	Sequence 1, Appli	C 783	16	1.1	5065	4	US-09-949-016-358	Sequence 358, App
711	16	1.1	2765	3	US-08-706-344C-1	Sequence 3, Appli	C 784	16	1.1	5086	4	US-09-949-016-11	Sequence 11, Appl
712	16	1.1	2765	3	US-08-706-344C-1	Sequence 3, Appli	C 785	16	1.1	5176	3	US-08-654-482-13	Sequence 13, Appl
713	16	1.1	2765	3	US-08-706-344C-1	Sequence 3, Appli	C 786	16	1.1	5325	4	US-09-919-172-75	Sequence 75, Appl
714	16	1.1	2765	3	US-08-706-344C-27	Sequence 27, Appl	C 787	16	1.1	5418	4	US-09-949-016-2477	Sequence 2477, Ap
715	16	1.1	2765	3	US-08-706-344C-29	Sequence 29, Appl	C 788	16	1.1	7152	4	US-09-492-709A-142	Sequence 142, App
716	16	1.1	2765	3	US-08-706-344C-31	Sequence 31, Appl	C 789	16	1.1	7231	4	US-09-949-016-13833	Sequence 13833, A
717	16	1.1	2791	2	US-08-967-101-1	Sequence 2, Appli	C 790	16	1.1	7233	4	US-09-949-016-12159	Sequence 12159, A
718	16	1.1	2791	2	US-08-967-101-1	Sequence 2, Appli	C 791	16	1.1	7432	1	US-07-852-260-1	Sequence 16479, A
719	16	1.1	2791	2	US-08-967-101-1	Sequence 2, Appli	C 792	16	1.1	7432	2	US-08-461-503-1	Sequence 1, Appli
720	16	1.1	2791	2	US-08-592-541-1	Sequence 1, Appli	C 793	16	1.1	7432	2	US-08-461-503-1	Sequence 1, Appli
721	16	1.1	2791	3	US-08-592-541-1	Sequence 1, Appli	C 794	16	1.1	7634	3	US-09-949-016-17332	Sequence 17332, A
722	16	1.1	2791	3	US-09-124-698-1	Sequence 1, Appli	C 795	16	1.1	8439	3	US-09-949-016-17332	Sequence 473, App
723	16	1.1	2791	3	US-09-124-698-1	Sequence 1, Appli	C 796	16	1.1	8546	4	US-09-949-016-15114	Sequence 15114, A
724	16	1.1	2791	3	US-09-127-480-1	Sequence 1, Appli	C 797	16	1.1	8546	4	US-09-949-016-16049	Sequence 16049, A
725	16	1.1	2791	3	US-08-496-841C-1	Sequence 1, Appli	C 798	16	1.1	9278	4	US-09-949-016-12716	Sequence 12716, A
726	16	1.1	2791	3	US-09-124-523-1	Sequence 1, Appli	C 799	16	1.1	9279	4	US-09-949-016-17423	Sequence 17423, A
727	16	1.1	2791	3	US-09-124-523-1	Sequence 1, Appli	C 800	16	1.1	9293	4	US-09-949-016-16801	Sequence 16801, A
728	16	1.1	2791	4	US-09-636-796A-1	Sequence 1, Appli	C 801	16	1.1	9442	4	US-09-949-016-12571	Sequence 12571, A
729	16	1.1	2791	4	US-09-636-796A-1	Sequence 1, Appli	C 802	16	1.1	10187	4	US-09-949-016-15877	Sequence 15877, A
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731	16	1.1	2791	4	US-08-431-048F-1	Sequence 1, Appli	C 804	16	1.1	10465	4	US-09-949-016-13136	Sequence 13136, A
732	16	1.1	2852	3	US-08-496-841C-133	Sequence 133, App	C 805	16	1.1	11272	4	US-09-341-461-1	Sequence 1, Appli
733	16	1.1	2852	4	US-09-063-950-1	Sequence 1, Appli	C 806	16	1.1	11272	4	US-09-949-016-15157	Sequence 15157, A
734	16	1.1	2906	4	US-09-485-473-6	Sequence 6, Appli	C 807	16	1.1	11633	4	US-09-949-016-3651	Sequence 3651, Ap
735	16	1.1	2906	4	US-09-907-794A-291	Sequence 291, App	C 808	16	1.1	12176	4	US-09-949-016-11	Sequence 11, Appl
736	16	1.1	2906	4	US-09-905-125A-291	Sequence 291, App	C 809	16	1.1	12225	2	US-08-822-445-11	Sequence 11, Appl
737	16	1.1	2906	4	US-09-902-775A-291	Sequence 291, App	C 810	16	1.1	12225	3	US-09-396-540-11	Sequence 11, Appl
738	16	1.1	2906	4	US-09-906-700-291	Sequence 291, App	C 811	16	1.1	12329	4	US-09-949-016-1079	Sequence 1079, Ap
739	16	1.1	2906	4	US-09-903-603A-291	Sequence 291, App	C 812	16	1.1	12360	4	US-09-949-016-14488	Sequence 14488, A
740	16	1.1	2906	4	US-09-904-920A-291	Sequence 291, App	C 813	16	1.1	12616	2	US-08-822-445-9	Sequence 9, Appli
741	16	1.1	2906	4	US-09-908-064-291	Sequence 291, App	C 814	16	1.1	12616	3	US-09-396-540-9	Sequence 9, Appli
742	16	1.1	2906	4	US-09-908-064-291	Sequence 291, App	C 815	16	1.1	12717	4	US-09-693-205A-9	Sequence 9, Appli
743	16	1.1	3037	4	US-09-906-618A-291	Sequence 291, App	C 816	16	1.1	12717	4	US-09-693-205A-13	Sequence 13, Appl
744	16	1.1	3046	1	US-09-949-016-5453	Sequence 291, App	C 817	16	1.1	12717	4	US-09-693-205A-14	Sequence 14, Appl
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746	16	1.1	3046	3	US-09-087-465-11	Sequence 1, Appli	C 819	16	1.1	12792	4	US-09-693-205A-1	Sequence 1, Appli
747	16	1.1	3046	3	US-09-087-465-11	Sequence 1, Appli	C 820	16	1.1	12793	4	US-09-693-205A-11	Sequence 11, Appl
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749	16	1.1	3046	4	US-08-023-655-1444	Sequence 1444, Ap	C 822	16	1.1	12793	4	US-09-949-016-12037	Sequence 12037, A
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ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/08876874
; Patent No. 5942405
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert
; APPLICANT: Bergema, Derek
; APPLICANT: Foley, James
; APPLICANT: Kumar, Chandrika
; APPLICANT: Sarau, Henry
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
; METHOD OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RATHER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,874
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,627
; FILING DATE: 16-JUN-1997
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELETYPE: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1449 base pairs
; TYPE: nucleic acid

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; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-876-874-1
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Best Local Similarity 100.0%; Pred. No. 0;
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|

RESULT 2

US-09-117-440-1
; Sequence 1, Application US/09117440
; Patent No. 6521418
; GENERAL INFORMATION:
; APPLICANT: Yes, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; TITLE OF INVENTION: EXTRACELLULAR DOMAIN
; FILE REFERENCE: SCR2041S
; CURRENT APPLICATION NUMBER: US/09/117,440
; EARLIER APPLICATION NUMBER: PCT/US97/01736
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: 60/010,808
; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1970
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1527)

Query Match 96.5%; Score 1398; DB 4; Length 1970;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACTACTCTACAGCCATGGAATGAG 60
|
Db 82 ATGGCGTCTTTCTGCTGAGACCAATTCACCTGACTACTCTACAGCCATGGAATGAG 141
|
QY 61 CCCACAGTAATCTCCATGGTCAATCTCAGCCTACTTTTACTGGATTGCCAGGC 120
|
|

Db 142 CCCCAGTAATTTCTCCATGGTCAATCTCAGCCTTACTTTTTTACTGGATTGCCAGGC 201
|
QY 121 AATGGGCTGGTGTCTGTGGGTGGCTGGCTGAAGATGACAGCGGACAGTGAACACAATTTGG 180
|
Db 202 AATGGGCTGGTGTCTGTGGGTGGCTGGCTGAAGATGACAGCGGACAGTGAACACAATTTGG 261
|
QY 181 TTCTCCACCTCACTCTGGGCGGACCTCTCTGCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
|
Db 262 TTCTCCACCTCACTCTGGGCGGACCTCTCTGCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 321
|
QY 241 CACTTGGCTCTCCAGGAGACAGTGGCCCTTACCGGAGGTTCTTATGCAAGCTCATCTCCCTCC 300
|
Db 322 CACTTGGCTCTCCAGGAGACAGTGGCCCTTACCGGAGGTTCTTATGCAAGCTCATCTCCCTCC 381
|
QY 301 ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCAATTTAGCCTTGAATGCG 360
|
Db 382 ATCATTTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCAATTTAGCCTTGAATGCG 441
|
QY 361 TGTCTTGGTGTATTCAGGCCAATCTGGTGTGAGATCATCGCAATGTAGGAGTGGCCTGC 420
|
Db 442 TGTCTTGGTGTATTCAGGCCAATCTGGTGTGAGATCATCGCAATGTAGGAGTGGCCTGC 501
|
QY 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATGTGATGTGATGTGATGTG 480
|
Db 502 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATGTGATGTGATGTGATGTG 561
|
QY 481 CGGGAATCTTCACTACAGACAACTAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
|
Db 562 CGGGAATCTTCACTACAGACAACTAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
|
QY 541 TCATTAGATTTACAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTGAACAATTT 600
|
Db 622 TCATTAGATTTACAGACTTTTATGGAGATCCACTAGAAAACAGTCTCTTGAACAATTT 681
|
QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTCTCTCTCTTCCAAACAATGAT 660
|
Db 682 GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTCTCTCTCTTCCAAACAATGAT 741
|
QY 661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGAGAT 720
|
Db 742 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTGAGAT 801
|
QY 721 TCATCTCTAGGGTCTGCTAGGTAACTAGTCAAAATCTGATCTCTTAATGATTTAAA 780
|
Db 802 TCATCTCTAGGGTCTGCTAGGTAACTAGTCAAAATCTGATCTCTTAATGATTTAAA 861
|
QY 781 CCTGCTGATGTGTCTCACCTAAATCCCACTGGGTTTCTTATGGAAGATCAGCAACC 840
|
Db 862 CCTGCTGATGTGTCTCACCTAAATCCCACTGGGTTTCTTATGGAAGATCAGCAACC 921
|
QY 841 AGCCACCTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 900
|
Db 922 AGCCACCTGGATAAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTTCCCTAGCGCT 981
|
QY 901 TCTAGCAATTTCTTACAGCTCTGAGTACCAAGGTTTCCAGGATTTATACAAATTTA 960
|
Db 982 TCTAGCAATTTCTTACAGCTCTGAGTACCAAGGTTTCCAGGATTTATACAAATTTA 1041
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QY 961 GGCCAAATTCAGATGACGATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1020
|
Db 1042 GGCCAAATTCAGATGACGATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1101
|
QY 1021 CTAGTGGTGGTCTCTGCTGCTGCTCTGTTATCATGATAGCTGTTTACAGCTTCAATTGTC 1080
|
Db 1102 CTAGTGGTGGTCTCTGCTGCTGCTCTGTTATCATGATAGCTGTTTACAGCTTCAATTGTC 1161
|
QY 1081 TTCCGAATGCAAAAGGGGCGCTTTCGCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGCTG 1140
|
Db 1162 TTCCGAATGCAAAAGGGGCGCTTTCGCCAAGTCTCAGAGCAAAACCTTTGAGTGGCCGCTG 1221
|
QY 1141 GTGGTGGTGGCTGCTCTTCTGCTGCTGCTGCAATTCATACCAATTTTGGAGTCTCTGTCA 1200
|
Db 1222 GTGGTGGTGGCTGCTCTTCTGCTGCTGCTGCAATTCATACCAATTTTGGAGTCTCTGTCA 1281
|

Qy 1441 ACTGTGTGA 1449
|||||
Db 1441 ACTGTGTGA 1449

RESULT 4
US-09-826-509-36/c
; Sequence 36, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 36
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-36

Query Match 1.9%; Score 28; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1419 CATTTCAGAAAGAAATAGTACAACTGTG 1446
|||||
Db 37 CATTTCAGAAAGAAATAGTACAACTGTG 10

RESULT 5
US-09-826-509-229
; Sequence 229, Application US/09826509.
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 229
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-229

Query Match 1.5%; Score 22; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1104 CGCCAAGTCTCAGAGCAAAACC 1125
|||||
Db 1 CGCCAAGTCTCAGAGCAAAACC 22

RESULT 6
US-09-826-509-230/c
; Sequence 230, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 230
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-230

Query Match 1.5%; Score 22; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1104 CGCCAAGTCTCAGAGCAAAACC 1125
|||||
Db 40 CGCCAAGTCTCAGAGCAAAACC 19

RESULT 7
US-09-170-496D-245
; Sequence 245, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-245

Query Match 1.4%; Score 21; DB 4; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 GGCAATGGGTGGTGGTGG 138
|||||
Db 178 GGCAATGGGTGGTGGTGG 198

RESULT 8
US-09-170-496D-269
; Sequence 269, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 269
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-269

Query Match 1.4%; Score 21; DB 4; Length 1071;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 GGCAATGGGCTGCTGCTGG 138
Db 178 GGCAATGGGCTGCTGCTGG 198

RESULT 9

US-09-902-540-1241
; Sequence 1241, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1241
; LENGTH: 28493
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(28493)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1241

Query Match 1.4%; Score 21; DB 4; Length 28493;
Best Local Similarity 100.0%; Pred. No. 2.1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 TGGGCTGCTGCTGGGTGGC 143
Db 27520 TGGGCTGCTGCTGGGTGGC 27540

RESULT 10

US-09-826-509-35
; Sequence 35, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 35
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-35

Query Match 1.3%; Score 19; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 16; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCTCTTCTCTGCTG 19

Db 14 ATGGGCTCTTCTCTGCTG 32

RESULT 11

US-09-949-016-19196
; Sequence 19196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19196
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19196

Query Match 1.3%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 19; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1295 CCTTCCTTTATGCCCTCTT 1313

Db 233 CCTTCCTTTATGCCCTCTT 251

RESULT 12

US-09-949-016-50598
; Sequence 50598, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50598
; LENGTH: 601

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-50598

Query Match 1.3%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 GACAGTGAACACAAATTGG 180
|||||
Db 377 GACAGTGAACACAAATTGG 395

RESULT 13

US-09-949-016-50599
; Sequence 50599, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50599
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-50599

Query Match 1.3%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 GACAGTGAACACAAATTGG 180
|||||
Db 481 GACAGTGAACACAAATTGG 499

RESULT 14

US-09-949-016-69461/c
; Sequence 69461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69461
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69461

Query Match 1.3%; Score 19; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1315 GGGAAAGATTTTAGGAAGA 1333
|||||
Db 121 GGGAAAGATTTTAGGAAGA 103

RESULT 15

US-09-949-016-69462/c
; Sequence 69462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69462
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69462

Query Match 1.3%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1315 GGGAAAGATTTTAGGAAGA 1333
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Db 396 GGGAAAGATTTTAGGAAGA 378

Search completed: April 11, 2005, 12:44:46
Job time : 295 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 12:41:32 ; Search time 904 Seconds

(without alignments)
9713.435 Million cell updates/sec

Title: US-10-764-649-1

Perfect score: 1449

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Post-processing: Listing first 1000 summaries

Database : Published Applications NA.*

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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1449	100.0	1449	10	US-09-751-708A-97
3	1449	100.0	1449	15	US-10-225-567A-77
4	1449	100.0	1449	16	US-10-206-395B-1
5	1449	100.0	1449	18	US-10-764-649-1
6	1449	100.0	1449	18	US-10-428-817A-93
7	1449	100.0	1849	15	US-10-017-161-759
8	1449	100.0	1849	17	US-10-292-798-661
9	1449	100.0	2096	18	US-10-723-860-6365
10	1398	96.5	1956	9	US-09-962-832-127
11	1398	96.5	1956	19	US-10-843-641A-6013
12	1398	96.5	2040	8	US-08-462-314-1
13	1398	96.5	2040	8	US-08-462-314-1
14	1398	96.5	2040	14	US-10-259-521-1
15	1398	96.5	2040	18	US-10-283-975A-63
16	1398	96.5	2040	18	US-10-723-860-2093
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18	1347	93.0	2040	10	US-09-925-302-214
19	1245	85.9	1449	10	US-09-826-509-464
20	1245	85.9	1449	19	US-10-925-095-464
21	330	22.8	453	10	US-09-918-995-14006
22	265	18.3	468	17	US-10-242-535A-27645
23	265	18.3	468	17	US-10-242-535A-27645
24	198	13.7	625	18	US-10-085-783A-27645
25	173	11.9	625	18	US-10-283-975A-367
26	163	11.2	611	18	US-10-350-923B-368
27	60	4.1	60	10	US-10-283-975A-368
28	50	3.5	50	17	US-09-908-975-14862
29	47	3.2	200	9	US-10-131-827-2597
30	47	3.2	200	9	US-09-892-206-4
31	47	3.2	2657	9	US-09-892-206-7
32	47	3.2	2657	9	US-09-892-206-1
33	28	1.9	37	10	US-10-764-649-9
34	28	1.9	37	10	US-09-826-509-36
35	28	1.9	197	9	US-10-925-095-36
36	25	1.7	7449	15	US-09-892-206-5
37	24	1.7	7449	15	US-10-311-455-249
38	22	1.5	40	10	US-10-311-455-250
39	22	1.5	40	10	US-09-826-509-229
40	22	1.5	40	10	US-09-826-509-230
41	22	1.5	40	19	US-10-925-095-229
42	22	1.5	65	10	US-10-925-095-230
43	21	1.4	32	8	US-09-908-975-27272
44	21	1.4	32	8	US-08-462-314-3
45	21	1.4	586	11	US-10-259-521-3
46	21	1.4	586	11	US-09-876-143-246
47	21	1.4	878	18	US-09-876-143-334
48	21	1.4	1071	14	US-10-437-963-59996
49	21	1.4	1071	14	US-10-226-102-3
50	21	1.4	1071	15	US-10-251-385-245
51	21	1.4	1071	15	US-10-251-385-269
52	21	1.4	1071	17	US-10-407-079-3
53	21	1.4	1071	19	US-10-225-567A-483
54	21	1.4	1797	14	US-10-684-206-3
55	21	1.4	1797	14	US-10-226-102-1
56	20	1.4	806	13	US-10-407-079-1
57	20	1.4	806	13	US-10-027-632-262704
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60	20	1.4	1379	17	US-10-172-118-321
61	20	1.4	1386	13	US-10-342-887-321
62	20	1.4	1386	13	US-10-027-632-95652
63	20	1.4	1386	13	US-10-027-632-95653
64	20	1.4	1386	17	US-10-027-632-95652
65	20	1.4	1579	9	US-10-027-632-95653
66	20	1.4	1579	9	US-09-911-150-1
67	20	1.4	1755	18	US-10-193-452-41
68	20	1.4	3245	17	US-10-159-563-266
69	20	1.4	4295	17	US-10-424-599-114731
70	19	1.3	32	8	US-10-437-963-101901
71	19	1.3	32	8	US-08-462-314-4
72	19	1.3	32	14	US-09-826-509-35
73	19	1.3	32	14	US-10-259-521-4
74	19	1.3	200	9	US-10-925-095-35
75	19	1.3	201	18	US-09-892-206-3
76	19	1.3	234	18	US-10-719-993-15999
77	19	1.3	406	18	US-10-437-963-76619
78	19	1.3	439	9	US-10-767-701-687
79	19	1.3	487	9	US-09-892-206-6
80	19	1.3	514	18	US-09-864-761-5373
81	19	1.3	520	16	US-10-425-115-11455
82	19	1.3	531	18	US-10-029-386-2193
83	19	1.3	574	17	US-10-767-701-10166
84	19	1.3	614	18	US-10-425-114-12288
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c 86	19	1.3	795	18	US-10-437-963-31323	Sequence 31323, A	159	18	1.2	636	13	US-10-027-632-290074	Sequence 290074,
c 87	19	1.3	1057	18	US-10-767-701-6910	Sequence 6910, Ap	160	18	1.2	636	17	US-10-027-632-290074	Sequence 290074,
c 88	19	1.3	1286	17	US-10-424-599-68010	Sequence 68010, A	c 161	18	1.2	650	13	US-10-027-632-205556	Sequence 205556,
c 89	19	1.3	1319	13	US-10-027-632-122900	Sequence 122900,	c 162	18	1.2	650	17	US-10-027-632-205557	Sequence 205557,
c 90	19	1.3	1319	13	US-10-027-632-122901	Sequence 122901,	c 163	18	1.2	650	17	US-10-027-632-205557	Sequence 205557,
c 91	19	1.3	1319	13	US-10-027-632-122902	Sequence 122902,	c 164	18	1.2	650	17	US-10-027-632-205557	Sequence 205557,
c 92	19	1.3	1319	17	US-10-027-632-122900	Sequence 122900,	c 165	18	1.2	676	17	US-10-027-632-205557	Sequence 205557,
c 93	19	1.3	1319	17	US-10-027-632-122901	Sequence 122901,	c 166	18	1.2	709	13	US-10-027-632-103805	Sequence 103805,
c 94	19	1.3	1319	17	US-10-027-632-122902	Sequence 122902,	c 167	18	1.2	709	17	US-10-027-632-103805	Sequence 103805,
c 95	19	1.3	1606	18	US-10-425-115-85679	Sequence 85679, A	c 168	18	1.2	754	18	US-10-425-115-95782	Sequence 95782, A
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c 98	19	1.3	2288	10	US-09-725-311-3	Sequence 3, Appli	c 171	18	1.2	850	17	US-10-027-632-153533	Sequence 153533,
c 99	19	1.3	2310	18	US-10-437-963-12274	Sequence 12274, A	c 172	18	1.2	865	13	US-10-027-632-38626	Sequence 38626, A
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c 106	19	1.3	34337	16	US-10-385-614-3	Sequence 3, Appli	c 179	18	1.2	1119	19	US-10-450-255-2	Sequence 2, Appli
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c 109	19	1.3	135800	13	US-10-087-192-898	Sequence 898, App	c 182	18	1.2	1230	17	US-10-425-114-20724	Sequence 20724, A
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C 296	17	1.2	378	18	US-10-425-115-68355	Sequence 68355, A	Sequence 236, App
C 297	17	1.2	380	10	US-09-803-719-2374	Sequence 2374, Ap	Sequence 236, App
C 298	17	1.2	383	18	US-10-472-724-7	Sequence 7, Appli	Sequence 236, App
C 299	17	1.2	395	11	US-09-987-899-133	Sequence 133, App	Sequence 236, App
C 300	17	1.2	397	13	US-10-027-632-292442	Sequence 292442,	Sequence 236, App
C 301	17	1.2	397	13	US-10-027-632-292443	Sequence 292443,	Sequence 236, App
C 302	17	1.2	397	13	US-10-027-632-292442	Sequence 292442,	Sequence 236, App
C 303	17	1.2	397	17	US-10-027-632-292443	Sequence 292443,	Sequence 236, App
C 304	17	1.2	400	10	US-09-803-719-413	Sequence 413, App	Sequence 236, App
C 305	17	1.2	405	17	US-10-335-977-2339	Sequence 2339, Ap	Sequence 236, App
C 306	17	1.2	410	10	US-09-814-353-4223	Sequence 4223, Ap	Sequence 236, App
C 307	17	1.2	410	18	US-10-653-047-10529	Sequence 10529, A	Sequence 236, App
C 308	17	1.2	415	18	US-10-653-047-4295	Sequence 4295, Ap	Sequence 236, App
C 309	17	1.2	420	17	US-10-424-599-66572	Sequence 66572, A	Sequence 236, App
C 310	17	1.2	422	10	US-09-918-995-4709	Sequence 4709, A	Sequence 236, App
C 311	17	1.2	431	13	US-10-040-739-1246	Sequence 1246, Ap	Sequence 236, App
C 312	17	1.2	441	9	US-09-864-761-27440	Sequence 27440, A	Sequence 236, App
C 313	17	1.2	441	9	US-09-604-287A-236	Sequence 236, App	Sequence 236, App
C 314	17	1.2	441	9	US-09-834-759-236	Sequence 236, App	Sequence 236, App
C 315	17	1.2	441	9	US-09-339-338-236	Sequence 236, App	Sequence 236, App
C 316	17	1.2	441	10	US-09-551-621-236	Sequence 236, App	Sequence 236, App
C 317	17	1.2	441	13	US-10-007-805-236	Sequence 236, App	Sequence 236, App
C 318	17	1.2	441	14	US-10-076-622-236	Sequence 236, App	Sequence 236, App
C 319	17	1.2	441	16	US-10-124-805-236	Sequence 236, App	Sequence 236, App
C 320	17	1.2	446	18	US-10-425-115-15312	Sequence 15312, A	Sequence 236, App
C 321	17	1.2	449	18	US-10-767-701-26352	Sequence 26352, A	Sequence 236, App
C 322	17	1.2	450	13	US-10-027-632-182261	Sequence 182261,	Sequence 236, App
C 323	17	1.2	450	13	US-10-027-632-182261	Sequence 182261,	Sequence 236, App
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C 325	17	1.2	450	17	US-10-027-632-182261	Sequence 182261,	Sequence 236, App
C 326	17	1.2	453	13	US-10-027-632-91858	Sequence 91858, A	Sequence 236, App
C 327	17	1.2	453	13	US-10-027-632-91858	Sequence 91858, A	Sequence 236, App
C 328	17	1.2	453	18	US-10-767-701-9539	Sequence 9539, Ap	Sequence 236, App
C 329	17	1.2	455	9	US-09-864-761-10798	Sequence 10798, A	Sequence 236, App
C 330	17	1.2	455	9	US-09-867-701-10397	Sequence 10397, A	Sequence 236, App
C 331	17	1.2	455	17	US-10-242-535A-24953	Sequence 24953, A	Sequence 236, App
C 332	17	1.2	455	17	US-10-085-783A-24953	Sequence 24953, A	Sequence 236, App
C 333	17	1.2	455	18	US-10-437-963-83097	Sequence 83097, A	Sequence 236, App
C 334	17	1.2	455	18	US-10-674-124A-6127	Sequence 6127, Ap	Sequence 236, App
C 335	17	1.2	457	16	US-10-362-939-5	Sequence 5, Appli	Sequence 236, App
C 336	17	1.2	457	18	US-10-425-115-49934	Sequence 49934, A	Sequence 236, App
C 337	17	1.2	458	14	US-10-198-846-2743	Sequence 2743, Ap	Sequence 236, App
C 338	17	1.2	462	15	US-10-128-714-2113	Sequence 2113, Ap	Sequence 236, App
C 339	17	1.2	465	18	US-10-425-115-37442	Sequence 37442, A	Sequence 236, App
C 340	17	1.2	472	13	US-10-027-632-287815	Sequence 287815,	Sequence 236, App
C 341	17	1.2	472	13	US-10-027-632-287815	Sequence 287815,	Sequence 236, App
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C 344	17	1.2	472	17	US-10-027-632-287815	Sequence 287815,	Sequence 236, App
C 345	17	1.2	472	18	US-10-027-632-287817	Sequence 287817,	Sequence 236, App
C 346	17	1.2	472	18	US-10-437-963-13703	Sequence 13703, A	Sequence 236, App
C 347	17	1.2	473	10	US-09-918-995-25092	Sequence 25092, A	Sequence 236, App
C 348	17	1.2	474	16	US-10-066-285-376	Sequence 376, App	Sequence 236, App
C 349	17	1.2	479	13	US-10-027-632-287806	Sequence 287806,	Sequence 236, App
C 350	17	1.2	479	17	US-10-027-632-287806	Sequence 287806,	Sequence 236, App
C 351	17	1.2	481	10	US-09-918-995-14552	Sequence 14552, A	Sequence 236, App
C 352	17	1.2	482	10	US-09-918-995-2811	Sequence 2811, Ap	Sequence 236, App
C 353	17	1.2	482	18	US-10-425-115-100398	Sequence 100398,	Sequence 236, App
C 354	17	1.2	486	14	US-10-066-243-1801	Sequence 1801, Ap	Sequence 236, App
C 355	17	1.2	500	13	US-10-027-632-71931	Sequence 71931, A	Sequence 236, App
C 356	17	1.2	500	13	US-10-027-632-73218	Sequence 73218, A	Sequence 236, App
C 357	17	1.2	500	17	US-10-027-632-71931	Sequence 71931, A	Sequence 236, App
C 358	17	1.2	500	17	US-10-027-632-73218	Sequence 73218, A	Sequence 236, App
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C 360	17	1.2	501	9	US-09-783-590-6485	Sequence 6485, Ap	Sequence 236, App
C 361	17	1.2	502	9	US-09-736-457-1463	Sequence 1463, Ap	Sequence 236, App
C 362	17	1.2	502	9	US-09-902-941-1463	Sequence 1463, Ap	Sequence 236, App
C 363	17	1.2	502	9	US-09-849-636-1463	Sequence 1463, Ap	Sequence 236, App
C 364	17	1.2	502	14	US-10-017-754-1463	Sequence 1463, Ap	Sequence 236, App
C 365	17	1.2	502	16	US-10-113-872-1463	Sequence 1463, Ap	Sequence 236, App
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C 378	17	1.2	549	17	US-10-424-599-88947	Sequence 88947, A	451	17	1.2	648	18	US-10-437-963-56415	Sequence 56415, A
C 379	17	1.2	550	13	US-10-027-632-106610	Sequence 106610, A	452	17	1.2	658	13	US-10-027-632-286264	Sequence 286264, A
C 380	17	1.2	550	13	US-10-027-632-106611	Sequence 106611, A	453	17	1.2	658	17	US-10-027-632-286264	Sequence 286264, A
C 381	17	1.2	550	17	US-10-027-632-106610	Sequence 106610, A	C 454	17	1.2	660	13	US-10-027-632-38062	Sequence 38062, A
C 382	17	1.2	550	17	US-10-027-632-106611	Sequence 106611, A	C 455	17	1.2	660	17	US-10-027-632-38062	Sequence 38062, A
C 383	17	1.2	562	13	US-10-027-632-279818	Sequence 279818, A	C 456	17	1.2	665	9	US-09-764-861-22	Sequence 22, Appl
C 384	17	1.2	562	13	US-10-027-632-279819	Sequence 279819, A	C 457	17	1.2	665	10	US-09-764-861-22	Sequence 22, Appl
C 385	17	1.2	562	17	US-10-027-632-279818	Sequence 279818, A	C 458	17	1.2	665	14	US-10-103-313-122	Sequence 122, App
C 386	17	1.2	563	17	US-10-027-632-279819	Sequence 279819, A	C 459	17	1.2	665	18	US-10-115-928-22	Sequence 22, Appl
C 387	17	1.2	563	10	US-09-814-353-16913	Sequence 16913, A	C 460	17	1.2	665	14	US-10-425-115-114517	Sequence 114517, A
C 388	17	1.2	565	9	US-09-731-872-11	Sequence 11, Appl	461	17	1.2	667	15	US-10-128-714-1113	Sequence 1113, Ap
C 389	17	1.2	565	10	US-09-876-997-11	Sequence 11, Appl	462	17	1.2	681	13	US-10-027-632-245839	Sequence 245839, A
C 390	17	1.2	567	16	US-10-029-386-20457	Sequence 20457, A	463	17	1.2	681	17	US-10-027-632-245839	Sequence 245839, A
C 391	17	1.2	573	18	US-10-767-701-15705	Sequence 15705, A	C 464	17	1.2	682	18	US-10-425-115-11815	Sequence 11815, A
C 392	17	1.2	575	9	US-09-880-107-2515	Sequence 2515, Ap	465	17	1.2	687	17	US-10-172-118-2669	Sequence 2669, Ap
C 393	17	1.2	579	13	US-10-027-632-192573	Sequence 192573, A	466	17	1.2	687	17	US-10-342-887-2669	Sequence 2669, Ap
C 394	17	1.2	579	15	US-10-128-714-7113	Sequence 7113, Ap	467	17	1.2	688	18	US-10-425-115-143047	Sequence 143047, A
C 395	17	1.2	579	17	US-10-027-632-192573	Sequence 192573, A	468	17	1.2	692	14	US-10-198-846-9418	Sequence 9418, Ap
C 396	17	1.2	582	16	US-10-029-386-20546	Sequence 20546, A	469	17	1.2	692	17	US-10-425-114-19025	Sequence 19025, A
C 397	17	1.2	582	17	US-10-424-599-116752	Sequence 116752, A	470	17	1.2	696	13	US-10-027-632-138895	Sequence 138895, A
C 398	17	1.2	585	18	US-10-437-963-79180	Sequence 79180, A	471	17	1.2	696	13	US-10-027-632-138896	Sequence 138896, A
C 399	17	1.2	586	13	US-10-027-632-89793	Sequence 89793, A	472	17	1.2	696	17	US-10-027-632-138895	Sequence 138895, A
C 400	17	1.2	586	13	US-10-027-632-89793	Sequence 89793, A	473	17	1.2	696	17	US-10-027-632-138896	Sequence 138896, A
C 401	17	1.2	586	13	US-10-027-632-317248	Sequence 317248, A	C 474	17	1.2	699	13	US-10-027-632-135674	Sequence 135674, A
C 402	17	1.2	586	13	US-10-027-632-317249	Sequence 317249, A	C 475	17	1.2	699	17	US-10-027-632-135674	Sequence 135674, A
C 403	17	1.2	586	17	US-10-027-632-89793	Sequence 89793, A	476	17	1.2	703	17	US-10-335-977-2340	Sequence 2340, Ap
C 404	17	1.2	586	17	US-10-027-632-89793	Sequence 89793, A	477	17	1.2	703	13	US-10-027-632-151721	Sequence 151721, A
C 405	17	1.2	586	17	US-10-027-632-317248	Sequence 317248, A	C 478	17	1.2	703	13	US-10-027-632-151722	Sequence 151722, A
C 406	17	1.2	586	17	US-10-027-632-317249	Sequence 317249, A	C 479	17	1.2	703	13	US-10-027-632-151723	Sequence 151723, A
C 407	17	1.2	586	18	US-10-437-963-32446	Sequence 32446, A	C 480	17	1.2	703	17	US-10-027-632-151721	Sequence 151721, A
C 408	17	1.2	587	13	US-10-027-632-216347	Sequence 216347, A	C 481	17	1.2	703	17	US-10-027-632-151722	Sequence 151722, A
C 409	17	1.2	587	13	US-10-027-632-216347	Sequence 216347, A	C 482	17	1.2	703	17	US-10-027-632-151723	Sequence 151723, A
C 410	17	1.2	587	17	US-10-027-632-216346	Sequence 216346, A	C 483	17	1.2	705	10	US-09-822-846-494	Sequence 494, App
C 411	17	1.2	587	17	US-10-027-632-216347	Sequence 216347, A	C 484	17	1.2	716	17	US-10-424-599-113111	Sequence 113111, A
C 412	17	1.2	591	18	US-10-767-701-31374	Sequence 31374, Ap	C 485	17	1.2	718	18	US-10-767-701-15374	Sequence 15374, A
C 413	17	1.2	593	18	US-10-767-701-31374	Sequence 31374, Ap	C 486	17	1.2	722	18	US-10-767-701-15374	Sequence 15374, A
C 414	17	1.2	598	9	US-10-021-323-15430	Sequence 15430, Ap	487	17	1.2	731	13	US-10-027-632-125599	Sequence 125599, A
C 415	17	1.2	598	9	US-09-764-887-108	Sequence 108, App	488	17	1.2	731	13	US-10-027-632-125599	Sequence 125599, A
C 416	17	1.2	599	13	US-10-027-632-234592	Sequence 234592, A	489	17	1.2	731	17	US-10-027-632-125599	Sequence 125599, A
C 417	17	1.2	599	14	US-10-073-361-108	Sequence 108, App	490	17	1.2	731	17	US-10-027-632-125600	Sequence 125600, A
C 418	17	1.2	599	17	US-10-027-632-234592	Sequence 234592, A	C 491	17	1.2	733	13	US-10-027-632-23536	Sequence 23536, A
C 419	17	1.2	600	13	US-10-027-632-232439	Sequence 232439, A	C 492	17	1.2	733	13	US-10-027-632-23537	Sequence 23537, A
C 420	17	1.2	600	13	US-10-027-632-232440	Sequence 232440, A	C 493	17	1.2	733	17	US-10-027-632-23536	Sequence 23536, A
C 421	17	1.2	600	13	US-10-027-632-232441	Sequence 232441, A	C 494	17	1.2	733	17	US-10-027-632-23537	Sequence 23537, A
C 422	17	1.2	600	17	US-10-027-632-232439	Sequence 232439, A	C 495	17	1.2	740	13	US-10-027-632-34002	Sequence 34002, A
C 423	17	1.2	600	17	US-10-027-632-232440	Sequence 232440, A	C 496	17	1.2	740	17	US-10-027-632-34002	Sequence 34002, A
C 424	17	1.2	600	17	US-10-027-632-232441	Sequence 232441, A	C 497	17	1.2	742	17	US-10-012-697-1175	Sequence 1175, Ap
C 425	17	1.2	601	18	US-10-021-323-15642	Sequence 15642, A	498	17	1.2	743	18	US-10-357-930-23719	Sequence 23719, A
C 426	17	1.2	604	13	US-10-027-632-231002	Sequence 231002, A	499	17	1.2	743	18	US-10-357-930-23719	Sequence 23719, A
C 427	17	1.2	604	17	US-10-027-632-231002	Sequence 231002, A	500	17	1.2	751	14	US-10-198-846-6528	Sequence 6528, Ap
C 428	17	1.2	607	18	US-10-767-701-23442	Sequence 23442, A	501	17	1.2	753	13	US-10-027-632-172193	Sequence 172193, A
C 429	17	1.2	611	13	US-10-027-632-210288	Sequence 210288, A	502	17	1.2	753	17	US-10-027-632-172193	Sequence 172193, A
C 430	17	1.2	611	13	US-10-027-632-210289	Sequence 210289, A	C 503	17	1.2	754	13	US-10-027-632-29980	Sequence 29980, A
C 431	17	1.2	611	13	US-10-027-632-210290	Sequence 210290, A	C 504	17	1.2	754	18	US-10-027-632-29980	Sequence 29980, A
C 432	17	1.2	611	17	US-10-027-632-210288	Sequence 210288, A	C 505	17	1.2	758	18	US-10-767-701-12696	Sequence 12696, A
C 433	17	1.2	611	17	US-10-027-632-210289	Sequence 210289, A	C 506	17	1.2	763	13	US-10-027-632-7931	Sequence 7921, Ap
C 434	17	1.2	611	17	US-10-027-632-210290	Sequence 210290, A	507	17	1.2	763	13	US-10-027-632-7931	Sequence 7931, Ap
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C 436	17	1.2	615	17	US-10-027-632-95980	Sequence 95980, A	509	17	1.2	763	17	US-10-027-632-7931	Sequence 7931, Ap
C 437	17	1.2	616	18	US-10-653-047-3834	Sequence 3834, Ap	510	17	1.2	768	17	US-10-425-114-26012	Sequence 26012, A
C 438	17	1.2	619	16	US-10-029-386-20768	Sequence 20768, A	C 511	17	1.2	773	13	US-10-027-632-130827	Sequence 130827, A
C 439	17	1.2	619	18	US-10-767-795-2916	Sequence 2916, Ap	C 512	17	1.2	773	13	US-10-027-632-130828	Sequence 130828, A
C 440	17	1.2	622	13	US-10-027-632-141368	Sequence 141368, A	C 513	17	1.2	773	13	US-10-027-632-130829	Sequence 130829, A
C 441	17	1.2	622	15	US-10-101-510-424	Sequence 424, App	C 514	17	1.2	773	17	US-10-027-632-130827	Sequence 130827, A
C 442	17	1.2	622	17	US-10-027-632-141368	Sequence 141368, A	C 515	17	1.2	773	17	US-10-027-632-130828	Sequence 130828, A
C 443	17	1.2	631	13	US-10-027-632-282033	Sequence 282033, A	C 516	17	1.2	773	17	US-10-027-632-130829	Sequence 130829, A
C 444	17	1.2	631	17	US-10-027-632-282033	Sequence 282033, A	C 517	17	1.2	782	18	US-10-027-632-157405	Sequence 157405, A
C 445	17	1.2	636	18	US-10-767-701-7311	Sequence 7311, Ap	C 518	17	1.2	783	17	US-10-425-115-157405	Sequence 157405, A
C 446	17	1.2	637	13	US-10-027-632-202892	Sequence 202892, A	519	17	1.2	797	17	US-10-425-114-1771	Sequence 1771, Ap
C 447	17	1.2	637	17	US-10-198-846-13314	Sequence 13314, A	C 520	17	1.2	805	13	US-10-027-632-157742	Sequence 157742, A
C 448	17	1.2	637	17	US-10-027-632-202892	Sequence 202892, A	C 521	17	1.2	805	17	US-10-027-632-157742	Sequence 157742, A
C 449	17	1.2	638	13	US-10-027-632-272474	Sequence 272474, A	522	17	1.2	807	14	US-10-198-846-13378	Sequence 13378, A

C 523	17	1.2	810	13	US-10-027-632-28729	Sequence 28729, A	596	17	1.2	1401	17	US-10-236-392-147	Sequence 147, App
C 524	17	1.2	810	17	US-10-027-632-28729	Sequence 28729, A	597	17	1.2	1401	17	US-10-236-392-149	Sequence 149, App
C 525	17	1.2	812	13	US-10-027-632-142384	Sequence 142384, A	C 598	17	1.2	1416	18	US-10-437-963-74676	Sequence 74676, A
C 526	17	1.2	812	13	US-10-027-632-142385	Sequence 142385, A	C 599	17	1.2	1422	18	US-09-864-761-10158	Sequence 10158, A
C 527	17	1.2	812	17	US-10-027-632-142384	Sequence 142384, A	600	17	1.2	1438	15	US-10-101-510-102	Sequence 102, App
C 528	17	1.2	812	17	US-10-027-632-142385	Sequence 142385, A	601	17	1.2	1438	17	US-10-101-510-102	Sequence 102, App
C 529	17	1.2	813	14	US-10-198-846-94208	Sequence 94208, A	602	17	1.2	1438	18	US-10-305-720-1426	Sequence 1426, App
C 530	17	1.2	829	18	US-10-437-963-92805	Sequence 92805, A	603	17	1.2	1438	18	US-10-283-975A-67	Sequence 67, Appl
C 531	17	1.2	830	14	US-10-198-846-6861	Sequence 6861, A	604	17	1.2	1441	16	US-10-098-871-19	Sequence 19, Appl
C 532	17	1.2	831	13	US-10-027-632-8734	Sequence 8734, A	605	17	1.2	1441	17	US-10-236-392-127	Sequence 127, App
C 533	17	1.2	831	18	US-10-027-632-8734	Sequence 8734, A	606	17	1.2	1441	17	US-10-236-392-133	Sequence 133, App
C 534	17	1.2	834	18	US-10-425-115-93961	Sequence 93961, A	607	17	1.2	1470	17	US-10-282-122A-26557	Sequence 26557, A
C 535	17	1.2	837	18	US-10-437-963-92472	Sequence 92472, A	608	17	1.2	1473	17	US-10-282-122A-28316	Sequence 28316, A
C 536	17	1.2	840	18	US-10-425-115-112238	Sequence 112238, A	C 608	17	1.2	1473	17	US-10-425-114-32731	Sequence 32731, A
C 537	17	1.2	843	18	US-10-437-963-17252	Sequence 17252, A	609	17	1.2	1498	14	US-10-004-551-29	Sequence 29, Appl
C 538	17	1.2	852	18	US-10-767-795-6370	Sequence 6370, A	610	17	1.2	1498	17	US-10-236-392-125	Sequence 125, App
C 539	17	1.2	858	18	US-10-767-795-6370	Sequence 6370, A	611	17	1.2	1527	13	US-10-027-632-257183	Sequence 257183, A
C 540	17	1.2	862	17	US-10-425-115-49703	Sequence 49703, A	612	17	1.2	1527	17	US-10-027-632-257183	Sequence 257183, A
C 541	17	1.2	867	18	US-10-468-372-8	Sequence 8, Appli	613	17	1.2	1528	18	US-10-437-963-3273	Sequence 3273, App
C 542	17	1.2	870	13	US-10-425-115-92923	Sequence 92923, A	C 614	17	1.2	1538	17	US-10-425-114-28117	Sequence 28117, A
C 543	17	1.2	870	13	US-10-027-632-138894	Sequence 138894, A	C 615	17	1.2	1545	9	US-09-922-138-6	Sequence 6, Appli
C 544	17	1.2	882	18	US-10-437-963-35107	Sequence 35107, A	C 616	17	1.2	1545	9	US-09-841-683-1	Sequence 1, Appli
C 545	17	1.2	886	17	US-10-425-114-18034	Sequence 18034, A	C 617	17	1.2	1545	18	US-10-620-845-1	Sequence 40, Appl
C 546	17	1.2	893	14	US-10-198-846-6536	Sequence 6536, A	C 618	17	1.2	1545	18	US-10-391-364-40	Sequence 114518, A
C 547	17	1.2	909	18	US-10-425-115-43139	Sequence 43139, A	C 619	17	1.2	1546	18	US-10-425-115-114518	Sequence 41062, A
C 548	17	1.2	915	17	US-10-425-115-43139	Sequence 43139, A	C 620	17	1.2	1569	18	US-10-425-115-41062	Sequence 107, App
C 549	17	1.2	923	17	US-10-425-114-19026	Sequence 19026, A	621	17	1.2	1581	9	US-09-729-674-107	Sequence 107, App
C 550	17	1.2	925	18	US-10-425-114-33204	Sequence 33204, A	622	17	1.2	1581	18	US-10-913-553-107	Sequence 107, App
C 551	17	1.2	942	15	US-10-739-930-2612	Sequence 2612, A	623	17	1.2	1584	9	US-09-764-861-68	Sequence 68, Appl
C 552	17	1.2	948	18	US-10-156-761-6198	Sequence 6198, A	624	17	1.2	1584	10	US-09-764-861-68	Sequence 68, Appl
C 553	17	1.2	953	15	US-10-767-701-15706	Sequence 15706, A	625	17	1.2	1584	14	US-10-103-313-636	Sequence 636, App
C 554	17	1.2	965	17	US-10-424-599-17050	Sequence 17050, A	626	17	1.2	1584	14	US-10-115-928-68	Sequence 68, Appl
C 555	17	1.2	969	18	US-10-767-701-8595	Sequence 8595, A	627	17	1.2	1620	17	US-10-468-372-7	Sequence 7, Appli
C 556	17	1.2	975	18	US-10-437-963-38330	Sequence 38330, A	628	17	1.2	1647	18	US-10-775-920-345	Sequence 345, App
C 557	17	1.2	981	17	US-10-424-599-74187	Sequence 74187, A	C 630	17	1.2	1665	9	US-09-771-161A-56	Sequence 56, Appl
C 558	17	1.2	984	17	US-10-425-114-21847	Sequence 21847, A	C 631	17	1.2	1673	9	US-09-861-696-4	Sequence 4, Appli
C 559	17	1.2	987	18	US-10-425-115-153717	Sequence 153717, A	C 632	17	1.2	1678	17	US-10-421-763-2	Sequence 2, Appli
C 560	17	1.2	1012	18	US-10-437-963-59791	Sequence 59791, A	633	17	1.2	1699	16	US-10-313-463-1	Sequence 1, Appli
C 561	17	1.2	1024	18	US-09-882-945A-259	Sequence 259, App	634	17	1.2	1725	17	US-10-236-392-69	Sequence 69, Appl
C 562	17	1.2	1024	18	US-10-807-114-259	Sequence 259, App	C 635	17	1.2	1735	16	US-10-029-386-20906	Sequence 20906, A
C 563	17	1.2	1026	18	US-10-767-701-8128	Sequence 8128, App	C 636	17	1.2	1735	18	US-09-864-761-19849	Sequence 19849, A
C 564	17	1.2	1054	18	US-10-767-701-1613	Sequence 1613, App	637	17	1.2	1739	18	US-10-739-930-442	Sequence 442, App
C 565	17	1.2	1054	18	US-10-767-701-1613	Sequence 1613, App	638	17	1.2	1748	13	US-10-001-887-52	Sequence 52, Appl
C 566	17	1.2	1057	17	US-10-425-114-33859	Sequence 33859, A	639	17	1.2	1748	18	US-10-958-863-52	Sequence 52, Appl
C 567	17	1.2	1068	17	US-09-864-761-26799	Sequence 26799, A	640	17	1.2	1749	18	US-10-775-920-340	Sequence 340, App
C 568	17	1.2	1068	15	US-10-251-385-1	Sequence 1, Appli	641	17	1.2	1784	17	US-10-424-599-35821	Sequence 35821, A
C 569	17	1.2	1068	15	US-10-251-385-163	Sequence 163, App	642	17	1.2	1820	17	US-10-272-811-3	Sequence 3, Appli
C 570	17	1.2	1068	15	US-10-225-567A-242	Sequence 242, App	643	17	1.2	1820	17	US-10-641-643-1031	Sequence 1031, App
C 571	17	1.2	1078	14	US-10-198-846-6662	Sequence 6662, App	644	17	1.2	1820	17	US-10-272-727-3	Sequence 3, Appli
C 572	17	1.2	1082	17	US-10-198-846-6889	Sequence 6889, App	645	17	1.2	1820	18	US-10-398-593-1	Sequence 1, Appli
C 573	17	1.2	1087	17	US-10-276-774-1167	Sequence 1167, App	646	17	1.2	1820	18	US-10-775-920-336	Sequence 336, App
C 574	17	1.2	1101	18	US-10-437-963-38335	Sequence 38335, A	647	17	1.2	1820	18	US-10-775-920-339	Sequence 339, App
C 575	17	1.2	1107	18	US-10-437-963-49442	Sequence 49442, A	648	17	1.2	1845	17	US-10-424-599-19558	Sequence 19558, A
C 576	17	1.2	1107	18	US-10-767-795-4996	Sequence 4996, App	649	17	1.2	1845	17	US-10-425-114-9159	Sequence 9159, App
C 577	17	1.2	1110	18	US-10-425-115-86092	Sequence 86092, A	C 650	17	1.2	1857	16	US-10-032-585-6435	Sequence 6435, App
C 578	17	1.2	1158	18	US-10-437-963-7051	Sequence 7051, App	651	17	1.2	1860	17	US-10-260-238-1524	Sequence 1524, App
C 579	17	1.2	1170	18	US-10-437-963-22115	Sequence 22115, A	652	17	1.2	1870	11	US-09-836-544-20	Sequence 20, Appl
C 580	17	1.2	1175	18	US-10-424-599-73509	Sequence 73509, A	653	17	1.2	1870	18	US-10-775-920-346	Sequence 346, App
C 581	17	1.2	1188	17	US-10-369-493-31701	Sequence 31701, A	C 654	17	1.2	1888	9	US-09-816-664-1	Sequence 1, Appli
C 582	17	1.2	1227	10	US-09-882-227-383	Sequence 383, App	C 655	17	1.2	1888	18	US-10-193-452-1	Sequence 1, Appli
C 583	17	1.2	1240	15	US-10-204-887-9	Sequence 9, Appli	656	17	1.2	1925	18	US-10-437-963-51206	Sequence 51206, A
C 584	17	1.2	1247	18	US-10-437-963-45753	Sequence 45753, A	657	17	1.2	1941	10	US-09-933-767-191	Sequence 191, App
C 585	17	1.2	1328	17	US-10-302-172-936	Sequence 936, App	658	17	1.2	1941	14	US-10-004-860-191	Sequence 191, App
C 586	17	1.2	1332	18	US-10-451-467A-453	Sequence 453, App	659	17	1.2	1941	14	US-10-023-282-191	Sequence 191, App
C 587	17	1.2	1332	19	US-10-741-849-6162	Sequence 6162, App	660	17	1.2	1942	17	US-10-305-720-1191	Sequence 1191, App
C 588	17	1.2	1356	17	US-10-424-599-11864	Sequence 11864, A	661	17	1.2	1942	17	US-10-272-811-23	Sequence 23, Appl
C 589	17	1.2	1363	9	US-09-263-959-283	Sequence 283, App	662	17	1.2	1942	17	US-10-272-727-23	Sequence 23, Appl
C 590	17	1.2	1389	17	US-10-236-392-71	Sequence 71, Appl	663	17	1.2	1942	18	US-10-775-920-337	Sequence 337, App
C 591	17	1.2	1389	17	US-10-236-392-137	Sequence 137, App	664	17	1.2	1944	15	US-10-084-817-84	Sequence 84, Appl
C 592	17	1.2	1389	17	US-10-236-392-139	Sequence 139, App	C 665	17	1.2	1951	9	US-09-822-830A-91	Sequence 91, Appl
C 593	17	1.2	1401	17	US-10-236-392-141	Sequence 141, App	666	17	1.2	1952	9	US-09-967-768A-195	Sequence 195, App
C 594	17	1.2	1401	17	US-10-236-392-143	Sequence 143, App	667	17	1.2	1952	9	US-09-954-531-585	Sequence 585, App
C 595	17	1.2	1401	17	US-10-236-392-145	Sequence 145, App	668	17	1.2	1952	19	US-10-843-641A-1652	Sequence 1652, App

669	17	1.2	1952	19	US-10-843-641A-6340	Sequence 6340, Ap	742	17	1.2	2635	14	US-10-023-282-121	Sequence 121, App
C 670	17	1.2	1954	16	US-10-420-845-2	Sequence 2, Appli	C 743	17	1.2	2660	18	US-10-755-889-31	Sequence 31, Appl
C 671	17	1.2	1956	9	US-09-864-761-3068	Sequence 3068, Ap	C 744	17	1.2	2667	15	US-10-128-714-113	Sequence 113, App
C 672	17	1.2	1978	17	US-10-425-114-660	Sequence 660, App	C 745	17	1.2	2670	18	US-10-437-963-73879	Sequence 73879, A
C 673	17	1.2	1986	13	US-10-194-163-150	Sequence 150, App	C 746	17	1.2	2677	13	US-10-194-163-959	Sequence 959, App
C 674	17	1.2	1990	18	US-10-437-963-28936	Sequence 28936, A	C 747	17	1.2	2693	9	US-09-764-861-67	Sequence 67, Appl
C 675	17	1.2	1995	18	US-10-425-115-138478	Sequence 138478, A	C 748	17	1.2	2693	9	US-09-764-861-69	Sequence 69, Appl
C 676	17	1.2	2001	9	US-09-841-683-3	Sequence 3, Appli	C 749	17	1.2	2693	9	US-09-764-861-70	Sequence 70, Appl
C 677	17	1.2	2001	18	US-10-620-845-3	Sequence 3, Appli	C 750	17	1.2	2693	10	US-09-764-861-67	Sequence 67, Appl
C 678	17	1.2	2024	9	US-09-867-569-1	Sequence 1, Appli	C 751	17	1.2	2693	10	US-09-764-861-69	Sequence 69, Appl
C 679	17	1.2	2024	14	US-10-218-574-1	Sequence 1, Appli	C 752	17	1.2	2693	10	US-09-764-861-70	Sequence 70, Appl
C 680	17	1.2	2066	18	US-10-437-963-61875	Sequence 61875, A	C 753	17	1.2	2693	14	US-10-103-313-635	Sequence 635, App
C 681	17	1.2	2093	17	US-10-112-944-123	Sequence 123, App	C 754	17	1.2	2693	14	US-10-103-313-637	Sequence 637, App
C 682	17	1.2	2105	18	US-10-468-406-17	Sequence 17, Appl	C 755	17	1.2	2693	14	US-10-103-313-638	Sequence 638, App
C 683	17	1.2	2116	18	US-10-775-920-342	Sequence 342, App	C 756	17	1.2	2693	14	US-10-115-928-67	Sequence 67, Appl
C 684	17	1.2	2132	17	US-10-262-445-118	Sequence 118, App	C 757	17	1.2	2693	14	US-10-115-928-69	Sequence 69, Appl
C 685	17	1.2	2135	18	US-10-425-115-73164	Sequence 73164, A	C 758	17	1.2	2693	14	US-10-115-928-70	Sequence 70, Appl
C 686	17	1.2	2196	17	US-10-369-493-27670	Sequence 27670, A	C 759	17	1.2	2727	18	US-10-437-963-98438	Sequence 98438, A
C 687	17	1.2	2203	9	US-09-739-907-39	Sequence 39, Appl	C 760	17	1.2	2729	17	US-10-264-237-1226	Sequence 1226, Ap
C 688	17	1.2	2203	11	US-09-938-671-39	Sequence 39, Appl	C 761	17	1.2	2737	15	US-10-176-306-10	Sequence 10, Appl
C 689	17	1.2	2206	19	US-10-935-998-39	Sequence 39, Appl	C 762	17	1.2	2739	14	US-10-109-562A-1	Sequence 1, Appli
C 690	17	1.2	2206	10	US-09-814-353-21128	Sequence 21128, A	C 763	17	1.2	2751	18	US-10-437-963-38332	Sequence 38332, A
C 691	17	1.2	2209	9	US-09-925-301-494	Sequence 494, App	C 764	17	1.2	2953	15	US-10-128-714-5113	Sequence 5113, Ap
C 692	17	1.2	2216	9	US-09-954-456-1977	Sequence 1977, Ap	C 765	17	1.2	2982	10	US-09-814-353-19609	Sequence 19609, A
C 693	17	1.2	2216	9	US-09-880-107-2436	Sequence 2436, Ap	C 766	17	1.2	3012	17	US-10-236-392-131	Sequence 131, App
C 694	17	1.2	2216	17	US-10-372-683-44	Sequence 44, Appl	C 767	17	1.2	3021	17	US-10-236-392-129	Sequence 129, App
C 695	17	1.2	2216	17	US-10-272-811-24	Sequence 24, Appl	C 768	17	1.2	3032	17	US-10-291-265-659	Sequence 659, App
C 696	17	1.2	2216	17	US-10-272-727-24	Sequence 24, Appl	C 769	17	1.2	3064	18	US-10-385-163-114	Sequence 114, App
C 697	17	1.2	2216	18	US-10-775-920-338	Sequence 338, App	C 770	17	1.2	3064	18	US-10-796-177-114	Sequence 114, App
C 698	17	1.2	2216	19	US-10-843-641A-5004	Sequence 5004, Ap	C 771	17	1.2	3078	17	US-10-172-118-1439	Sequence 1439, Ap
C 699	17	1.2	2224	14	US-10-059-585-11	Sequence 11, Appl	C 772	17	1.2	3078	17	US-10-342-887-1439	Sequence 1439, Ap
C 700	17	1.2	2226	18	US-10-335-053-219	Sequence 219, App	C 773	17	1.2	3078	17	US-10-236-392-135	Sequence 135, App
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C 702	17	1.2	2232	17	US-10-027-632-110384	Sequence 110384, A	C 775	17	1.2	3085	17	US-10-104-047-377	Sequence 377, App
C 703	17	1.2	2238	18	US-10-437-963-710823	Sequence 710823, A	C 776	17	1.2	3088	9	US-09-529-063-72	Sequence 72, Appl
C 704	17	1.2	2240	17	US-10-311-034-39	Sequence 39, Appl	C 777	17	1.2	3088	16	US-10-414-378-72	Sequence 72, Appl
C 705	17	1.2	2245	17	US-10-231-956A-153	Sequence 153, App	C 778	17	1.2	3139	17	US-10-260-238-889	Sequence 889, App
C 706	17	1.2	2280	17	US-09-925-301-24	Sequence 24, Appl	C 779	17	1.2	3155	16	US-10-240-965-102	Sequence 102, App
C 707	17	1.2	2287	17	US-10-104-047-1539	Sequence 1539, Ap	C 780	17	1.2	3224	18	US-10-775-920-341	Sequence 341, App
C 708	17	1.2	2301	17	US-10-425-114-26283	Sequence 26283, A	C 781	17	1.2	3242	17	US-10-062-674-2110	Sequence 2110, Ap
C 709	17	1.2	2340	17	US-10-641-643-359	Sequence 359, App	C 782	17	1.2	3263	17	US-10-264-049-894	Sequence 894, App
C 710	17	1.2	2347	16	US-10-362-939-1	Sequence 1, Appli	C 783	17	1.2	3279	13	US-10-027-632-114128	Sequence 114128, A
C 711	17	1.2	2362	17	US-10-466-759-13	Sequence 13, Appl	C 784	17	1.2	3279	13	US-10-027-632-114129	Sequence 114129, A
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C 713	17	1.2	2369	17	US-10-424-599-30244	Sequence 30244, A	C 786	17	1.2	3279	17	US-10-027-632-114129	Sequence 114129, A
C 714	17	1.2	2389	8	US-08-979-847-48	Sequence 48, Appl	C 787	17	1.2	3306	18	US-10-437-963-100862	Sequence 100862, A
C 715	17	1.2	2389	16	US-10-430-442-52	Sequence 52, Appl	C 788	17	1.2	3309	9	US-09-925-298-273	Sequence 273, App
C 716	17	1.2	2389	16	US-10-114-104-48	Sequence 48, Appl	C 789	17	1.2	3318	16	US-10-102-806-273	Sequence 273, App
C 717	17	1.2	2436	17	US-10-468-372-6	Sequence 6, Appli	C 790	17	1.2	3318	16	US-10-420-845-3	Sequence 3, Appli
C 718	17	1.2	2436	18	US-10-357-930-30141	Sequence 30141, A	C 791	17	1.2	3318	16	US-10-421-763-3	Sequence 3, Appli
C 719	17	1.2	2466	9	US-09-922-138-4	Sequence 4, Appli	C 792	17	1.2	3336	14	US-10-004-551-27	Sequence 27, Appl
C 720	17	1.2	2466	18	US-10-391-364-38	Sequence 38, Appl	C 793	17	1.2	3336	14	US-10-236-392-123	Sequence 123, App
C 721	17	1.2	2473	10	US-09-814-353-22034	Sequence 22034, A	C 794	17	1.2	3348	17	US-10-282-122A-26061	Sequence 26061, A
C 722	17	1.2	2484	17	US-10-080-334-79	Sequence 79, Appl	C 795	17	1.2	3385	16	US-10-420-845-1	Sequence 1, Appli
C 723	17	1.2	2488	9	US-09-962-832-231	Sequence 231, App	C 796	17	1.2	3405	17	US-10-291-265-187	Sequence 187, App
C 724	17	1.2	2488	18	US-10-789-378-31	Sequence 31, Appl	C 797	17	1.2	3416	18	US-10-930-213-293	Sequence 293, App
C 725	17	1.2	2488	19	US-10-482-029-127	Sequence 127, App	C 798	17	1.2	3416	18	US-10-723-860-1566	Sequence 1566, Ap
C 726	17	1.2	2488	19	US-10-843-641A-6117	Sequence 6117, Ap	C 799	17	1.2	3424	17	US-10-094-749-634	Sequence 634, App
C 727	17	1.2	2503	18	US-10-676-248B-80	Sequence 80, Appl	C 800	17	1.2	3424	17	US-10-437-963-93433	Sequence 93433, A
C 728	17	1.2	2505	15	US-10-176-306-12	Sequence 12, Appl	C 801	17	1.2	3655	18	US-10-276-774-918	Sequence 918, App
C 729	17	1.2	2505	17	US-10-467-434-22	Sequence 22, Appl	C 802	17	1.2	3655	18	US-10-437-963-93433	Sequence 93433, A
C 730	17	1.2	2520	10	US-09-880-107-3685	Sequence 3685, Ap	C 803	17	1.2	3677	17	US-10-405-877-46	Sequence 46, Appl
C 731	17	1.2	2520	10	US-09-960-706-1049	Sequence 1049, Ap	C 804	17	1.2	3694	17	US-10-405-877-24	Sequence 24, Appl
C 732	17	1.2	2520	17	US-09-873-319-696	Sequence 696, App	C 805	17	1.2	3704	17	US-10-405-877-24	Sequence 24, Appl
C 733	17	1.2	2560	17	US-10-236-392-153	Sequence 153, App	C 806	17	1.2	3708	18	US-10-357-930-23334	Sequence 23334, A
C 734	17	1.2	2577	9	US-09-529-063-71	Sequence 71, Appl	C 807	17	1.2	3708	18	US-10-357-930-23334	Sequence 23334, A
C 735	17	1.2	2577	16	US-10-414-378-71	Sequence 71, Appl	C 808	17	1.2	3809	9	US-09-764-847-1158	Sequence 1158, Ap
C 736	17	1.2	2592	17	US-10-236-392-151	Sequence 151, App	C 809	17	1.2	3809	14	US-10-092-154-1158	Sequence 1158, Ap
C 737	17	1.2	2607	18	US-10-437-963-1460	Sequence 1460, Ap	C 810	17	1.2	3837	18	US-10-723-860-5986	Sequence 5986, Ap
C 738	17	1.2	2620	18	US-10-723-860-5366	Sequence 5366, Ap	C 811	17	1.2	3930	9	US-09-847-874A-2	Sequence 2, Appli
C 739	17	1.2	2629	17	US-10-152-319A-1954	Sequence 1954, Ap	C 812	17	1.2	3930	9	US-10-458-162-2	Sequence 2, Appli
C 740	17	1.2	2635	10	US-09-933-767-121	Sequence 121, App	C 813	17	1.2	3960	14	US-10-197-666A-95	Sequence 95, Appl
C 741	17	1.2	2635	14	US-10-004-860-121	Sequence 121, App	C 814	17	1.2				

C 815	17	1.2	3975	17	US-10-311-034-34	Sequence 34, Appl	C 888	17	1.2	31314	9	US-09-764-877-3875	Sequence 3875, Ap
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US-09-751-708A-97

; Sequence 97, Application US/09751708A

; Publication No. US20030157113A1

; GENERAL INFORMATION:

; APPLICANT: TERMAN, David S

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

; FILE REFERENCE: 751708

; CURRENT APPLICATION NUMBER: US/09/751,708A

; CURRENT FILING DATE: 2002-10-15

; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 166

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 97

; LENGTH: 1449

; TYPE: DNA

; ORGANISM: Homo sapiens

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; LOCATION: (1)..(1449)

; OTHER INFORMATION:

US-09-751-708A-97

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Qy 181 TTCTCTCCACTCACCTTGGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
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Qy 1441 ACTGTGTGA 1449
Db 1441 ACTGTGTGA 1449

```

```

RESULT 6
US-10-428-817A-93
; Sequence 93, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1449)

```

US-10-428-817A-93

Query Match 100.0%; Score 1449; DB 18; Length 1449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACGCCATGGATGAG 60
DB 1 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACGCCATGGATGAG 60

QY 61 CCCCAGTAATCTCTCCATGTCATCTCAGCCCTTACTTTTACTGGGATTCGACGGC 120
DB 61 CCCCAGTAATCTCTCCATGTCATCTCAGCCCTTACTTTTACTGGGATTCGACGGC 120

QY 121 AATGGCTGGTGTCTGCGTGGCTGGCTGAGATGACGGGACAGTGAACAAATTTGG 180
DB 121 AATGGCTGGTGTCTGCGTGGCTGGCTGAGATGACGGGACAGTGAACAAATTTGG 180

QY 181 TTCTCCACCTCACCCTTGGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
DB 181 TTCTCCACCTCACCCTTGGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240

QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGGTTCCATGCAAGCTCATCCCTCC 300
DB 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGGTTCCATGCAAGCTCATCCCTCC 300

QY 301 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTGCAATAGGCTGGATCGC 360
DB 301 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTGCAATAGGCTGGATCGC 360

QY 361 TGTCTTGGTATTCAAGCCATCTGGTGTGAGATCATCGCAATGTAGGATGGCTGCG 420
DB 361 TGTCTTGGTATTCAAGCCATCTGGTGTGAGATCATCGCAATGTAGGATGGCTGCG 420

QY 421 TCTATCTGTGATGATCTGGGTGTGGCTTTTGTGATGTGATCTCTGTTTCTGTGATC 480
DB 421 TCTATCTGTGATGATCTGGGTGTGGCTTTTGTGATGTGATCTCTGTTTCTGTGATC 480

QY 481 CGGGAATCTTCACTACAGAACCAATATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 540
DB 481 CGGGAATCTTCACTACAGAACCAATATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 540

QY 541 TCATTAGATTATCCAGATTTTATGGATCCACTAGAAACAGCTCTCTGAAACATTT 600
DB 541 TCATTAGATTATCCAGATTTTATGGATCCACTAGAAACAGCTCTCTGAAACATTT 600

QY 601 GTTCAGCGCTCGGAGAAATGAATGATAGGTAGATCTCTCTCTCTTCCAAACAAATGAT 660
DB 601 GTTCAGCGCTCGGAGAAATGAATGATAGGTAGATCTCTCTCTCTTCCAAACAAATGAT 660

QY 661 CATCTTGGACAGTCCCACCTGTCTTCCAACTCAACATTTTCAAGACCTTCTCGAGAT 720
DB 661 CATCTTGGACAGTCCCACCTGTCTTCCAACTCAACATTTTCAAGACCTTCTCGAGAT 720

QY 721 TCACCTCCCTAGGGTCTCTGATGTTTACAGTCAAAATCTGTATCTTAATGATTTAAA 780
DB 721 TCACCTCCCTAGGGTCTCTGATGTTTACAGTCAAAATCTGTATCTTAATGATTTAAA 780

QY 781 CCTGCTGATGTGCTCACTCAAAATCCCAGTGGTTCCTTATTGAAGATCAGCAAAACC 840
DB 781 CCTGCTGATGTGCTCACTCAAAATCCCAGTGGTTCCTTATTGAAGATCAGCAAAACC 840

QY 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTCTCCAGGCT 900
DB 841 AGCCCACTGGATTAATCTGATGCTTTTCTCTACTCAATTTAAAGCTGTCTCCAGGCT 900

QY 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATTAATTTA 960
DB 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATTAATTTA 960

QY 961 GGCCTAATTCACAGATGACGATCAAGTGCACCAACCCCTCTGTCGCAATTAACGATCACTAGG 1020
DB 961 GGCCTAATTCACAGATGACGATCAAGTGCACCAACCCCTCTGTCGCAATTAACGATCACTAGG 1020
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RESULT 7

US-10-017-161-759
; Sequence 759, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIHO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 759
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1849)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(829)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1106)..(1649)
US-10-017-161-759

Query Match 100.0%; Score 1449; DB 15; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACGCCATGGATGAG 60
DB 201 ATGGCGTCTTCTCTGCTGAGACCAATCAACTGACCTACTCTCACGCCATGGATGAG 260
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QY 61 CCCCAGTAATCTCTCCATGGTCATCTTCAGCCCTTACTTTTACTGGGATGCCAGGC 120
Db 261 CCCCAGTAATCTCTCCATGGTCATCTTCAGCCCTTACTTTTACTGGGATGCCAGGC 320
QY 121 AATGGCTGGTCTGTGGGTGGCTGGCCCTGAAGATGACGCGAGCAGTGAACACAAATTTGG 180
Db 321 AATGGCTGGTCTGTGGGTGGCTGGCCCTGAAGATGACGCGAGCAGTGAACACAAATTTGG 380
QY 181 TTCCTCCACCTCACTTGGCGGAACTCTCTCTGTGGCCCTCTCTGGCCCTTCTCGCTGGCT 240
Db 381 TTCCTCCACCTCACTTGGCGGAACTCTCTCTGTGGCCCTCTCTGGCCCTTCTCGCTGGCT 440
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGTTCCATGCAAGCTCATCCCTCC 300
Db 441 CACTTGGCTCTCCAGGACAGTGGCCCTACGCGAGTTCCATGCAAGCTCATCCCTCC 500
QY 301 ATCATTTGCTCCCAACATGTTTGGCCAGTGTCTTCTGTCTTACTGCAATAGCTGTGATGCG 360
Db 501 ATCATTTGCTCCCAACATGTTTGGCCAGTGTCTTCTGTCTTACTGCAATAGCTGTGATGCG 560
QY 361 TGTCTTGTGGTATTCAGCCCAATCTGTGTGAGCAATCATCGCAATGATAGGATGCCCTGC 420
Db 561 TGTCTTGTGGTATTCAGCCCAATCTGTGTGAGCAATCATCGCAATGATAGGATGCCCTGC 620
QY 421 TCTATCTGTGATGATCTGGGTGGTGGCTTTTGTGATGTCATTCCTGTGTCTGTGTAC 480
Db 621 TCTATCTGTGATGATCTGGGTGGTGGCTTTTGTGATGTCATTCCTGTGTCTGTGTAC 680
QY 481 CGGGAATCTTCACTACAGACAAACATAATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 540
Db 681 CGGGAATCTTCACTACAGACAAACATAATAGATGTGGCTCAAAATTTGGTCTCTCCAGC 740
QY 541 TCATATGATATTCAGACATTTTATGGAGATCCATAGAAAACAGTCTCTTGAACATTT 600
Db 741 TCATATGATATTCAGACATTTTATGGAGATCCATAGAAAACAGTCTCTTGAACATTT 800
QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTTCACAAACAAATGAT 660
Db 801 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTCTCTCTTTCACAAACAAATGAT 860
QY 661 CATCTTTGGACAGTCCCCACTGTCTTCCAACTCAAACTTCAAAAGACCTTCTGCAGAT 720
Db 861 CATCTTTGGACAGTCCCCACTGTCTTCCAACTCAAACTTCAAAAGACCTTCTGCAGAT 920
QY 721 TCATCTCTAGGGTCTGCTAGGTATACAGTCAAAATCTGTATCTTAATGATTTAAA 780
Db 921 TCATCTCTAGGGTCTGCTAGGTATACAGTCAAAATCTGTATCTTAATGATTTAAA 980
QY 781 CCTGTGATGTGCTCACTCAAAATCCCAAGTGGTTCCTATTGAAGATCACGAAACC 840
Db 981 CCTGTGATGTGCTCACTCAAAATCCCAAGTGGTTCCTATTGAAGATCACGAAACC 1040
QY 841 AGCCCACTGGATACTCTGATGTTTTCTCTACTCAATTAAGCTGTCCCTAGCGCT 900
Db 1041 AGCCCACTGGATACTCTGATGTTTTCTCTACTCAATTAAGCTGTCCCTAGCGCT 1100
QY 901 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATACAAATTA 960
Db 1101 TCTAGCAATCTCTTACAGTCTGAGTACCAAGGTTTCCAGGATTTATACAAATTA 1160
QY 961 GSCCAATTCACAGATGACATCAAGTGCACACCCCTCTGTGGCAATTAACGATCACTAGG 1020
Db 1161 GSCCAATTCACAGATGACATCAAGTGCACACCCCTCTGTGGCAATTAACGATCACTAGG 1220
QY 1021 CTAGTGTGGTTCCTCTGCGCTCTGTATCATGATAGCTGTTCAGCTTCAATGTC 1080
Db 1221 CTAGTGTGGTTCCTCTGCGCTCTGTATCATGATAGCTGTTCAGCTTCAATGTC 1280
QY 1081 TTCCGAATGCAAGGGCGCTTCCGCAAGTCTCAGACAAACCTTTCGATGCGCGTG 1140
Db 1281 TTCCGAATGCAAGGGCGCTTCCGCAAGTCTCAGACAAACCTTTCGATGCGCGTG 1340
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QY 1141 GTGTGTGGCTGTCTTTCTTGTCTGTGGACTCCATACCACTTTTGGAGTCTGTCA 1200
Db 1341 GTGTGTGGCTGTCTTTCTTGTCTGTGGACTCCATACCACTTTTGGAGTCTGTCA 1400
QY 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGTCTGGGATCATGTATGC 1260
Db 1401 TTGCTTACTGACCCAGAAACTCCCTTGGGAAAACTCTGATGTCTGGGATCATGTATGC 1460
QY 1261 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTTCTGGGAAA 1320
Db 1461 ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCTTTATGCCCTTCTGGGAAA 1520
QY 1321 GATTTTAGGAAGAAGCAAGCAGTCCATTGAGGAAATTTCTGGAGGAGCCCTTCAGTGAG 1380
Db 1521 GATTTTAGGAAGAAGCAAGCAGTCCATTGAGGAAATTTCTGGAGGAGCCCTTCAGTGAG 1580
QY 1381 GAGTCAACAGTTCCACCCACTGTCCCTCAAACTAATGTCTATTCAGAAAGAAATAGTACA 1440
Db 1581 GAGTCAACAGTTCCACCCACTGTCCCTCAAACTAATGTCTATTCAGAAAGAAATAGTACA 1640
QY 1441 ACTGTGTGA 1449
Db 1641 ACTGTGTGA 1649
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RESULT 8

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US-10-292-798-661
; Sequence 661, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: SUMA, MAKIYO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 661
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1849)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1649)
US-10-292-798-661
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Query Match 100.0%; Score 1449; DB 17; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGCGCTTTCTCTGTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 60
Db 201 ATGGCGCTTTCTCTGTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 260
QY 61 CCCCAGTAATCTCTCCATGGTCACTTACGCTTACTTTTACTGGGATGCCAGGC 120
Db 261 CCCCAGTAATCTCTCCATGGTCACTTACGCTTACTTTTACTGGGATGCCAGGC 320
QY 121 AATGGCTGGTCTGTGGGTGGCTGGCCCTGAAGATGACGCGAGCAGTGAACACAAATTTGG 180
Db 321 AATGGCTGGTCTGTGGGTGGCTGGCCCTGAAGATGACGCGAGCAGTGAACACAAATTTGG 380
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QY 191 TTCTCTCAGCTCACTTGGGGAACCTCTCTGTGCTGCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
Db 381 TTCTCTCAGCTCACTTGGGGAACCTCTCTGTGCTGCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 440
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGCGAGGTTCTTATGCAAGCTCATCCCTCC 300
Db 441 CACTTGGCTCTCCAGGACAGTGGCCCTTACGCGAGGTTCTTATGCAAGCTCATCCCTCC 500
QY 301 ATCATTTGCTCAACATGTTTGCAGTGTCTTCTGCTTACTGCTCATTTAGCTTGGATCGC 360
Db 501 ATCATTTGCTCAACATGTTTGCAGTGTCTTCTGCTTACTGCTCATTTAGCTTGGATCGC 560
QY 361 TGTCTTGTGTATTCAGGCAATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 561 TGTCTTGTGTATTCAGGCAATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 421 TCTATCTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 621 TCTATCTGTGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY 481 CGGGAATCTTCACTACAGAACCAATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 540
Db 681 CGGGAATCTTCACTACAGAACCAATATAGATGTGCTCAAAATTTGGTCTCTCCAGC 740
QY 541 TCATTAGATTTACAGACTTTTATGAGATCCACTAGAAACAGGTCTCTTGAACAATTT 600
Db 741 TCATTAGATTTACAGACTTTTATGAGATCCACTAGAAACAGGTCTCTTGAACAATTT 800
QY 601 GTTCAGCGCTGGAGAAATGATAGTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 801 GTTCAGCGCTGGAGAAATGATAGTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 860
QY 661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTCAGAT 720
Db 861 CATCTTGGACAGTCCCACTGTCTTCAACCTCAACATTTCAAGACCTTCTCAGAT 920
QY 721 TCATCTCTAGGGTCTGCTAGGTAAAGTCAAGTCAAAATCTGATTTAAATGATTTAA 780
Db 921 TCATCTCTAGGGTCTGCTAGGTAAAGTCAAGTCAAAATCTGATTTAAATGATTTAA 980
QY 781 CTTGCTGATGTCTCACTTAAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 981 CTTGCTGATGTCTCACTTAAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
QY 841 AGCCCACTGGATAAATCTGATGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 1041 AGCCCACTGGATAAATCTGATGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1100
QY 901 TCTAGCAATCTCTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1101 TCTAGCAATCTCTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
QY 961 GSCCAATTCACAGATGACATCAAGTCCCAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 1161 GSCCAATTCACAGATGACATCAAGTCCCAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220
QY 1021 CTAGTGGTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1221 CTAGTGGTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280
QY 1081 TTCCCAATTCACAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1281 TTCCCAATTCACAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1340
QY 1141 GTGGTGGTGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1341 GTGGTGGTGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1400
QY 1201 TTGCTTACTGACCCAGAACTCCCTTTGGGAAACTCTGATGCTCTGGGATCATGTATGC 1260
Db 1401 TTGCTTACTGACCCAGAACTCCCTTTGGGAAACTCTGATGCTCTGGGATCATGTATGC 1460
QY 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTCTCTTTATGCTGCTCTTGGGAAA 1320
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Db 1461 ATTGCTCTAGCATCTGCCAATAGTGTCTTTAATCCCTCTCTTTATGCTCTCTTGGGAAA 1520
QY 1321 GATTTTAGAAGAAAGCAAGCAGTCCATTTCAGGAAATCTTGGAGGAGCCCTTCAGTGA 1380
Db 1521 GATTTTAGAAGAAAGCAAGCAGTCCATTTCAGGAAATCTTGGAGGAGCCCTTCAGTGA 1580
QY 1381 GAGCTCACAGCTTCCACCCACTGCTCCCTCAAAACATGTCATTTGAGAAAGAAATAGTACA 1440
Db 1581 GAGCTCACAGCTTCCACCCACTGCTCCCTCAAAACATGTCATTTGAGAAAGAAATAGTACA 1640
QY 1441 ACTGTGTGA 1449
Db 1641 ACTGTGTGA 1649
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RESULT 9

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US-10-723-860-6365
; Sequence 6365, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIORITY FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6365
; LENGTH: 2096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-6365
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Query Match 100.0%; Score 1449; DB 18; Length 2096;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGGCTCTTTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCCGATGGAATGAG 60
Db 156 ATGGGCTCTTTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCCGATGGAATGAG 215
QY 61 CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTTTACTGGGATGCGCAGC 120
Db 216 CCCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTTTACTGGGATGCGCAGC 275
QY 121 AATGGCTGGTGTCTGCTGGGTGGCTGGCTGAGATGCGCGACAGTGAACACAATTTGG 180
Db 276 AATGGCTGGTGTCTGCTGGGTGGCTGGCTGAGATGCGCGACAGTGAACACAATTTGG 335
QY 181 TTCTCTCAGCTCACCTTGGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCTGCT 240
Db 336 TTCTCTCAGCTCACCTTGGCGGACCTCTCTGCTGCTGCTCTCTGCTGCTCTCTGCTGCTGCT 395
QY 241 CACTTGGCTCTCCAGGACAGTGGGCTTACGCGAGGTTCTTATGCAAGCTCATCCCTCC 300
Db 396 CACTTGGCTCTCCAGGACAGTGGGCTTACGCGAGGTTCTTATGCAAGCTCATCCCTCC 455
QY 301 ATCATTTGCTCAACATGTTTGCAGTGTCTTCTGCTGCTTACTGCAATAGCTTGGATCGC 360
Db 456 ATCATTTGCTCAACATGTTTGCAGTGTCTTCTGCTGCTTACTGCAATAGCTTGGATCGC 515
QY 361 TGTCTTGTGATTTCAAGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 516 TGTCTTGTGATTTCAAGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
QY 421 TCTATCTGATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Db 576 TCTATCTGTGGATGATCTGGTGGTGGCTTTTGTGATGTGCATTCCTGCTGTGTGATC 635
  QY CGGGAATCTTCACTACAGAACCATATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 636 CGGGAATCTTCACTACAGAACCATATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 695
  QY TCATTAGATTATCCAGATCTTTATGGAGATCCACTAGAAACAGAGTCTCTTGAACAATTT 600
Db 696 TCATTAGATTATCCAGATCTTTATGGAGATCCACTAGAAACAGAGTCTCTTGAACAATTT 755
  QY GTTCAGCGCTGGAGAAATGAATAGATAGTGTAGATCTCTCTTTTCCAAACAAATGAT 660
Db 756 GTTCAGCGCTGGAGAAATGAATAGATAGTGTAGATCTCTCTTTTCCAAACAAATGAT 815
  QY CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTTCAAGACCTTCTGCAGAT 720
Db 816 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTTCAAGACCTTCTGCAGAT 875
  QY TCACCTCCCTAGGGTCTCTAGGTGTTAAACAAGTCAAAATCTGTATCTAAATGATTATAA 780
Db 876 TCACCTCCCTAGGGTCTCTAGGTGTTAAACAAGTCAAAATCTGTATCTAAATGATTATAA 935
  QY CTGTGATGTGTCTCACTAAATCCCAAGTGGTTCCTATTTGAAGATCAAGAAACC 840
Db 936 CTGTGATGTGTCTCACTAAATCCCAAGTGGTTCCTATTTGAAGATCAAGAAACC 995
  QY AGCCCACTGGATCACTGTGATCTTCTCTCTACTCAATTTAAAGCTGTTCCTAGCGCT 900
Db 996 AGCCCACTGGATCACTGTGATCTTCTCTCTACTCAATTTAAAGCTGTTCCTAGCGCT 1055
  QY TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTTA 960
Db 1056 TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTAACAATTTA 1115
  QY GGCCCAATTCAGATGAGATCAAGTGCCAAACCCCTCTGCTGGCAATTAACGATCACTAGG 1020
Db 1116 GGCCCAATTCAGATGAGATCAAGTGCCAAACCCCTCTGCTGGCAATTAACGATCACTAGG 1175
  QY CTAGTGTGGTGTCTCTGCTGCTCTCTTATCATGATAGCTGTGTTACAGCTTCAATGTC 1080
Db 1176 CTAGTGTGGTGTCTCTGCTGCTCTCTTATCATGATAGCTGTGTTACAGCTTCAATGTC 1235
  QY TTCCGAATGCAAAAGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1140
Db 1236 TTCCGAATGCAAAAGGGCGCTTCCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGTG 1295
  QY GTGTGTGGTGTCTCTTCTGTCTGCTGGACTCCATACCAATTTTGGAGTCTGTGCA 1200
Db 1296 GTGTGTGGTGTCTCTTCTGTCTGCTGGACTCCATACCAATTTTGGAGTCTGTGCA 1355
  QY TTGCTTACTGACCCAGAAACTCCCTTGGGGAACCTCTGATGTCTGGGATCATGTATGC 1260
Db 1356 TTGCTTACTGACCCAGAAACTCCCTTGGGGAACCTCTGATGTCTGGGATCATGTATGC 1415
  QY ATTGCTTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCCTTTGGGAAA 1320
Db 1416 ATTGCTTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCCTTTGGGAAA 1475
  QY GATTTTAGGAAGAAGCAAGCAGTCCATTCAGGAAATCTGGAGGAGCCCTTCAGTGAG 1380
Db 1476 GATTTTAGGAAGAAGCAAGCAGTCCATTCAGGAAATCTGGAGGAGCCCTTCAGTGAG 1535
  QY GAGCTCACAGTCTCCACCCTGCTCCCTCAAACTGTCATTTTCAAGAAAGAAATAGTACA 1440
Db 1536 GAGCTCACAGTCTCCACCCTGCTCCCTCAAACTGTCATTTTCAAGAAAGAAATAGTACA 1595
  QY ACTGTGGA 1449
Db 1596 ACTGTGGA 1604

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; Sequence 127, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 127
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-127

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Query Match 96.5%; Score 1398; DB 9; Length 1956;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGTCTTCTCTGCTGAGACCAATTTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
Db 82 ATGGCGTCTTCTCTGCTGAGACCAATTTCAACTGACCTACTCTCACAGCCATGGAATGAG 141
QY 61 CCCCGAGTAATTCCTCCATGTCATTTCTAGCCCTTACTTTTTTACTGGGATTCGAGGC 120
Db 142 CCCCGAGTAATTCCTCCATGTCATTTCTAGCCCTTACTTTTTTACTGGGATTCGAGGC 201
QY 121 AATGGCGTGTGCTGTGGTGGCTGGCTGAAGATGACGCGACAGTGAAACACAAATTTGG 180
Db 202 AATGGCGTGTGCTGTGGTGGCTGGCTGAAGATGACGCGACAGTGAAACACAAATTTGG 261
QY 181 TTCTTCCACCTCACTCTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 240
Db 262 TTCTTCCACCTCACTCTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTGCTGCT 321
QY 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGCGAGGTTCTATGCAAGCTCATGCCCTTCC 300
Db 322 CACTTGGCTCTCCAGGACAGTGGCCCTTACGCGAGGTTCTATGCAAGCTCATGCCCTTCC 381
QY 301 ATCAATGCTCAACATGTTTCCAGTGTCTTCCAGTGTCTTCCAGTGTCTTCCAGTGTCT 360
Db 382 ATCAATGCTCAACATGTTTCCAGTGTCTTCCAGTGTCTTCCAGTGTCTTCCAGTGTCT 441
QY 361 TGTCTTGTGTTATTTCAAGCCAAATCTGGTGTGTCAGAAATCATCGCAATGTAGGATGCGCTGC 420
Db 442 TGTCTTGTGTTATTTCAAGCCAAATCTGGTGTGTCAGAAATCATCGCAATGTAGGATGCGCTGC 501
QY 421 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATGTGATGTGATGTGATGT 480
Db 502 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATGTGATGTGATGTGATGT 561
QY 481 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db 562 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 621
QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAATTT 600
Db 622 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAACAGGTCTCTTGAACAATTT 681
QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTTCTCTCTTTCACAACTATGAT 660
Db 682 GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTTCTCTCTTTCACAACTATGAT 741
QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTGTCATTTTCAAGAAAGAAATAGTACA 720
Db 742 CATCTTGGACAGTCCCACTGTCTTCCAACTCAAACTGTCATTTTCAAGAAAGAAATAGTACA 801

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QY 721 TCACCTCCCTAGGGTCTCTAGGTTAAACAGTCAAAATCTGTATCTAATGATTTAAA 780
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 QY 802 TCACCTCCCTAGGGTCTCTAGGTTAAACAGTCAAAATCTGTATCTAATGATTTAAA 861
 Db |||||||
 QY 781 CCTGCTGATGGTCTCACCTAAATCCCAAGTGGTTCCTATTGAAGATCACGAAC 840
 Db |||||||
 QY 862 CCTGCTGATGGTCTCACCTAAATCCCAAGTGGTTCCTATTGAAGATCACGAAC 921
 Db |||||||
 QY 841 AGCCCACTGGATCACTGTAGTCTCTCTCTACTCATTTAAAGCTGTTCCTAGCGCT 900
 Db |||||||
 QY 922 AGCCCACTGGATCACTGTAGTCTCTCTCTACTCATTTAAAGCTGTTCCTAGCGCT 981
 Db |||||||
 QY 901 TCTAGCAATCTCTAGGCTCTGAGCTACACAGGTTTCCAGGATTTATACAAATTA 960
 Db |||||||
 QY 982 TCTAGCAATCTCTAGGCTCTGAGCTACACAGGTTTCCAGGATTTATACAAATTA 1041
 Db |||||||
 QY 961 GCCCAATTCACAGATGAGATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1020
 Db |||||||
 QY 1042 GCCCAATTCACAGATGAGATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1101
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 QY 1102 TAGTGGTGGTCT 1161
 Db |||||||
 QY 1081 TTCCGAATCCAAAGGGCGCTTCGCCAAGTCTCAGACCAAAACCTTTGGAGTGGCGGTG 1140
 Db |||||||
 QY 1162 TTCCGAATCCAAAGGGCGCTTCGCCAAGTCTCAGACCAAAACCTTTGGAGTGGCGGTG 1221
 Db |||||||
 QY 1141 GTGGTGGTGGTCT 1200
 Db |||||||
 QY 1222 GTGGTGGTGGTCT 1281
 Db |||||||
 QY 1201 TTGCTTACGACCCAGAAACTCCCTTTGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1260
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 QY 1282 TTGCTTACGACCCAGAAACTCCCTTTGGGAAAACTCTGATGCTCTGGGATCATGTATGC 1341
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 QY 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTAATCCCTTCTTATGCTCTTGGGAAA 1320
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 QY 1342 ATTGCTCTAGCATCTGCCAATAGTGTCTTAATCCCTTCTTATGCTCTTGGGAAA 1401
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 QY 1321 GATTTTAGGAGAAAGCAAGGAGTCCATTCAGGAAATCTGGAGGAGCCCTTCAGTGAG 1380
 Db |||||||
 QY 1402 GATTTTAGGAGAAAGCAAGGAGTCCATTCAGGAAATCTGGAGGAGCCCTTCAGTGAG 1461
 Db |||||||
 QY 1381 GAGCTCACAGTTCACCCACCTGTCCCTCAAAAGTCAATTCAGAAAGAAATAGTACA 1440
 Db |||||||
 QY 1462 GAGCTCACAGTTCACCCACCTGTCCCTCAAAAGTCAATTCAGAAAGAAATAGTACA 1521
 Db |||||||
 QY 1441 ACTGTGTGA 1449
 Db |||||||
 QY 1522 ACTGTGTGA 1530
 Db |||||||

RESULT 11

US-10-843-641A-6013
 ; Sequence 6013, Application US/10843641A
 ; Publication No. US20050064454A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avalon Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; TITLE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 689290-189
 ; CURRENT APPLICATION NUMBER: US/10/843,641A
 ; CURRENT FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: US/09/873,367
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US/09/954,531
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/09/954,456
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/962,436
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/962,832

QY 1 ATGGCGTCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 60
 Db |||||||
 QY 82 ATGGCGTCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG 141
 Db |||||||
 QY 61 CCCCCAGTAATCTCTCCATGCTCACTCAGCCCTTACTTTTACTGGGATGCGAGGC 120
 Db |||||||
 QY 142 CCCCCAGTAATCTCTCCATGCTCACTCAGCCCTTACTTTTACTGGGATGCGAGGC 201
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 QY 121 AATGGCTGGTGTCTGCTGGGTGGCTGGCTGAAGATGCGGAGACAGTGAACAATTTGG 180
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 QY 202 AATGGCTGGTGTCTGCTGGGTGGCTGGCTGAAGATGCGGAGACAGTGAACAATTTGG 261
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 QY 181 TTCTCCACCTCACTTGGCGGAGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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 QY 262 TTCTCCACCTCACTTGGCGGAGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321
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 QY 241 CACTTGGCTCTCCAGGAGACAGTGGCCCTTACGCGAGTTCCTATGCAAGCTCATCCCTCC 300
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 QY 322 CACTTGGCTCTCCAGGAGACAGTGGCCCTTACGCGAGTTCCTATGCAAGCTCATCCCTCC 381
 Db |||||||
 QY 301 ATCATGTCCTCAACATGTTTGGCAGTGTCTCTGCTTACTGCCCATTAGCCTGATGCG 360
 Db |||||||
 QY 382 ATCATGTCCTCAACATGTTTGGCAGTGTCTCTGCTTACTGCCCATTAGCCTGATGCG 441
 Db |||||||
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 Db |||||||
 QY 502 TCTATCTGTGATGTATCTGGGTGGTGGCTTTTGTGATGTGATTCCTCTGTGTCTGTATC 561
 Db |||||||
 QY 481 CGGGAATCTCTACATACAGAACCATTAATAGATGTGGGTACAAATTTGGTCTCTCCAGC 540
 Db |||||||
 QY 562 CGGGAATCTCTACATACAGAACCATTAATAGATGTGGGTACAAATTTGGTCTCTCCAGC 621
 Db |||||||
 QY 541 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGGCTCTCTTGAACAATTT 600
 Db |||||||
 QY 622 TCATTAGATTTCCAGACTTTTATGGAGATCCACTAGAAACAGGCTCTCTTGAACAATTT 681
 Db |||||||
 QY 601 GTTCAGCGCCTGGAGAAATGAATGATAGTGTAGATTCCTCTCTTTTCCAAACAAATGAT 660
 Db |||||||
 QY 682 GTTCAGCGCCTGGAGAAATGAATGATAGTGTAGATTCCTCTCTTTTCCAAACAAATGAT 741
 Db |||||||
 QY 661 CATCTTGGACAGTCCCACTGTCTTCCAACTGCTCAAACTTCAAGACCTTCTCAGAT 720
 Db |||||||
 QY 742 CATCTTGGACAGTCCCACTGTCTTCCAACTGCTTCCAACTTCAAGACCTTCTCAGAT 801
 Db |||||||
 QY 721 TCACCTCCCTAGGGTCTCTGCTAGGTTAAACAGTCAAAATCTGTATCTAATGATTTAAA 780
 Db |||||||

Query Match 96.5%; Score 1398; DB 19; Length 1956;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-843-641A-6013
 ; ORGANISM: Homo sapiens
 ; TYPE: DNA
 ; LENGTH: 1956
 ; SOFTWARE: PatentIn version 3.0
 ; NUMBER OF SEQ ID NOS: 8447
 ; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.

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Db 802 TCACCTCCCTAGGGTCTGCTAGGTTTAAAGTCAAAATCTGATCTAAATGATTTAAA 861
Qy 781 CCTGCTGATGCTGCTACCTAAATCCCGAGTGGTTCCTATTGAAGATCACGAACC 840
Db 862 CCTGCTGATGCTGCTACCTAAATCCCGAGTGGTTCCTATTGAAGATCACGAACC 921
Qy 841 AGCCCACTGGGAACTCTGATGCTTTCTCTACTCATTTAAAGCTGTCCTCAGCGCT 900
Db 922 AGCCCACTGGGAACTCTGATGCTTTCTCTACTCATTTAAAGCTGTCCTCAGCGCT 981
Qy 901 TCTAGCAATTCCTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTAATCAATTTA 960
Db 982 TCTAGCAATTCCTCTACGAGTCTGAGCTACCAAGGTTTCCAGGATTAATCAATTTA 1041
Qy 961 GGCCAAATTCACAGATGAGATCAAGTGGCAACACCCCTCGTGGCAATTAACGATCACTAGG 1020
Db 1042 GGCCAAATTCACAGATGAGATCAAGTGGCAACACCCCTCGTGGCAATTAACGATCACTAGG 1101
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Db 1102 CTAGTGGTGGGTTTCTGCTGCCCTCTGTTATCATGATGAGCTGTTTACAGCTTCATTGTC 1161
Qy 1081 TTCCGAATGCAAAAGGGCGGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGCTG 1140
Db 1162 TTCCGAATGCAAAAGGGCGGCTTCGCCAAGTCTCAGAGCAAAACCTTTTCGAGTGGCCGCTG 1221
Qy 1141 GTGGTGGTGGCTGCTTTCTTGCTGCTGGACTCAATACCAATTTTGGAGTCTCTGCA 1200
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Db 1282 TTGCTTACTGACCCAGAACTCCCTTGGGGAAGTCTGATGCTCTGGGATCATGATGC 1341
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Db 1342 ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTTATGCCCCTCTTGGGGAAA 1401
Qy 1321 GATTTAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1402 GATTTAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1461
Qy 1381 GAGCTCACAGCTTCCACCACTGCTCCCTCAAAATGTCATTTCAAGAAAGAAATAGTACA 1440
Db 1462 GAGCTCACAGCTTCCACCACTGCTCCCTCAAAATGTCATTTCAAGAAAGAAATAGTACA 1521
Qy 1441 ACTGTGTGA 1449
Db 1522 ACTGTGTGA 1530

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RESULT 12
US-10-367-035-1
; Sequence 1, Application US/10367035
; Publication No. US20030187244A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; FILE REFERENCE: TSRI 511.1D1
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: PCY/US97/01736
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 60/010,808
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1970

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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)...(1527)
US-10-367-035-1

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Query Match 96.5%; Score 1398; DB 16; Length 1970;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ATGGCGTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCAGCAATGGAATGAG 60
Db 82 ATGGCGTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCAGCAGCAATGGAATGAG 141
Qy 61 CCCCGAGTAATTCCTCCATGGTCAATCTCAGCCTTACTTTTTTACTGGGATTCGACGCG 120
Db 142 CCCCGAGTAATTCCTCCATGGTCAATCTCAGCCTTACTTTTTTACTGGGATTCGACGCG 201
Qy 121 AATGGCGTGGTCTGCTGGGCTGGCTGAGATGACGCGACAGTGAACACAAATTTGG 180
Db 202 AATGGCGTGGTCTGCTGGGCTGGCTGAGATGACGCGACAGTGAACACAAATTTGG 261
Qy 181 TTCCTCCACCTCACCCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 240
Db 262 TTCCTCCACCTCACCCTTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCT 321
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Db 322 CACTTGGCTCTCCAGGGACAGTGGCCCTAOCGGAGGTTCTCTATGCAAGCTCATGCCCTCC 381
Qy 301 ATCAATGCTCCCAATGTTTCCAGTGTCTCTCTGCTTACTGCTTACTGCTTACTGCTTACTGCT 360
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Db 442 TGTCTTGTGTPATTCAGGCCAATCTGGTGTGTCAGAAATCATCGCAATGTAGGATGSCCTGC 501
Qy 421 TCTATCTGTGATGATATCTGGGCTGGTGGCTTTTGTGATGTCATCTCTGCTGCTGCTGCTGCT 480
Db 502 TCTATCTGTGATGATATCTGGGCTGGTGGCTTTTGTGATGTCATCTCTGCTGCTGCTGCTGCT 561
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Db 562 CGGAAATCTTCACTACAGACCAATATAGATGTGGCTACAAATTTGGTCTCTTCCAGC 621
Qy 541 TCATTAGATTAATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT 600
Db 622 TCATTAGATTAATCCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT 681
Qy 601 GTTCAGCGCGCTGGAGAAATGAATGATAGGTTAGATCCTTCTCTTTTCCAAACAAATGAT 660
Db 682 GTTCAGCGCGCTGGAGAAATGAATGATAGGTTAGATCCTTCTCTTTTCCAAACAAATGAT 741
Qy 661 CATCCTTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAGACCTTTCTGACAGAT 720
Db 742 CATCCTTTGGACAGTCCCACTGTCTTCCAACTCAAAATTTCAAGACCTTTCTGACAGAT 801
Qy 721 TCATCTCCCTAGGCTTCTGCTAGGTTAAACAGTCAAAATCTGTAATCTTAATGATTTAAA 780
Db 802 TCATCTCCCTAGGCTTCTGCTAGGTTAAACAGTCAAAATCTGTAATCTTAATGATTTAAA 861
Qy 781 CCTGCTGATGCTCTCAGCTTAAATCCCAAGTGGTTCCTTATTTGAGATCAGGAACC 840
Db 862 CCTGCTGATGCTCTCAGCTTAAATCCCAAGTGGTTCCTTATTTGAGATCAGGAACC 921
Qy 841 AGCCCACTGGGAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTCCTCCTAGCGCT 900
Db 922 AGCCCACTGGGAACTCTGATGCTTTTCTCTCTACTCATTTAAAGCTGTCCTCCTAGCGCT 981
Qy 901 TCTAGCAATTCCTTCTAGGAGTCTGAGCTACCAAGGTTTCCAGGATTAATCAATTTA 960

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Db 1113 GGCCAAATTCACAGATGACGATCAAGTGCACACACCCCTCGTGGCAATTAACGATCACTAGG 1172
QY 1021 CTAGTGGTGGTTTCTCTGCTGCTCTGTTATCATGATGAGCTGTTCAGCTTCAATGTC 1080
Db 1173 CTAGTGGTGGTTTCTCTGCTGCTCTGTTATCATGATGAGCTGTTCAGCTTCAATGTC 1232
QY 1081 TTCCGAATGCAAGGGCGGCTTCGCCAAGTCTCAGACCAAAACCTTTTCGAGTGGCCGTG 1140
Db 1233 TTCCGAATGCAAGGGCGGCTTCGCCAAGTCTCAGACCAAAACCTTTTCGAGTGGCCGTG 1292
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Db 1353 TTGCTTACTGACCCGAAACTCTCTTGGGAAACTCTGATGCTCTGGGATCATGTATGC 1412
QY 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTAACTCCCTTCTTATGCCCTCTTGGGAAA 1320
Db 1413 ATTGCTCTAGCATCTGCCAATAGTGTCTTAACTCCCTTCTTATGCCCTCTTGGGAAA 1472
QY 1321 GATTTTAGGAAGAAAGCAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1380
Db 1473 GATTTTAGGAAGAAAGCAGGAGTCCATTCAGGGAATTTCTGGAGGAGCCCTTCAGTGAG 1532
QY 1381 GAGCTCAGAGTTCACCCACTGCTCCCTCAACATGTCATTTAGAAAGAAATAGTACA 1440
Db 1533 GAGCTCAGAGTTCACCCACTGCTCCCTCAACATGTCATTTAGAAAGAAATAGTACA 1592
QY 1441 ACTGTGTGA 1449
Db 1593 ACTGTGTGA 1601

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RESULT 14
US-10-259-521-1
; Sequence 1, Application US/10259521
; Publication No. US20030022310A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/259,521
; FILING DATE: 30-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,314
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: PCT/US95/01992
; FILING DATE: 17 FEB 1995
; ATTORNEY/AGENT INFORMATION:

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; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-382 (PF159)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2040 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-259-521-1

Query Match 96.5%; Score 1398; DB 14; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGAATGAG 60
Db 153 ATGGCGCTCTTCTCTGCTGAGACCAATTCACCTGACCTACTCTCACAGCCATGGAATGAG 212
QY 61 CCCCAGTAAATTCCTCCATGGTCAATTCAGCCCTTACTTTTTTACTGGGATGCCAGGC 120
Db 213 CCCCAGTAAATTCCTCCATGGTCAATTCAGCCCTTACTTTTTTACTGGGATGCCAGGC 272
QY 121 AATGGCTGGTGTCTGGTGGCTGGCTGAGATGACAGGGACAGTGAACACAAATTTGG 180
Db 273 AATGGCTGGTGTCTGGTGGCTGGCTGAGATGACAGGGACAGTGAACACAAATTTGG 332
QY 181 TTCTTCCACCTCACTTGGGGGACCTCTCTGCTGCTCTCTCTGCTCTCTCTGCTGCT 240
Db 333 TTCTTCCACCTCACTTGGGGGACCTCTCTGCTGCTCTCTCTGCTCTCTCTGCTGCT 392
QY 241 CACTTGGCTCTCCAGGGACAGTGGCCCTCAGCGAGGTTCTTATGCAAGCTCATCCCCCTCC 300
Db 393 CACTTGGCTCTCCAGGGACAGTGGCCCTCAGCGAGGTTCTTATGCAAGCTCATCCCCCTCC 452
QY 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTAGCTAGCTGATGCTG 360
Db 453 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTAGCTAGCTGATGCTG 512
QY 361 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGCTGCTG 420
Db 513 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGAGATCATCGCAATGTAGGATGCTGCTG 572
QY 421 TCTATCTGTGAGATGATCTGGGTGGTGGCTTTTGTGATGTCATTCCTGTGTTGCTGTAC 480
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QY 481 CGGAAATCTTCACTACAGACAAACATAATAGATGTGCTACAAATTTGGTCTCTCCAGC 540
Db 633 CGGAAATCTTCACTACAGACAAACATAATAGATGTGCTACAAATTTGGTCTCTCCAGC 692
QY 541 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAAGCTCTCTTGAACAACTT 600
Db 693 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAAAGCTCTCTTGAACAACTT 752
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Db 873 TCACCTCCCTAGGGGTTCTGTAGGTTTACAAAGTCAAAATCTGTATTTCTAATGATTTAAA 932
QY 781 CCTGCTGATGGTCTCACCTAAAATCCCGAGTGGGTTTCTTATTTGAAGATCACGAAACC 840

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Qy	1021	CTAGTGGTGGTTCCTCTGTCGCCCTCTGTATTATCATGATAGCCTGTTACAGCTTCATTGTC	1080
Db	1173	CTAGTGGTGGTTCCTCTGTCGCCCTCTGTATTATCATGATAGCCTGTTACAGCTTCATTGTC	1232
Qy	1081	TTCCGAATGCAAGGGCGCTTCGCCAAGTCTCAGACAAACCTTTGAGTGGCCGTG	1140
Db	1233	TTCCGAATGCAAGGGCGCTTCGCCAAGTCTCAGACAAACCTTTGAGTGGCCGTG	1292
Qy	1141	GTGCTGGTGGTGTCTTTCTTGTCTGCTGGACTCCATACCAATTTTGGAGTCCGTCA	1200
Db	1293	GTGCTGGTGGTGTCTTTCTTGTCTGCTGGACTCCATACCAATTTTGGAGTCCGTCA	1352
Qy	1201	TTGCTTACTGACCCAGAACTCCCTTTGGGAAAACCTGTGATGTCCTGGGATCATGTATGC	1260
Db	1353	TTGCTTACTGACCCAGAACTCCCTTTGGGAAAACCTGTGATGTCCTGGGATCATGTATGC	1412
Qy	1261	ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCCCTTATGCCCTCTTGGGAAA	1320
Db	1413	ATTGCTCTAGCATCTGCCAATAGTTGCTTTAATCCCTTCCCTTATGCCCTCTTGGGAAA	1472
Qy	1321	GATTTAGGAAGAAAGCAAGGAGTCCATTGAGGAATTTCTGGAGGAGCCCTTCAGTGAG	1380
Db	1473	GATTTAGGAAGAAAGCAAGGAGTCCATTGAGGAATTTCTGGAGGAGCCCTTCAGTGAG	1532
Qy	1381	GAGCTCACACGTTCCACCCACTGTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA	1440
Db	1533	GAGCTCACACGTTCCACCCACTGTCCCTCAACAAATGTCAATTCAGAAAGAAATAGTACA	1592
Qy	1441	ACTGTGTGA	1449
Db	1593	ACTGTGTGA	1601

Search completed: April 11, 2005, 16:14:21
Job time : 937 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:53 ; Search time 5116 Seconds

(without alignments)
10780.908 Million cell updates/sec

Title: US-10-764-649-1

Perfect score: 1449
Sequence: 1 atggcgctttctctgtga.....gaaatagtaacaactgtgtga 1449

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
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8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	1449	9	AY410247 Homo sapi
2	1449	100.0	1885	3	CR601349 full-length
3	1449	100.0	1888	3	CR590169 full-length
4	1449	100.0	1899	3	CR623914 full-length
5	1449	100.0	1910	3	CR591233 full-length
6	1449	100.0	1951	3	CR609272 full-length
7	830	57.3	1137	5	CR396411 BX396411
8	793	54.7	1092	5	CR381444 BX381444
9	779	53.8	797	5	CR095575 BX095575
10	776	53.6	934	5	CR337391 BX337391
11	763	52.7	1122	5	CR395616 BX395616
12	688	47.5	1112	4	BM562131 AGENCOURT
13	687	47.4	859	5	BM355871 BX355871
14	687	47.4	1093	5	BM920604 AGENCOURT
15	651	44.9	1124	4	BM546347 AGENCOURT
16	648	44.7	1067	5	BM919467 AGENCOURT
17	619	42.7	1093	1	AL513912 AL513912
18	615	42.4	799	7	CO957263 AGENCOURT
19	613	42.3	716	6	CB054504 NISC gm04
20	582	40.2	1035	5	BM381109 BX381109
21	576	39.8	969	4	BM804784 AGENCOURT
22	566	39.1	816	6	CD520940 AGENCOURT
23	533	36.8	1449	9	AY410248 Pan trogl
24	525	36.2	704	5	EX482976 DKF2p686A

25	525	36.2	849	4	BI821479	
26	512	35.3	582	5	BP320435	
27	510	35.2	803	7	CO957262	
C	28	496	34.2	729	6	CD102504
29	495	34.2	579	5	BP291658	
30	490	33.8	582	5	BP343952	
31	485	33.5	585	5	BP344756	
32	476	32.9	663	6	CD685945	
33	474	32.7	945	6	CA488766	
34	472	32.6	579	5	BP345808	
35	457	31.5	728	1	AU138812	
36	450	31.1	668	6	CD638412	
37	440	30.4	582	5	BP299521	
38	428	29.5	583	5	BP281114	
39	427	29.5	582	5	BP253595	
40	427	29.5	887	4	BI769086	
41	421	29.1	518	2	AW949379	
42	408	28.2	560	6	CD685958	
43	402	27.7	582	5	BP287326	
44	391	27.0	752	1	AV712421	
45	387	26.7	869	6	AGENCYCOURT	
46	385	26.6	556	2	BE696096	
47	366	25.3	582	5	BP219768	
48	358	24.7	582	5	BP344978	
49	357	24.6	581	5	BP201197	
50	351	24.2	1067	5	BP378071	
C	51	351	24.2	1089	5	EX381443
52	350	24.2	588	6	CD703934	
53	336	23.2	583	5	BP320399	
C	54	334	23.1	1055	5	EX381108
55	334	23.1	1143	6	CD252156	
56	320	22.1	471	7	R92269	
57	310	21.4	484	7	R77881	
C	58	289	19.9	1173	5	EX378155
C	59	287	19.8	718	6	CD743134
60	279	19.3	353	6	CB053853	
61	278	19.2	387	7	CR737963	
62	273	18.8	440	6	CB054358	
63	256	17.7	831	4	BI911839	
64	255	17.6	630	2	AW581977	
C	65	254	17.5	672	9	AG057384
C	66	253	17.5	387	2	BF062475
C	67	253	17.5	978	5	EX378070
68	247	17.0	583	5	BP271083	
69	239	16.5	976	5	EX381073	
C	70	238	16.4	680	6	CD364825
71	230	15.9	319	7	T49050	
C	72	212	14.6	643	6	CA307734
73	210	14.5	331	2	BF900259	
C	74	210	14.5	877	1	AI356589
C	75	200	13.8	393	2	AW390510
C	76	190	13.1	648	6	CB054503
C	77	187	12.9	660	7	CF530088
C	78	180	12.4	997	5	EX337390
C	79	180	12.4	1111	5	EX395615
C	80	161	11.1	377	1	AA296709
C	81	161	11.1	760	1	AI146335
82	154	10.6	334	7	RO1558	
83	151	10.4	381	1	AA039537	
84	145	10.0	300	1	AU099242	
85	144	9.9	510	7	CF769647	
86	132	9.1	256	7	T91438	
87	132	9.1	414	1	AA477030	
C	88	124	8.6	719	5	BM991860
C	89	121	8.4	553	1	AA523398
C	90	117	8.1	734	4	BG538100
C	91	102	7.0	515	1	AI032041
C	92	102	7.0	934	5	EX355870
C	93	99	6.8	514	4	AA683528
C	94	96	6.6	541	4	BG057281
C	95	85	6.6	550	1	AI719023
C	96	85	5.9	233	4	BI024173
C	97	78	5.4	533	1	AA039538

C 98	77	5.3	578	2	AW182643	171	24	1.7	342	5	BY175401	BY175401
C 99	71	4.9	548	1	AA476919	172	24	1.7	342	5	BY178190	BY178190
C 100	66	4.6	481	1	AI373719	173	24	1.7	342	5	BY180001	BY180001
C 101	51	3.5	233	4	BI024173	174	24	1.7	343	5	BY177320	BY177320
C 102	50	3.5	509	6	CA419088	175	24	1.7	345	5	BY181276	BY181276
C 103	49	3.4	107	5	BQ347598	176	24	1.7	345	5	BY181276	BY181276
C 104	43	3.2	406	6	BY546914	177	24	1.7	350	5	BY18474	BY18474
C 105	47	3.2	414	6	BY524950	178	24	1.7	351	5	BY175023	BY175023
C 106	47	3.2	439	6	BY530275	179	24	1.7	351	5	BY180132	BY180132
C 107	47	3.2	444	6	BY530301	180	24	1.7	351	5	BY203034	BY203034
C 108	47	3.2	552	4	BG694555	181	24	1.7	352	5	BY210671	BY210671
C 109	47	3.2	595	1	AI528007	182	24	1.7	353	5	BY177138	BY177138
C 110	47	3.2	630	2	BB665738	183	24	1.7	353	5	BY178435	BY178435
C 111	47	3.2	637	6	BY722246	184	24	1.7	357	5	BY202942	BY202942
C 112	47	3.2	654	6	BY724477	185	24	1.7	365	5	BY176640	BY176640
C 113	47	3.2	665	6	BY747807	186	24	1.7	373	5	BY170246	BY170246
C 114	47	3.2	671	6	BY747635	187	24	1.7	374	5	BY199798	BY199798
C 115	47	3.2	680	4	BI111760	188	24	1.7	380	5	BY200538	BY200538
C 116	47	3.2	710	6	BY763666	189	24	1.7	392	5	BY201922	BY201922
C 117	47	3.2	737	7	CN265199	190	24	1.7	411	5	BY154992	BY154992
C 118	47	3.2	739	2	BE377743	191	24	1.7	411	5	BY154992	BY154992
C 119	47	3.2	744	4	BI854110	192	23	1.6	601	4	BM781338	BM781338
C 120	47	3.2	1434	9	AI410249	193	22	1.6	766	9	CC947080	CC947080
C 121	47	3.2	2931	3	AK054017	194	22	1.5	222	9	CE220852	CE220852
C 122	46	3.2	596	5	BQ272246	195	22	1.5	374	6	BY526992	BY526992
C 123	45	3.1	572	1	AI240061	196	22	1.5	376	6	BY698616	BY698616
C 124	40	2.8	522	4	BF998237	197	22	1.5	378	6	BY524121	BY524121
C 125	37	2.6	929	5	EX381072	198	22	1.5	379	6	BY541725	BY541725
C 126	35	2.4	88	1	AA707210	199	22	1.5	396	5	BY522558	BY522558
C 127	35	2.4	297	7	RS6715	200	22	1.5	400	5	BY521795	BY521795
C 128	35	2.4	414	6	BI547178	201	22	1.5	401	6	BY527186	BY527186
C 129	35	2.4	914	4	BI151088	202	22	1.5	402	6	BY525624	BY525624
C 130	34	2.3	449	1	AI47563	203	22	1.5	417	6	BY537778	BY537778
C 131	28	1.9	330	5	BI190095	204	22	1.5	421	6	BY538998	BY538998
C 132	28	1.9	332	5	BI188504	205	22	1.5	422	5	BY487792	BY487792
C 133	28	1.9	335	5	BI189816	206	22	1.5	442	6	BY553805	BY553805
C 134	28	1.9	335	5	BY210296	207	22	1.5	447	6	BY548533	BY548533
C 135	28	1.9	336	5	BY181624	208	22	1.5	494	6	BY551636	BY551636
C 136	28	1.9	338	5	BY175342	209	22	1.5	520	1	AI313927	AI313927
C 137	28	1.9	338	5	BY195119	210	22	1.5	551	8	AZ374258	AZ374258
C 138	28	1.9	342	5	BI185193	211	22	1.5	647	8	AZ977005	AZ977005
C 139	28	1.9	345	5	BI180090	212	22	1.5	698	6	BY763781	BY763781
C 140	28	1.9	345	5	BI205985	213	22	1.5	719	7	CF271708	CF271708
C 141	28	1.9	346	5	BI184693	214	22	1.5	876	2	BF137570	BF137570
C 142	28	1.9	348	5	BY176524	215	21	1.4	217	4	BM102562	BM102562
C 143	28	1.9	348	5	BY191230	216	21	1.4	294	2	BB605118	BB605118
C 144	28	1.9	354	5	BY192327	217	21	1.4	315	5	BY519334	BY519334
C 145	28	1.9	356	5	BY192148	218	21	1.4	328	7	DI5163	DI5163
C 146	28	1.9	358	5	BI182152	219	21	1.4	406	1	AI699908	AI699908
C 147	28	1.9	363	5	BY182270	220	21	1.4	588	2	BF513073	BF513073
C 148	28	1.9	363	5	BY203248	221	21	1.4	591	9	CL981113	CL981113
C 149	28	1.9	364	5	BY195200	222	21	1.4	621	4	BI791553	BI791553
C 150	28	1.9	366	5	BY209545	223	21	1.4	626	6	CA753583	CA753583
C 151	28	1.9	367	5	BY202474	224	21	1.4	654	6	CD381728	CD381728
C 152	28	1.9	368	5	BI192305	225	21	1.4	694	7	CF147779	CF147779
C 153	28	1.9	370	5	BI179831	226	21	1.4	747	9	AG156138	AG156138
C 154	28	1.9	396	5	BY201901	227	21	1.4	765	4	BI156714	BI156714
C 155	28	1.9	402	5	BY172520	228	21	1.4	768	6	CD559558	CD559558
C 156	28	1.9	404	5	BY207825	229	21	1.4	773	6	CD559561	CD559561
C 157	28	1.9	406	5	BI183111	230	21	1.4	803	6	CD559560	CD559560
C 158	28	1.9	407	5	BI183231	231	21	1.4	834	9	CC586141	CC586141
C 159	28	1.9	415	6	BY526107	232	21	1.4	845	9	CG276465	CG276465
C 160	28	1.9	539	1	AI527986	233	21	1.4	985	9	CG276465	CG276465
C 161	27	1.9	573	4	BI345859	234	21	1.4	1037	2	BF317473	BF317473
C 162	26	1.8	357	5	BY179536	235	21	1.4	1054	5	EX335173	EX335173
C 163	26	1.8	453	1	AA156435	236	20	1.4	193	4	BF998236	BF998236
C 164	25	1.7	363	5	BY202285	237	20	1.4	198	5	BQ905527	BQ905527
C 165	24	1.7	294	5	BI185716	238	20	1.4	208	4	EG828367	EG828367
C 166	24	1.7	328	5	BY181497	239	20	1.4	237	5	BU007256	BU007256
C 167	24	1.7	339	5	BY175501	240	20	1.4	247	5	EX630653	EX630653
C 168	24	1.7	339	5	BY179882	241	20	1.4	297	2	D46366	D46366
C 169	24	1.7	339	5	BI185446	242	20	1.4	347	2	AW938811	AW938811
C 170	24	1.7	341	5	BI190842	243	20	1.4	351	9	CL956832	CL956832

244	20	1.4	352	6	CA725033	CA725033 wds3f.pk0	317	20	1.4	640	9	CR277472	Forward s
c 246	20	1.4	356	4	BG316076	BG316076 sabs5906.	318	20	1.4	641	5	BU012473	BU012473 QGJ2A08.Y
247	20	1.4	370	4	BJ322668	BJ322668	c 319	20	1.4	644	2	BB324156	BB324156
248	20	1.4	371	5	BY209532	BY209532 BY209532	320	20	1.4	648	4	CG284952	CG284952 602409210
249	20	1.4	390	1	AA221119	AA221119 mv05903.r	321	20	1.4	651	9	CL167656	CL167656 104 364 1
c 250	20	1.4	392	5	BQ994212	BQ994212 QGF6722.Y	c 322	20	1.4	658	4	BJ283311	BJ283311 BJ283311
c 251	20	1.4	396	2	AW378786	AW378786 PM0-HT022	c 323	20	1.4	658	4	BJ316395	BJ316395 BJ316395
c 252	20	1.4	397	6	C91808	C91808 C91808 Rice	c 324	20	1.4	658	4	BM671310	BM671310 UI-E-CQ1-
c 253	20	1.4	398	6	C72173	C72173 C72173 Rice	c 325	20	1.4	659	4	BM671310	BM671310 UI-E-CQ1-
254	20	1.4	401	6	BY524159	BY524159 BY524159	c 326	20	1.4	660	4	BJ285633	BJ285633 BJ285633
255	20	1.4	405	5	BY201953	BY201953 BY201953	c 327	20	1.4	666	9	CE322467	CE322467 tigr-g88-
256	20	1.4	409	5	BY511486	BY511486 BY511486	c 328	20	1.4	669	4	BJ292503	BJ292503 BJ292503
257	20	1.4	410	6	BY541443	BY541443 BY541443	c 329	20	1.4	675	4	BJ302017	BJ302017 BJ302017
258	20	1.4	417	2	BE494459	BE494459 WHE1254.A	c 330	20	1.4	676	4	BJ308759	BJ308759 BJ308759
259	20	1.4	420	6	CA602993	CA602993 wr1.pk002	c 331	20	1.4	676	7	CN338572	CN338572 170004280
260	20	1.4	427	1	AI181838	AI181838 uh87h06.r	c 332	20	1.4	677	6	CD920491	CD920491 G608.117F
261	20	1.4	431	6	BY536057	BY536057 BY536057	c 333	20	1.4	678	7	CF544617	CF544617 Hd wx17 6
c 262	20	1.4	435	9	CR030926	CR030926 Forward s	c 334	20	1.4	680	6	CD926752	CD926752 GR45.001P
c 263	20	1.4	442	6	C72603	C72603 C72603 Rice	c 335	20	1.4	681	5	BM980472	BM980472 UI-CF-EN1
c 264	20	1.4	447	2	AW734053	AW734053 sk86a03.Y	c 336	20	1.4	681	5	BM980472	BM980472 UI-CF-EN1
c 265	20	1.4	447	4	BU295686	BU295686 BU295686	c 337	20	1.4	684	4	BM575446	BM575446 170006871
c 266	20	1.4	456	6	BY556081	BY556081 BY556081	c 338	20	1.4	684	9	CE799109	CE799109 tigr-g88-
c 267	20	1.4	458	4	BI903239	BI903239 id23h04.Y	c 339	20	1.4	691	7	CF544307	CF544307 Hd wx17 6
c 268	20	1.4	458	9	BX002075	BX002075 Arabidops	c 340	20	1.4	691	9	CR256946	CR256946 Forward s
c 269	20	1.4	462	1	AU223139	AU223139 AU223139	c 341	20	1.4	693	4	BJ307832	BJ307832 BJ307832
270	20	1.4	471	4	BU289359	BU289359 BU289359	c 342	20	1.4	707	6	CD938715	CD938715 OV.10M05
c 271	20	1.4	476	1	AI120694	AI120694 ub71f02.r	c 343	20	1.4	710	4	BU278259	BU278259 BJ278259
c 272	20	1.4	477	4	BJ231304	BJ231304 BJ231304	c 344	20	1.4	712	5	BQ875664	BQ875664 QG18L23.Y
c 273	20	1.4	484	7	CK874451	CK874451 SGPI35660	c 345	20	1.4	715	8	BJ232084	BJ232084 BJ232084
c 274	20	1.4	492	1	AI960251	AI960251 sc80h06.Y	c 346	20	1.4	715	8	B2411520	B2411520 OGAAR29TM
c 275	20	1.4	498	9	AJ593320	AJ593320 Arabidops	c 347	20	1.4	720	4	BJ311066	BJ311066 BJ311066
c 276	20	1.4	500	6	BY555506	BY555506 Arabidops	c 348	20	1.4	724	9	AG489659	AG489659 Mus muscu
c 277	20	1.4	504	5	BQ033102	BQ033102 UI-1-CF0-	c 349	20	1.4	729	6	CB681539	CB681539 OSUNE1070
c 278	20	1.4	506	7	CF075819	CF075819 Hd wx17 6	c 350	20	1.4	731	8	B2411509	B2411509 OGAAR29TC
c 279	20	1.4	506	7	CV064386	CV064386 WNE110d11	c 351	20	1.4	733	4	BJ298963	BJ298963 BJ298963
c 280	20	1.4	514	1	AI131306	AI131306 u338f06.x	c 352	20	1.4	752	4	BI832103	BI832103 603077713
c 281	20	1.4	518	4	BU306085	BU306085 BJ306085	c 353	20	1.4	759	9	CG691141	CG691141 QGVBL22TH
c 282	20	1.4	523	6	CB174261	CB174261 OR_2o39D0	c 354	20	1.4	768	4	BU295085	BU295085 BJ295085
c 283	20	1.4	524	9	CE501952	CE501952 tigr-g88-	c 355	20	1.4	774	6	CA321799	CA321799 UI-M-FX0-
c 284	20	1.4	526	7	CF277767	CF277767 14ETL--03	c 356	20	1.4	785	4	BI520586	BI520586 6030771509
c 285	20	1.4	535	4	BJ007443	BJ007443 BJ007443	c 357	20	1.4	787	5	BQ885701	BQ885701 AGENCOURT
c 286	20	1.4	536	2	BE494096	BE494096 WHE1277.G	c 358	20	1.4	790	8	B2516514	B2516514 BOMQ86TF
c 287	20	1.4	536	5	BU765198	BU765198 sabs5h02.	c 359	20	1.4	815	8	CC332252	CC332252 OGAAR29TV
c 288	20	1.4	544	7	CK874273	CK874273 SGPI35475	c 360	20	1.4	823	6	CB630920	CB630920 OS11EB08C
c 289	20	1.4	545	8	AZ579964	AZ579964 LM0368E02	c 361	20	1.4	826	5	BU428396	BU428396 603958037
c 290	20	1.4	550	4	BJ004551	BJ004551 BJ004551	c 362	20	1.4	826	9	CG366237	CG366237 OGVGB68TV
c 291	20	1.4	556	7	CR807027	CR807027 p8RB019XG	c 363	20	1.4	827	8	BH430711	BH430711 BOMNS57TF
c 292	20	1.4	568	4	BJ305485	BJ305485 BJ305485	c 364	20	1.4	829	8	BH701823	BH701823 BOMNS57TF
c 293	20	1.4	568	9	CE283179	CE283179 tigr-g88-	c 365	20	1.4	834	8	CNS03867	AL256840 Tetraodon
c 294	20	1.4	569	5	BP267157	BP267157 BP267157	c 366	20	1.4	845	8	AZ688325	AZ688325 ENTLN77TR
c 295	20	1.4	573	6	CD449387	CD449387 Hd wx17 0	c 367	20	1.4	851	5	BQ097080	BQ097080 tigr-g88-
c 296	20	1.4	579	5	BP213978	BP213978 BP213978	c 368	20	1.4	855	9	CR253112	CR253112 Forward s
c 297	20	1.4	579	7	CO231932	CO231932 WS0052.B2	c 369	20	1.4	859	9	CG258209	CG258209 OGI1DC77TV
c 298	20	1.4	581	4	BU280812	BU280812 BU280812	c 370	20	1.4	861	8	BH132944	BH132944 ENTLN22TF
c 299	20	1.4	581	5	BP266628	BP266628 BP266628	c 371	20	1.4	864	9	CL964195	CL964195 OeIFCC010
c 300	20	1.4	581	5	BP269939	BP269939 BP269939	c 372	20	1.4	868	5	BX391653	BX391653 BX391653
c 301	20	1.4	582	5	BM864122	BM864122 BM864122	c 373	20	1.4	891	8	BH154324	BH154324 601504403
c 302	20	1.4	593	3	CG684541	CG684541 tigr-g88-	c 374	20	1.4	890	2	BE614336	BE614336 601504403
c 303	20	1.4	598	7	CF334928	CF334928 JMT--04-G	c 375	20	1.4	902	5	BQ293938	BQ293938 AGENCOURT
c 304	20	1.4	602	4	BU300256	BU300256 BU300256	c 376	20	1.4	909	7	CF582696	CF582696 AGENCOURT
c 305	20	1.4	604	1	AI727007	AI727007 ENLGH1710	c 377	20	1.4	909	8	AZ686423	AZ686423 ENTLN77TR
c 306	20	1.4	608	7	CK326075	CK326075 Hd wx17 7	c 378	20	1.4	913	8	BH132368	BH132368 ENTLN77TR
c 307	20	1.4	616	5	BM931434	BM931434 UI-E-EJ1-	c 379	20	1.4	917	9	CG373433	CG373433 AGENCOURT
c 308	20	1.4	616	6	CB853037	CB853037 UI-CF-FN0	c 380	20	1.4	923	5	BQ928115	BQ928115 AGENCOURT
c 309	20	1.4	618	4	BJ3119052	BJ3119052 BJ3119052	c 381	20	1.4	930	8	AZ548645	AZ548645 ENTLN77TR
c 310	20	1.4	624	4	BJ313303	BJ313303 BJ313303	c 382	20	1.4	935	8	BH155404	BH155404 ENTLN77TR
c 311	20	1.4	626	6	CA699446	CA699446 wtk.p000	c 383	20	1.4	936	5	BQ957853	BQ957853 AGENCOURT
c 312	20	1.4	629	1	AI727476	AI727476 ENLGH1805	c 384	20	1.4	944	5	BX335973	BX335973 BX335973
c 313	20	1.4	631	7	CF311536	CF311536 ABF--06-M	c 385	20	1.4	956	8	CC194345	CC194345 CH261-182
c 314	20	1.4	634	4	BJ278092	BJ278092 BJ278092	c 386	20	1.4	964	4	BI105732	BI105732 602892327
c 315	20	1.4	637	4	BJ288805	BJ288805 BJ288805	c 387	20	1.4	978	1	AL538635	AL538635 AL538635
c 316	20	1.4	638	4	BJ321912	BJ321912 BJ321912	c 388	20	1.4	981	5	AX464154	AX464154 BX464154
							c 389	20	1.4	1647	3	CR603019	CR603019 full-length

390	20	1.4	2063	3.	HSN805656	AL834223 Homo sapi	463	19	1.3	434	1	AI495528
391	20	1.4	2742	3	AK032903	Mus muscu	464	19	1.3	434	8	AQ401153
392	20	1.4	3209	3	AK046771	Mus muscu	C 465	19	1.3	435	1	AA437958
393	19	1.3	162	9	CL964447	ObiFC0010	C 466	19	1.3	438	5	BQ975082
394	19	1.3	196	8	AQ005846	CIT-HSP-2	C 467	19	1.3	442	2	BF154591
395	19	1.3	206	2	BE495582	WHE1291-1	468	19	1.3	444	7	CV430264
396	19	1.3	207	7	U21460	Huma	469	19	1.3	445	7	CO549561
397	19	1.3	266	2	BE593034	WS1_93_E0	470	19	1.3	451	1	AU265728
398	19	1.3	272	9	CL308629	Q3S0467-1	471	19	1.3	451	1	CR850891
399	19	1.3	278	5	BQ913491	QHA7K017.Y	472	19	1.3	454	7	CV429195
400	19	1.3	285	5	BQ028892	BH251970	C 473	19	1.3	455	2	AW236886
401	19	1.3	291	8	BH251970	SALK_0124	474	19	1.3	455	2	AW236886
402	19	1.3	299	5	BU022276	QHEG619.Y	C 475	19	1.3	462	2	CV429371
403	19	1.3	305	8	CC097231	CSU-K34.1	C 476	19	1.3	462	2	AW233450
404	19	1.3	307	5	BQ915225	QHEG619.Y	C 477	19	1.3	462	7	CK721587
405	19	1.3	308	5	BQ578814	QHEG619.Y	C 478	19	1.3	462	7	CK721587
406	19	1.3	311	4	BQ48709	QHEG619.Y	479	19	1.3	462	9	CL697298
407	19	1.3	312	7	CNS19764	QO103.B3	480	19	1.3	475	7	CV237580
408	19	1.3	323	5	BU027588	QHEG619.Y	481	19	1.3	477	6	BY531328
409	19	1.3	324	5	BU020081	QHEG619.Y	482	19	1.3	477	6	BY531328
410	19	1.3	328	4	BI487941	QHEG619.Y	483	19	1.3	478	7	CV431625
411	19	1.3	331	5	BQ911513	QHA17G45	C 484	19	1.3	480	6	CA181184
412	19	1.3	331	5	BY184899	QHA17G45	C 485	19	1.3	480	6	CA181184
413	19	1.3	337	1	AV630939	AV630939	C 486	19	1.3	483	5	BQ901746
414	19	1.3	341	5	BQ338119	RC5-NN108	C 487	19	1.3	483	5	BQ901746
415	19	1.3	342	8	AQ086311	HS_3168.A	C 488	19	1.3	484	8	BH074785
416	19	1.3	344	5	BQ909634	QHA11M18	C 489	19	1.3	486	7	CK851620
417	19	1.3	345	5	BU021922	QHEF02.Y	C 490	19	1.3	490	7	CK851620
418	19	1.3	347	5	BQ915259	QHEF02.Y	C 491	19	1.3	492	1	AV778686
419	19	1.3	347	5	BQ202529	QHEF02.Y	492	19	1.3	494	2	BF649702
420	19	1.3	349	5	BQ209198	BY209198	493	19	1.3	494	2	BF649702
421	19	1.3	351	5	BQ967571	QHEB30D22	C 494	19	1.3	496	7	CF674282
422	19	1.3	351	9	CE058029	QHEB30D22	C 495	19	1.3	500	5	BQ607004
423	19	1.3	351	9	CE058029	QHEB30D22	C 496	19	1.3	501	6	CA109415
424	19	1.3	352	1	AV116969	AV116969	C 497	19	1.3	502	7	CNS18181
425	19	1.3	364	8	BH862215	SAUK_0891	C 498	19	1.3	503	6	CD115317
426	19	1.3	366	9	CR132605	Forward s	C 499	19	1.3	506	8	AZ225879
427	19	1.3	368	5	BY172974	BY172974	C 500	19	1.3	511	4	BI320861
428	19	1.3	369	7	CN026145	UMC-P4C1V	C 501	19	1.3	515	6	CA068751
429	19	1.3	370	5	BQ496237	EST050466	C 502	19	1.3	515	6	CA068751
430	19	1.3	371	7	CN913723	Q30108ABM	C 503	19	1.3	516	6	CA068150
431	19	1.3	378	5	BU025635	QHEG10H23	C 504	19	1.3	519	4	BI452317
432	19	1.3	382	7	CN517539	CN517539	C 505	19	1.3	521	2	BF732169
433	19	1.3	383	7	RI2626	YF57401.r1	C 506	19	1.3	521	4	BJ298799
434	19	1.3	386	8	AQ852817	QHEB30D22	C 507	19	1.3	523	4	BJ298799
435	19	1.3	392	2	BF220394	QHEB30D22	C 508	19	1.3	523	5	BQ903339
436	19	1.3	393	2	BF220394	QHEB30D22	C 509	19	1.3	524	7	CK852207
437	19	1.3	397	5	BQ901630	QHEB30D22	C 510	19	1.3	525	6	CD934886
438	19	1.3	397	5	BU028174	QHEB30D22	C 511	19	1.3	528	7	CV138331
439	19	1.3	397	5	BU058532	QHEB30D22	C 512	19	1.3	530	4	BG593544
440	19	1.3	398	5	BQ979001	QHEB30D22	C 513	19	1.3	531	8	AZ025689
441	19	1.3	398	5	BY183760	QHEB30D22	C 514	19	1.3	532	7	CN882660
442	19	1.3	399	5	BY183760	QHEB30D22	C 515	19	1.3	533	7	CN882660
443	19	1.3	405	9	CR276745	Reverse s	C 516	19	1.3	534	2	BE113412
444	19	1.3	406	2	BE358938	Reverse s	C 517	19	1.3	534	5	BQ606996
445	19	1.3	407	7	CV431261	CV431261	C 518	19	1.3	537	6	CB878455
446	19	1.3	410	5	BI183424	BI183424	C 519	19	1.3	537	6	CB878455
447	19	1.3	413	1	AI619419	AI619419	C 520	19	1.3	541	7	CV188709
448	19	1.3	414	5	BP070003	BP070003	C 521	19	1.3	543	5	BQ628255
449	19	1.3	415	1	AA169149	AA169149	C 522	19	1.3	544	7	CK853480
450	19	1.3	417	8	AQ734792	QHEB30D22	C 523	19	1.3	545	5	BQ904017
451	19	1.3	418	1	AA452856	AA452856	C 524	19	1.3	545	7	CK851836
452	19	1.3	419	6	CD650473	CD650473	C 525	19	1.3	547	2	BE100786
453	19	1.3	420	6	CA225590	CA225590	C 526	19	1.3	547	6	CA143834
454	19	1.3	422	5	CA225590	CA225590	C 527	19	1.3	548	5	BQ903041
455	19	1.3	422	5	CA225590	CA225590	C 528	19	1.3	550	1	AA015502
456	19	1.3	426	7	CK273503	CK273503	C 529	19	1.3	552	4	BM407027
457	19	1.3	426	8	AQ683898	HS_5455.B	C 530	19	1.3	554	2	BE112439
458	19	1.3	428	7	CV431444	CV431444	C 531	19	1.3	556	6	CA873500
459	19	1.3	429	1	AV810552	AV810552	C 532	19	1.3	556	8	BZ096955
460	19	1.3	432	6	CB259775	23-E9536	C 533	19	1.3	557	7	CV430110
461	19	1.3	433	5	BQ628072	sa080609	C 534	19	1.3	559	6	CA096548
462	19	1.3	433	8	AQ009448	CIT-HSP-2	C 535	19	1.3	564	7	CV430283

C 536	19	1.3	565	6	CA199091	CA199091	SCAGFL108	C 609	19	1.3	635	7	CN941740	CN941740	010919AVB
C 537	19	1.3	566	7	CN938434	CN938434	010615AVB	610	19	1.3	635	7	CV430017	CV430017	53005.1 A
C 538	19	1.3	567	6	CA167223	CA167223	SCCSCB100	C 611	19	1.3	636	6	CA191866	CA191866	SCCST1C0
C 539	19	1.3	572	4	CN522156	CN522156	Q00122.B3	612	19	1.3	637	2	BB163723	BB163723	BB163723
C 540	19	1.3	573	4	BI504769	BI504769	BB170009A	613	19	1.3	637	8	B2114966	B2114966	CH230-459
C 541	19	1.3	573	7	CN910024	CN910024	030124ABL	614	19	1.3	639	2	BE414399	BE414399	SCU009.D0
C 542	19	1.3	576	7	CV431876	CV431876	56535.1 A	615	19	1.3	639	2	CK853006	CK853006	13696 SCo
C 543	19	1.3	578	7	CN941746	CN941746	010919AVB	C 616	19	1.3	640	7	CN900073	CN900073	010723ABA
C 544	19	1.3	578	7	CN947957	CN947957	020805AVB	617	19	1.3	641	7	CV429444	CV429444	52061.1 A
C 545	19	1.3	580	7	CK271263	CK271263	EST717341	618	19	1.3	641	7	CV431970	CV431970	56706.1 A
C 546	19	1.3	580	7	CK854557	CK854557	15744 SCo	C 619	19	1.3	641	8	B2806511	B2806511	PUGAA23TB
C 547	19	1.3	581	7	CK854565	CK854565	15744 SCo	C 620	19	1.3	641	9	CG978462	CG978462	CH240 169
C 548	19	1.3	584	5	BM933447	BM933447	56535.1 A	621	19	1.3	642	7	CK853197	CK853197	13928 SCo
C 549	19	1.3	584	7	CV431352	CV431352	55563.1 A	C 622	19	1.3	642	9	CG966251	CG966251	PUIKPS58TD
C 550	19	1.3	585	5	BQ807090	BQ807090	WHE3586.F	C 623	19	1.3	643	7	CK276309	CK276309	EST722387
C 551	19	1.3	586	7	CF675495	CF675495	ta020D05	C 624	19	1.3	643	7	CN881074	CN881074	010425AAS
C 552	19	1.3	586	7	CN888238	CN888238	010603AAW	C 625	19	1.3	643	7	CN911904	CN911904	021217ABM
C 553	19	1.3	587	7	CN944825	CN944825	011003AVB	C 626	19	1.3	644	7	CV431667	CV431667	56122.1 A
C 554	19	1.3	588	7	CN968096	CN968096	010412AAO	C 627	19	1.3	645	7	CN912586	CN912586	021218ABM
C 555	19	1.3	591	7	CF653861	CF653861	ta077D02	C 628	19	1.3	648	7	CK852281	CK852281	12703 SCo
C 556	19	1.3	591	7	CF777382	CF777382	ta099h11	C 629	19	1.3	648	9	CE755835	CE755835	tiGrF-g88-
C 557	19	1.3	591	7	CK852341	CK852341	12788 SCo	C 630	19	1.3	649	6	CA178255	CA178255	SCRFST104
C 558	19	1.3	591	7	CV429907	CV429907	52839.1 A	C 631	19	1.3	649	7	CN944225	CN944225	011002AVB
C 559	19	1.3	592	9	CG357826	CG357826	QGYCA22TV	C 632	19	1.3	651	7	CN881347	CN881347	010427AAS
C 560	19	1.3	593	7	CF602372	CF602372	ta041e05	C 633	19	1.3	652	4	BJ233326	BJ233326	BJ233326
C 561	19	1.3	593	9	CL555374	CL555374	OB_Ba000	C 634	19	1.3	652	7	CV431281	CV431281	55438.1 A
C 562	19	1.3	595	7	CN355967	CN355967	170004182	C 635	19	1.3	654	6	CA144832	CA144832	SCSRFT207
C 563	19	1.3	596	6	CD209456	CD209456	HS1_42.A1	C 636	19	1.3	654	7	CO203414	CO203414	180012.B2
C 564	19	1.3	596	7	CV430822	CV430822	54607.1 A	C 637	19	1.3	654	7	CV429797	CV429797	52670.1 A
C 565	19	1.3	598	7	CV431378	CV431378	55611.1 A	C 638	19	1.3	655	9	CE817820	CE817820	tiGrF-g88-
C 566	19	1.3	599	7	CK952959	CK952959	13640 SCo	C 639	19	1.3	656	4	BJ231855	BJ231855	RJ231855
C 567	19	1.3	599	7	CN912217	CN912217	021217ABM	C 640	19	1.3	656	7	CK851826	CK851826	12094 SCo
C 568	19	1.3	600	6	CA242185	CA242185	SCEPFL308	C 641	19	1.3	659	6	CA105545	CA105545	SCJFHR1C0
C 569	19	1.3	601	7	CV429265	CV429265	51763.1 A	C 642	19	1.3	659	7	CV430826	CV430826	54612.1 A
C 570	19	1.3	601	9	CL909681	CL909681	OA_ABa000	C 643	19	1.3	659	7	CV431142	CV431142	55153.1 A
C 571	19	1.3	602	7	CO416907	CO416907	MGf+3011k	C 644	19	1.3	661	7	CN881335	CN881335	010427AAS
C 572	19	1.3	603	5	BUB82682	BUB82682	UM80TH02	C 645	19	1.3	662	6	CA133907	CA133907	SCE2RT201
C 573	19	1.3	603	6	CB074677	CB074677	V-B-11D07	C 646	19	1.3	662	9	CE409592	CE409592	tiGrF-g88-
C 574	19	1.3	606	9	CL917585	CL917585	OA_ABa002	C 647	19	1.3	663	1	AJ779303	AJ779303	RJ779303
C 575	19	1.3	607	2	BE336326	BE336326	6F01087092	C 648	19	1.3	663	5	BQ483673	BQ483673	WHE3511.C
C 576	19	1.3	607	4	BG457955	BG457955	NOF036G08P	C 649	19	1.3	663	6	CA261319	CA261319	SCCCLB200
C 577	19	1.3	608	7	CN955637	CN955637	MGf+3001P	C 650	19	1.3	664	6	CA260483	CA260483	SCSBR303
C 578	19	1.3	609	7	CK269631	CK269631	EST715709	C 651	19	1.3	665	4	BJ401851	BJ401851	RJ401851
C 579	19	1.3	610	6	CD423167	CD423167	SAL_27.B0	C 652	19	1.3	665	6	CA124632	CA124632	SCQGLR108
C 580	19	1.3	611	7	CV431717	CV431717	56221.1 A	C 653	19	1.3	665	8	B2840476	B2840476	31557 in
C 581	19	1.3	612	1	AL961097	AL961097	AL961097	C 654	19	1.3	666	8	B2840476	B2840476	CH240 288
C 582	19	1.3	613	7	CF119968	CF119968	MTU10CS.P	C 655	19	1.3	668	6	CA193525	CA193525	SCCCCL7C0
C 583	19	1.3	613	7	CF425677	CF425677	lad42g10	C 656	19	1.3	668	7	CK271262	CK271262	EST717340
C 584	19	1.3	613	9	CL412745	CL412745	RPC144_43	C 657	19	1.3	670	5	BQ818317	BQ818317	1030070A0
C 585	19	1.3	614	6	CA105467	CA105467	SCJFHR1C0	C 658	19	1.3	672	7	CK276918	CK276918	EST722996
C 586	19	1.3	614	7	CF656984	CF656984	ta067d11	C 659	19	1.3	673	7	CN911238	CN911238	021119ABM
C 587	19	1.3	614	7	CO502101	CO502101	59341.1 I	C 660	19	1.3	675	6	CA198833	CA198833	SCCST3C1
C 588	19	1.3	615	7	CF602111	CF602111	ta039c10	C 661	19	1.3	675	7	CK276308	CK276308	EST722386
C 589	19	1.3	615	7	CK852651	CK852651	13204 SCo	C 662	19	1.3	679	6	CA198342	CA198342	SCCCFL300
C 590	19	1.3	616	7	CK852860	CK852860	13500 SCo	C 663	19	1.3	679	7	CV431202	CV431202	55287.1 A
C 591	19	1.3	617	6	CA081597	CA081597	SCAGAM201	C 664	19	1.3	680	7	CN888550	CN888550	010604AAW
C 592	19	1.3	617	9	BM125647	BM125647	Danilo ter	C 665	19	1.3	684	4	CV429218	CV429218	51687.1 A
C 593	19	1.3	618	4	BG739595	BG739595	EM1_82.G0	C 666	19	1.3	685	4	BJ208530	BJ208530	EJ208530
C 594	19	1.3	618	7	CK953751	CK953751	14649 SCo	C 667	19	1.3	685	6	CD928654	CD928654	GR45_1051
C 595	19	1.3	619	7	CV429462	CV429462	52092.1 A	C 668	19	1.3	685	9	CL602783	CL602783	OB_Ba007
C 596	19	1.3	624	6	CA242130	CA242130	SCEPFL308	C 669	19	1.3	686	6	CA086343	CA086343	SCMCAW208
C 597	19	1.3	624	7	CN909938	CN909938	030123ABL	C 670	19	1.3	688	7	CV431777	CV431777	56350.1 A
C 598	19	1.3	627	7	CK852333	CK852333	12776 SCo	C 671	19	1.3	689	7	CN011760	CN011760	WHE3888.D
C 599	19	1.3	628	7	CV431840	CV431840	56475.1 A	C 672	19	1.3	690	4	BG124031	BG124031	EST469677
C 600	19	1.3	629	7	CN940121	CN940121	010702AVB	C 673	19	1.3	691	4	BJ215799	BJ215799	RJ215799
C 601	19	1.3	630	8	B27868	B27868	T1D16TFD TA	C 674	19	1.3	691	6	CA222676	CA222676	SCBGPL405
C 602	19	1.3	631	6	CK176679	CK176679	SCMGST105	C 675	19	1.3	691	7	CN939179	CN939179	010616AVB
C 603	19	1.3	631	7	CK288637	CK288637	EST751359	C 676	19	1.3	692	7	CN943553	CN943553	010927AVB
C 604	19	1.3	631	7	CN888584	CN888584	010604AAW	C 677	19	1.3	693	8	BH924712	BH924712	odh7f08
C 605	19	1.3	632	6	CD885085	CD885085	F1_118003	C 678	19	1.3	693	9	TA371D10Q	TA371D10Q	TA371D10Q
C 606	19	1.3	632	7	CN912306	CN912306	021217ABM	C 679	19	1.3	695	8	B2432917	B2432917	BONDPT15TF
C 607	19	1.3	633	5	BM163396	BM163396	EX616396	C 680	19	1.3	696	6	CB327832	CB327832	UI-R-FS0-
C 608	19	1.3	635	4	BG365941	BG365941	HVSME1000	C 681	19	1.3	696	7	CK269630	CK269630	EST715708

682	19	1.3	702	6	CA089699	CA089699	SCSGAM207	19	1.3	1045	8	CC213898	CC213898	CH261-76F
c 683	19	1.3	706	8	BH963348	BH963348	odj07b12.	c 755	19	1.3	1052	9	CNS05604	AL323553
c 684	19	1.3	714	4	B0238874	B0238874	odj07b12.	c 756	19	1.3	1062	9	CL979525	Tetraodon
c 685	19	1.3	714	6	CA176541	CA176541	SCMCST105	c 757	19	1.3	1125	8	CC211415	CH261-74F
c 686	19	1.3	714	8	BH545184	BH545184	BOGR61TF	c 758	19	1.3	1158	8	CC211179	CH261-186
c 687	19	1.3	715	2	AW964143	AW964143	EST376216	c 759	19	1.3	1169	8	CC253315	CH261-33C
c 688	19	1.3	716	6	CD210487	CD210487	HSL_51_CO	c 760	19	1.3	1223	9	CG753205	PO48-1-HO
c 689	19	1.3	717	6	CA113136	CA113136	SCEZLB100	c 761	19	1.3	1252	9	CG755082	PO50-3-HO
c 690	19	1.3	719	9	AG142368	AG142368	Pan trogl	c 762	19	1.3	1298	6	CD248845	AGENCOURT
c 691	19	1.3	721	9	CR806042	CR806042	GROAAA27D	c 763	19	1.3	1332	8	CC243450	CH261-75H
c 692	19	1.3	723	6	CA220723	CA220723	SCEZFLA40	c 764	19	1.3	1332	8	AG029775	Pan trogl
c 693	19	1.3	725	5	BX8662631	BX8662631	BM862631	c 765	19	1.3	1490	9	AG029775	CH261-75H
c 694	19	1.3	730	8	AZ854464	AZ854464	2M0158L02	c 766	19	1.3	1505	3	CR647476	Tetraodon
c 695	19	1.3	731	9	CL695934	CL695934	PR1017C_H	c 767	19	1.3	2044	3	CNS0A7DR	Arabidops
c 696	19	1.3	732	2	BS060390	BS060390	HVSNB9001	c 768	19	1.3	2286	3	AK038048	Mus muscu
c 697	19	1.3	733	7	CR880201	CR880201	010417AAS	c 769	19	1.3	2494	3	AK041947	Mus muscu
c 698	19	1.3	735	7	CR944750	CR944750	011003AVB	c 770	19	1.3	2675	3	AK078871	Mus muscu
c 699	19	1.3	736	7	CNS98198	CNS98198	Mdftr3021e	c 771	19	1.3	3921	3	BC036725	Mus muscu
c 700	19	1.3	737	7	CO063932	CO063932	est_k_bre	c 772	18	1.2	1016	6	CB104995	K-EST0086
c 701	19	1.3	738	2	BE414590	BE414590	SCU011_D0	c 773	18	1.2	1036	6	CB104809	K-EST0052
c 702	19	1.3	741	7	CNS19414	CNS19414	Q00104_B3	c 774	18	1.2	1059	9	CL953791	OstrUA003
c 703	19	1.3	749	7	CF438012	CF438012	EST674357	c 775	18	1.2	1359	1	AG025146	Oryza sat
c 704	19	1.3	749	8	BZ234763	BZ234763	CH230-333	c 776	18	1.2	1501	1	AV283968	Arabidops
c 705	19	1.3	750	9	CR223769	CR223769	Reverse s	c 777	18	1.2	1558	8	AZ041463	RPCL-23-3
c 706	19	1.3	754	4	B0434172	B0434172	Bj434172	c 778	18	1.2	1572	2	BF478952	WHE2015_F
c 707	19	1.3	755	8	CC451351	CC451351	ZMWBBC033	c 779	18	1.2	1762	2	AW179451	687011D01
c 708	19	1.3	760	6	CR834952	CR834952	BN45_043LC	c 780	18	1.2	1797	7	D43055	D43055_Rice
c 709	19	1.3	764	6	CA209118	CA209118	SCEZADICL	c 781	18	1.2	1838	8	AF222045	AF222045
c 710	19	1.3	765	6	CA140160	CA140160	SCEZRT202	c 782	18	1.2	2114	4	BU543031	BU543031
c 711	19	1.3	765	7	CNS147406	CNS147406	WOUNDI_49	c 783	18	1.2	2122	7	CGN81266	001008AAG
c 712	19	1.3	766	6	CA083163	CA083163	SCBFAW212	c 784	18	1.2	2169	9	CG793312	ZMWBBC030
c 713	19	1.3	768	9	CT750849	CT750849	ZMWBBC013	c 785	18	1.2	2191	1	AA798479	AA798479 vx75b08.r
c 714	19	1.3	771	4	BG436890	BG436890	602488884	c 786	18	1.2	2289	9	AL772065	Arabidops
c 715	19	1.3	772	7	CV429427	CV429427	52035_1_A	c 787	18	1.2	2312	5	AW880263	OV0-OT003
c 716	19	1.3	773	9	CG274257	CG274257	OGXFL13TV	c 788	18	1.2	2333	2	BF357674	BF357674
c 717	19	1.3	775	7	CNS21158	CNS21158	Q0002112	c 789	18	1.2	2336	6	CA919099	CA919099
c 718	19	1.3	780	9	CG816597	CG816597	100002112	c 790	18	1.2	2431	1	AV431014	AV431014
c 719	19	1.3	795	9	CL973673	CL973673	QsIFCC024	c 791	18	1.2	2434	5	BU014054	BU014054
c 720	19	1.3	800	5	BQ215527	BQ215527	SEAGNCOURT	c 792	18	1.2	2441	1	AV097722	AV097722
c 721	19	1.3	802	4	BG783656	BG783656	SEAGNCOURT	c 793	18	1.2	2442	1	BE530555	M77P21STM
c 722	19	1.3	804	8	CC119540	CC119540	NDL_3B16	c 794	18	1.2	2477	7	CR758226	CR758226
c 723	19	1.3	804	9	CG120335	CG120335	PUJGJ18TB	c 795	18	1.2	2477	7	CR759164	CR759164
c 724	19	1.3	807	7	CK200607	CK200607	FGAS00912	c 796	18	1.2	2477	7	CA693601	CA693601
c 725	19	1.3	807	9	AG431636	AG431636	Mus muscu	c 797	18	1.2	2502	6	BA0403690	BA0403690
c 726	19	1.3	808	7	CR176697	CR176697	Reverse s	c 798	18	1.2	2502	6	BZ897235	BZ897235
c 727	19	1.3	813	7	CO544332	CO544332	LyEST1208	c 799	18	1.2	2522	8	CE086992	tigr-gss-
c 728	19	1.3	817	9	BX150885	BX150885	Danio rer	c 800	18	1.2	2522	2	BF560189	BF560189
c 729	19	1.3	824	7	CF437922	CF437922	EST674267	c 801	18	1.2	2532	2	AA911208	AA911208
c 730	19	1.3	830	5	BX701663	BX701663	BX701663	c 802	18	1.2	2552	1	BB097885	BB097885
c 731	19	1.3	831	9	CNS03DCB	CNS03DCB	Tetraodon	c 803	18	1.2	2592	9	CG418600	CG418600
c 732	19	1.3	832	9	CNS033V8	CNS033V8	AL247373	c 804	18	1.2	2688	9	BQ982560	BQ982560
c 733	19	1.3	837	8	CL108978	CL108978	NDL_5B20	c 805	18	1.2	2722	5	BQ982560	BQ982560
c 734	19	1.3	845	2	CNS04EPV	CNS04EPV	AL301972	c 806	18	1.2	2767	7	CO960723	CO960723
c 735	19	1.3	848	2	AW983197	AW983197	HVSNB9000	c 807	18	1.2	2768	8	BH865950	BH865950
c 736	19	1.3	860	9	CG120333	CG120333	PUJGJ18TB	c 808	18	1.2	2785	5	BQ848727	BQ848727
c 737	19	1.3	865	9	CL566731	CL566731	OB_Ba003	c 809	18	1.2	2792	2	BB309019	BB309019
c 738	19	1.3	870	4	CR191133	CR191133	Forward s	c 810	18	1.2	2801	1	AI960888	AI960888
c 739	19	1.3	877	4	BI102423	BI102423	602889606	c 811	18	1.2	2809	9	LBAF022F12	LBAF022F12
c 740	19	1.3	877	6	CD557356	CD557356	AGENCOURT	c 812	18	1.2	2821	1	AU090543	AU090543
c 741	19	1.3	877	9	CNS03RAN	CNS03RAN	AL257000	c 813	18	1.2	2821	1	AV864083	AV864083
c 742	19	1.3	890	9	CG954206	CG954206	MBEIK07TF	c 814	18	1.2	2845	5	BQ864265	BQ864265
c 743	19	1.3	904	5	CG094125	CG094125	PUJF25TB	c 815	18	1.2	2845	5	BQ864265	BQ864265
c 744	19	1.3	906	5	BU223429	BU223429	603947365	c 816	18	1.2	2895	5	BU013823	BU013823
c 745	19	1.3	910	8	BZ692458	BZ692458	SP_Ba002	c 817	18	1.2	2909	9	CE239192	CE239192
c 746	19	1.3	917	7	CK275662	CK275662	EST721740	c 818	18	1.2	2931	1	AU194267	AU194267
c 747	19	1.3	924	7	CNS39634	CNS39634	AGENCOURT	c 819	18	1.2	2945	5	BQ988389	BQ988389
c 748	19	1.3	944	9	CL057663	CL057663	CH216-850	c 820	18	1.2	2959	5	CE759753	tigr-gss-
c 749	19	1.3	964	7	CF436302	CF436302	EST672647	c 821	18	1.2	2968	8	CC001696	CC001696
c 750	19	1.3	972	5	BU506051	BU506051	AGENCOURT	c 822	18	1.2	2982	2	BB253141	BB253141
c 751	19	1.3	976	8	CL466903	CL466903	SAIL_1263	c 823	18	1.2	3085	5	BQ852306	BQ852306
c 752	19	1.3	976	8	BZ694646	BZ694646	SP_Ba004	c 824	18	1.2	3094	4	BJ168439	BJ168439
c 753	19	1.3	1017	9	EST783670	EST783670	EST783670	c 825	18	1.2	3132	4	BB541332	BB541332
c 754	19	1.3	1042	9	CNS05B29	CNS05B29	AL330462	c 826	18	1.2	3176	6	CA970585	CA970585
								c 827	18	1.2	3199	9	CE024287	tigr-gss-

C 828	18	1.2	320	4	BI412771	BI412771	602988418	C 901	18	1.2	408	6	CA696183	CA696183	wlmk8.pk0
C 829	18	1.2	320	7	W41902	W41902	mc64h02.r1	C 902	18	1.2	411	1	AA796035	AA796035	vo68a10.r
C 831	18	1.2	322	1	A1526963	A1526963	uj48e04.x	C 903	18	1.2	411	7	CF647599	CF647599	3530_1_45
832	18	1.2	323	1	AI73631	AI73631	QST254731	904	18	1.2	415	1	AA684069	AA684069	vm52h07.r
833	18	1.2	324	5	BU006897	BU006897	EGH12L16.	905	18	1.2	415	6	BY576110	BY576110	BY576110
834	18	1.2	325	7	CV260283	CV260283	WS02013.B	C 906	18	1.2	416	6	BY688210	BY688210	BY688210
835	18	1.2	326	5	BQ84566	BQ84566	QSA19N12.	C 907	18	1.2	416	8	BH918689	BH918689	3526_1_62
836	18	1.2	328	5	BQ863873	BQ863873	QGC25B14.	908	18	1.2	417	1	AJ558334	AJ558334	AJ558334
837	18	1.2	330	5	BU000629	BU000629	QGG25H08.	909	18	1.2	417	1	AA615819	AA615819	vo99g04.r
838	18	1.2	340	5	BY175732	BY175732	BY175732	910	18	1.2	417	5	BP769707	BP769707	BP769707
839	18	1.2	340	9	CL226727	CL226727	ZMWBBC000	C 911	18	1.2	417	5	BU441370	BU441370	604142680
840	18	1.2	345	1	AA080494	AA080494	mm88h10.r	912	18	1.2	418	1	AA655862	AA655862	vs41g04.r
841	18	1.2	346	8	B48826	B48826	RPC111-3K19	913	18	1.2	419	1	AA560165	AA560165	vl17e12.r
842	18	1.2	349	8	A2906914	A2906914	RPCI-24-1	C 914	18	1.2	420	1	AA474573	AA474573	vh02h09.r
843	18	1.2	350	5	BP083998	BP083998	BP083998	915	18	1.2	420	9	AG247969	AG247969	lotue cor
844	18	1.2	350	6	CB071707	CB071707	TGESTzye9	C 916	18	1.2	421	1	AV429594	AV429594	AV429594
845	18	1.2	350	6	CB072117	CB072117	TGESTzyf0	917	18	1.2	422	1	AU092120	AU092120	AU092120
846	18	1.2	352	9	BX653609	BX653609	Arabidops	918	18	1.2	423	6	AQ437212	AQ437212	HS 5147.A
847	18	1.2	352	9	CE535501	CE535501	tigr-g88-	C 919	18	1.2	425	6	CD998283	CD998283	QBF11c0f.
848	18	1.2	353	1	AA690664	AA690664	vu5g01.r	C 920	18	1.2	426	2	BE673384	BE673384	BB673384
849	18	1.2	354	2	BB841804	BB841804	BB841804	C 921	18	1.2	426	8	CC051270	CC051270	SALK_0041
850	18	1.2	354	5	BY316612	BY316612	BY316612	C 922	18	1.2	427	2	BB686166	BB686166	BB686166
851	18	1.2	357	7	CV261181	CV261181	WS02016.B	C 923	18	1.2	427	2	BE862685	BE862685	UI-N-BHO-
852	18	1.2	358	9	CG652171	CG652171	OST414695	C 924	18	1.2	427	4	BM195711	BM195711	C0315B12-
853	18	1.2	360	1	AJ474182	AJ474182	AJ474182	925	18	1.2	427	6	BY579171	BY579171	BY579171
854	18	1.2	360	2	AM577306	AM577306	RC5-BT050	926	18	1.2	427	6	CF041105	CF041105	QC121h01.
855	18	1.2	362	2	BE398845	BE398845	WHE0027.A	C 927	18	1.2	428	1	AU282283	AU282283	AU282283
856	18	1.2	362	5	BP085741	BP085741	BP085741	928	18	1.2	428	1	AA462757	AA462757	vf91c10.r
857	18	1.2	362	5	BQ984518	BQ984518	QGE2d07.Y	929	18	1.2	428	2	AW823704	AW823704	uf59b02.Y
858	18	1.2	362	7	W08159	W08159	mb42d04.r1	930	18	1.2	428	4	BM195743	BM195743	UI-N-AOO-
859	18	1.2	363	7	W15844	W15844	mb53a11.r1	C 931	18	1.2	428	5	BP769610	BP769610	BP769610
860	18	1.2	363	8	CC051269	CC051269	SALK_0041	932	18	1.2	428	5	BP769610	BP769610	BP769610
861	18	1.2	364	6	CA287633	CA287633	SCSFSD206	933	18	1.2	430	1	AV664602	AV664602	tigr-g88-
862	18	1.2	364	6	CA301426	CA301426	SCCSD2C0	C 934	18	1.2	430	1	AV664602	AV664602	AV664602
863	18	1.2	364	9	CR311426	CR311426	Medicago	935	18	1.2	430	5	BQ623630	BQ623630	USDA-FP.0
864	18	1.2	365	7	CV270346	CV270346	WS0151.B2	936	18	1.2	431	1	AA028370	AA028370	mi17b12.r
865	18	1.2	366	5	BY160900	BY160900	BY160900	937	18	1.2	431	6	CA962910	CA962910	TGESTzye6
866	18	1.2	367	2	BF878967	BF878967	RCL-ET013	C 938	18	1.2	432	1	AA823434	AA823434	VP39f11.r
867	18	1.2	367	8	AO2060462	AO2060462	RPCI-23-4	C 939	18	1.2	432	5	BY479773	BY479773	BY479773
868	18	1.2	368	9	CE512766	CE512766	tigr-g88-	C 940	18	1.2	432	8	AQ011167	AQ011167	F21120TRB
869	18	1.2	373	6	BY527618	BY527618	BY527618	C 941	18	1.2	432	8	AQ080385	AQ080385	HS_2204.A
870	18	1.2	374	1	A1876657	A1876657	u61f12.x	C 942	18	1.2	433	1	AA749254	AA749254	ny04b03.s
871	18	1.2	376	2	BE517517	BE517517	WHE0627.C	943	18	1.2	434	5	BQ983428	BQ983428	QGE19B16.
872	18	1.2	379	4	BI522835	BI522835	603175945	944	18	1.2	434	7	CV429554	CV429554	52280_1.A
873	18	1.2	379	5	BP060297	BP060297	BP060297	C 945	18	1.2	435	1	AA774578	AA774578	a127d09.s
874	18	1.2	381	5	BP054996	BP054996	BP054996	946	18	1.2	436	1	AJ559087	AJ559087	AJ559087
875	18	1.2	382	1	AI326621	AI326621	mm88h10.Y	C 947	18	1.2	436	1	AJ801236	AJ801236	AJ801236
876	18	1.2	383	1	AV841771	AV841771	AV841771	C 948	18	1.2	436	8	AQ686813	AQ686813	nbx00731
877	18	1.2	387	5	BY495049	BY495049	BY495049	C 949	18	1.2	437	6	CB071390	CB071390	TGESTzye9
878	18	1.2	387	6	CB152774	CB152774	K-EST0210	950	18	1.2	437	6	CA564184	CA564184	K0323B10-
879	18	1.2	389	7	CV262711	CV262711	WS0202.B2	C 951	18	1.2	439	8	AZ705791	AZ705791	RPCI-23-2
880	18	1.2	390	8	AZ972157	AZ972157	2M0245122	C 952	18	1.2	441	2	BE137631	BE137631	ug65f10.Y
881	18	1.2	391	2	AW145952	AW145952	um35a09.x	953	18	1.2	442	1	AA839749	AA839749	vw51c03.r
882	18	1.2	391	2	BE487921	BE487921	177070.BA	C 954	18	1.2	442	1	A1125358	A1125358	q92h11.x
883	18	1.2	392	1	AJ558850	AJ558850	AJ558850	C 955	18	1.2	443	6	CA621196	CA621196	w11n.pk00
884	18	1.2	392	7	N26386	N26386	YW76b10.r1	C 956	18	1.2	443	6	CA621196	CA621196	w11n.pk00
885	18	1.2	394	2	BF116791	BF116791	uz02c11.Y	C 957	18	1.2	444	1	AU282824	AU282824	AU282824
886	18	1.2	394	6	BY698362	BY698362	BY698362	C 958	18	1.2	444	4	BG354457	BG354457	947037D06
887	18	1.2	395	2	BF612310	BF612310	daal17b10.	C 959	18	1.2	444	8	BH914730	BH914730	3526_1_44
888	18	1.2	397	2	BE428481	BE428481	MTD007.E0	C 960	18	1.2	445	1	AA466433	AA466433	vg86f08.r
889	18	1.2	397	4	BM238782	BM238782	K0523C11-	961	18	1.2	445	6	CB748740	CB748740	BB748740
890	18	1.2	397	5	BX644651	BX644651	DKF2P781E	C 962	18	1.2	445	6	CB744429	CB744429	AMGNNUC.N
891	18	1.2	400	2	BB755639	BB755639	BB755639	C 963	18	1.2	446	5	BF063751	BF063751	BP063751
892	18	1.2	401	9	CE209176	CE209176	tigr-g88-	C 964	18	1.2	447	2	BF512676	BF512676	UI-H-BW1-
893	18	1.2	402	5	BP084921	BP084921	BP084921	C 965	18	1.2	447	2	AW012493	AW012493	uc05f04.Y
894	18	1.2	403	1	AJ5011743	AJ5011743	AJ5011743	C 966	18	1.2	448	1	AU264530	AU264530	vr94e02.r
895	18	1.2	404	5	BY159935	BY159935	BY159935	C 967	18	1.2	449	1	AA683906	AA683906	vr94e02.r
896	18	1.2	404	8	BZ915151	BZ915151	CH240_57D	C 968	18	1.2	449	1	A1196933	A1196933	ui68b05.x
897	18	1.2	404	9	CE019668	CE019668	tigr-g88-	969	18	1.2	449	2	AW597177	AW597177	ej74e07.Y
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900	18	1.2	408	5	BQ334355	BQ334355	QV1-MT013	C 972	18	1.2	451	2	CE106437	CE106437	tigr-g88-

C 974	18	1.2	452	2	BF717405	BF717405 fd42c08.y
C 975	18	1.2	453	2	BF404667	BF404667 UI-R-CAL-
C 976	18	1.2	454	1	AA693698	AA693698 zi55a08.s
C 977	18	1.2	454	1	AV597591	AV597591 AV597591
C 978	18	1.2	454	2	BF417903	BF417903 UI-R-CAL-
C 979	18	1.2	454	2	AW261519	AW261519 um8f02.x
C 980	18	1.2	455	5	BP610542	BP610542 BP610542
C 981	18	1.2	455	9	CR357208	CR357208 Arabinidops
C 982	18	1.2	456	9	CE166799	CE166799 tigr-g8s-
C 983	18	1.2	457	1	AA634353	AA634353 zu75a03.s
C 984	18	1.2	459	1	AI120869	AI120869 ub73c08.x
C 985	18	1.2	459	1	AV780847	AV780847 AV780847
C 986	18	1.2	459	7	CK091199	CK091199 F058P85.3
C 987	18	1.2	459	8	B24336	B24336 F1715TF IGF
C 988	18	1.2	459	8	BH172324	BH172324 SALK 0055
C 989	18	1.2	459	8	BZ858262	BZ858262 CH240.220
C 990	18	1.2	460	1	AV777620	AV777620 AV777620
C 991	18	1.2	460	8	AQ122817	AQ122817 HS 3088.A
C 992	18	1.2	462	1	AI181374	AI181374 ub83f12.r
C 993	18	1.2	462	6	CD317412	CD317412 StrPa621.
C 994	18	1.2	463	8	AQ221184	AQ221184 HS 2258.B
C 995	18	1.2	464	1	AI117211	AI117211 ub83g12.r
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C 997	18	1.2	465	9	AG236866	AG236866 Lotus cor
C 998	18	1.2	465	9	CE814544	CE814544 tigr-g8s-
C 999	18	1.2	466	8	BH213695	BH213695 SALK 0095
1000	18	1.2	466	8	BH427100	BH427100 BGI_X76TF
RESULT 1						
AY410247						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
COMMENT						
FEATURES						
source						
gene						
ORIGIN						


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Qy      1081  TTCCGAATGCAAAAGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTCGAGTGCCCGTG 1140
Db      1081  TTCCGAATGCAAAAGGGCGCTTCGCCAAGTCTCAGAGCAAAACCTTCGAGTGCCCGTG 1140
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Db      1141  GTGGTGGTGGCTGTCTTCTGCTGCTGGACTCATACCAACATTTTGGAGTCCGTGCA 1200
Qy      1201  TTGCTTACTGACCCAGCAAACTCCCTTGGGGAAAACCTCTGATGCTCTGGGATCATGTATGC 1260
Db      1201  TTGCTTACTGACCCAGCAAACTCCCTTGGGGAAAACCTCTGATGCTCTGGGATCATGTATGC 1260
Qy      1261  ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCTCTTGGGGAAA 1320
Db      1261  ATTGCTCTAGCATCTGCCAATAGTGTCTTAAATCCCTTCTTATGCCCCTCTTGGGGAAA 1320
Qy      1321  GATTTAGGAAGAAAGCAAGCAGTCCATTCAGGGAATCTGGAGGAGCCTTCAGTGAG 1380
Db      1321  GATTTAGGAAGAAAGCAAGCAGTCCATTCAGGGAATCTGGAGGAGCCTTCAGTGAG 1380
Qy      1381  GAGCTCACACGCTTCCACCCACTGTCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1440
Db      1381  GAGCTCACACGCTTCCACCCACTGTCCTCAAAACATGTCAATTCAGAAAGAAATAGTACA 1440
Qy      1441  ACTGTGTGA 1449
Db      1441  ACTGTGTGA 1449

RESULT 2
CR601349
LOCUS      CR601349      1885 bp      mRNA      linear      HTC 2i-JUL-2004
DEFINITION full-length cDNA clone CS0D1065YH15 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR601349
VERSION   CR601349.1 GI:50482156
KEYWORDS  HTC; CNSLT cDNA.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1885)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
           http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
           Faraday Avenue
           Genoscope.
REFERENCE 2. (bases 1 to 1885)
AUTHORS   Genoscope.
TITLE     Direct Submision
JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
           - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
           end enriched, double-strand cDNA was digested with Not I and cloned
           into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
           was normalized. Library was constructed by Life Technologies, a
           division of Invitrogen.
FEATURES   Location/Qualifiers
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               /mol_type="mRNA"
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               /clone="CS0D1065YH15"
               /tissue_type="Placenta Cot 25-normalized"
               /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      100.0%; Score 1449; DB 3; Length 1885;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      79  ATGCGCTTTTCTCTGCTGAGACCAATTCAACTGACCTTCTCTCAGCCATGGAATGAG 138
Qy      61  CCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTACTGGGATGTCAGGC 120
Db      139  CCCCAGTAATCTCTCCATGGTCAATCTCAGCCCTTACTTTTACTGGGATGTCAGGC 198
Qy      121  AATGGCTGGTGTCTGCTGGGCTGGCTGAAGATGACGCGGACAGTGAACACAAATTTGG 180
Db      199  AATGGCTGGTGTCTGCTGGGCTGGCTGAAGATGACGCGGACAGTGAACACAAATTTGG 258
Qy      181  TTCTTCCACCTCACTTGGCGGACCTCTCTGTGCGCTCTCTCTGCGCTTCTCTGCGCT 240
Db      259  TTCTTCCACCTCACTTGGCGGACCTCTCTGTGCGCTCTCTCTGCGCTTCTCTGCGCT 318
Qy      241  CACTTGGCTCTCCAGGAGCAGTGGCCCTACGGCAGGTTCTCTATGCAAGCTCATCCCTCC 300
Db      319  CACTTGGCTCTCCAGGAGCAGTGGCCCTACGGCAGGTTCTCTATGCAAGCTCATCCCTCC 378
Qy      301  ATCAATGTCCTCAACATGTTTGCAGATGCTCTTCTGCTTACTTGCCTATAGCTGATGCG 360
Db      379  ATCAATGTCCTCAACATGTTTGCAGATGCTCTTCTGCTTACTTGCCTATAGCTGATGCG 438
Qy      361  TGTCTTGGTATTCAAGCCCAATCTGGTGTGAGATCATGCAATGTAGGAGTGGCCTGCG 420
Db      439  TGTCTTGGTATTCAAGCCCAATCTGGTGTGAGATCATGCAATGTAGGAGTGGCCTGCG 498
Qy      421  TCTATCTGTGATGATCTGGGTGGTGGCTTTTGTGATGTGCATTCCTGTGTTCTGTGAT 480
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Qy      481  CGGAAATCTTCACTACAGACAACCATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db      559  CGGAAATCTTCACTACAGACAACCATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 618
Qy      541  TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAATTT 600
Db      619  TCATTAGATTATCAGACTTTTATGGAGATCCACTAGAAACAGGTCTCTTGAACAATTT 678
Qy      601  GTTCAGCGCTGGAGAAATGAATCATAGTGTAGATCTCTCTCTTTTCCAAACAATGAT 660
Db      679  GTTCAGCGCTCTGGAGAAATGAATCATAGTGTAGATCTCTCTCTTTTCCAAACAATGAT 738
Qy      661  CATCTTGGACAGTCCCACCTGTCTTCCAACTCAAAACATTTCAAAGACCTTCTGAGAT 720
Db      739  CATCTTGGACAGTCCCACCTGTCTTCCAACTCAAAACATTTCAAAGACCTTCTGAGAT 798
Qy      721  TCATCTCCTAGGGGTTCTGTAGGTAAACAAGTCAAAATCTGTATTTCTAATGTATTAAA 780
Db      799  TCATCTCCTAGGGGTTCTGTAGGTAAACAAGTCAAAATCTGTATTTCTAATGTATTAAA 858
Qy      781  CCTGCTGATGTCTCACTCACTTAAATCCCAGTGGGTTTCTTATTGAAGATCAGAAACC 840
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Qy      841  AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTAGCGCT 900
Db      919  AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTAGCGCT 978
Qy      901  TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACATTTTA 960
Db      979  TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTACATTTTA 1038
Qy      961  GGCCAAATTCAGATGAGCATCAAGTGCACACCCCTCGTGGCAATTAACGATCACTAGG 1020
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Qy      1021  CTAGTGGTGGGTTTCTCTGCTGCGCTCTCTGTATCATGATAGCCTGTATACAGTTCAATTGTC 1080

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Qy 1321 GATTTTAGGAAGAAGCAAGGAGTCCATTAGGGAATCTGGAGGAGCCCTTCAGTGAG 1380

Db 1399 GATTTTAGGAAGAAGCAAGGAGTCCATTAGGGAATCTGGAGGAGCCCTTCAGTGAG 1458

Qy 1381 GAGCTCACAGTTCACCCACTGTCCTTCAAACTCAATGTCAATTCAGAAAGAAATAGTACA 1440

Db 1459 GAGCTCACAGTTCACCCACTGTCCTTCAAACTCAATGTCAATTCAGAAAGAAATAGTACA 1518

Qy 1441 ACTGTGTGA 1449

Db 1519 ACTGTGTGA 1527

RESULT 3

CR590169

LOCUS

DEFINITION

Full-length cDNA clone CSODI003YE01 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION

CR590169

VERSION

CR590169.1 GI:50470976

KEYWORDS

HTC; CNSLT cDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1888)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization.

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation.1600
Faraday Avenue

2 (bases 1 to 1888)

Genoscope.

REFERENCE

2 (bases 1 to 1888)

Genoscope.

TITLE

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.

FEATURES

Location/Qualifiers

1..1888

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="CSODI003YE01"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

Query Match 100.0%; Score 1449; DB 3; Length 1888;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGTCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 60

Db 69 ATGGCGTCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 128

Qy 61 CCCCAGTAATTCCTCCATGCTCATCTCAGCCCTTACTCTTTTACTGGGATGCCAGGC 120

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QY 1441 ACTGTGTGA 1449
Db 1509 ACTGTGTGA 1517

RESULT 4
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LOCUS full-length cDNA clone CS0D1016YJ19 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR623914
VERSION CR623914.1 GI:50504721
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1899)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
REFERENCE 2 (bases 1 to 1899)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/clone="CS0D1016YJ19"
/tissue_type="Placenta Cot 25-normalized"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 AATGGGCTGGTGTGTGGGTGGCTGAGAGTGCAGCGGACAGTGAACACAATTTGG 180
Db 188 AATGGGCTGGTGTGTGGGTGGCTGAGAGTGCAGCGGACAGTGAACACAATTTGG 247
QY 181 TTCTCCACCTCACCCTTGGGGGACCTCCTCTGCTGCTCTCTCTCTGCTTCTGCTGCT 240
Db 248 TTCTCCACCTCACCCTTGGGGGACCTCCTCTGCTGCTCTCTCTCTGCTTCTGCTGCT 307
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Db 308 CACTTGGCTCTCCAGGACAGTGGCCCTAGCGGAGGTTTCTTATGCAAGCTCATCCCCCTCC 367
QY 301 ATCAATGTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTTACTGCT 360
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QY 541 TCATTAGATTTATCAGACTTTTATGGAGATCCACTAGAAAACAGCTCTTCTGAAAACATT 600
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QY 601 GTTCAGCGCTGGAGAAATGAATGATAGTGTAGATCTCTCTCTTCTTCCAAACAAATGAT 660
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QY 661 CATCTTTGGACAGTCCCACCTGTCTTCCAACTCAAACTTCAAAAGACCTTCTGAGAT 720
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QY 721 TCATCTCCCTAGGGTCTGCTAGTGTAAAGTCAAAATCTGTATTCTTAATGATTTAAA 780
Db 788 TCATCTCCCTAGGGTCTGCTAGTGTAAAGTCAAAATCTGTATTCTTAATGATTTAAA 847
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QY 841 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTTAGCGCT 900
Db 908 AGCCCACTGGATAACTCTGATGCTTTTCTCTACTCATTTTAAAGCTGTTCCTTAGCGCT 967
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Oy 1201 TTGCTTACTGACCCAGAAACTCCCTTGGGGAAAACTCTGATGCTCGGTGATATGC 1260
Db 1279 TTGCTTACTGACCCAGAAACTCCCTTGGGGAAAACTCTGATGCTCGGTGATATGC 1338
Oy 1261 ATTGCTCTAGCATCTGCCAATAGTGTCTTAACTCCCTTCCCTTATGCGCTCTTGGGAAA 1320
Db 1339 ATTGCTCTAGCATCTGCCAATAGTGTCTTAACTCCCTTCCCTTATGCGCTCTTGGGAAA 1398
Oy 1321 GATTTAGGAAGAAGCAAGGAGTCCATTAGGGAATTTGGAGGAGCCCTTCAGTGA 1380
Db 1399 GATTTAGGAAGAAGCAAGGAGTCCATTAGGGAATTTGGAGGAGCCCTTCAGTGA 1458
Oy 1381 GAGCTCACAGTTCACCCACTGCTCCCTCAACCAATGTCATTTAGAAAGAAATAGTACA 1440
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Oy 1441 ACTGTGTA 1449
Db 1519 ACTGTGTA 1527

RESULT 6
LOCUS CR609272 1951 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI061YC05 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR609272
VERSION CR609272.1 GI:50490079
KEYWORDS HTC; CNSLT_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1951)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1951)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1.1951
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI061YC05"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 100.0%; Score 1449; DB 3; Length 1951;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGGCGTCTTCTCTGCTGAGACCAATTCACCTGACTCTCACGCCATGGATGAG 60
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Db 128 CCCCCAGTAATTCCTCCATGGTCAATTCAGCCTTACTTTTTTACTGGGATGCCAGGC 187
Oy 121 AATGGGCTGTGTCTGGGTGGCTGTGAAGATGACGGGACAGTGAACACAAATTTGG 180
Db 188 AATGGGCTGTGTCTGGGTGGCTGTGAAGATGACGGGACAGTGAACACAAATTTGG 247
Oy 181 TTCTCCACCTCACTTTGGGGGACCTCTCTGCTGCTCTCTCTGCGCTTCTCGCTGCT 240
Db 248 TTCTCCACCTCACTTTGGGGGACCTCTCTGCTGCTCTCTCTGCGCTTCTCGCTGCT 307
Oy 241 CACTTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTTCTATGCAAGCTCATCCCCCTCC 300
Db 308 CACTTTGGCTCTCCAGGGACAGTGGCCCTACGGCAGGTTTCTATGCAAGCTCATCCCCCTCC 367
Oy 301 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGATAGGCTGTGATCGC 360
Db 368 ATCAATGCTCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCGATAGGCTGTGATCGC 427
Oy 361 TGTCTGTGTGTAATTCAGGCCAACTCTGCTGTCAGAAATCATGCAATGTAGGATGCGCTGC 420
Db 428 TGTCTGTGTGTAATTCAGGCCAACTCTGCTGTCAGAAATCATGCAATGTAGGATGCGCTGC 487
Oy 421 TCTATCTGTGGATGATCTGGGTGGTGGCTTTTGTGATGTGCATTTCTCTGTTTCTGTGATC 480
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Oy 721 TCCTCCCTAGGGGTCTCTGCTAGGTAAACAGTCAAAATCTGATTTCTTAATGATTTTAAA 780
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Oy 781 CCTGCTGATGTGTCTCACCTTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 840
Db 848 CCTGCTGATGTGTCTCACCTTAAATCCCAAGTGGGTTTCTTATTTGAAGATCACGAAACC 907
Oy 841 AGCCACTGGANATCTGATGCTTTCTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 900
Db 908 AGCCACTGGANATCTGATGCTTTCTCTCTACTCATTTTAAAGCTGTTCCCTAGCGCT 967
Oy 901 TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTTACAATTTA 960
Db 968 TCTAGCAATTCCTTCTAGAGTCTGAGCTACCAAGGTTTCCAGGATTTATTTACAATTTA 1027
Oy 961 GGCCAAATTCAGATGAGATCAAGTGCACACACCCCTCTGGTGGCAATAACGATCACTAGG 1020
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Oy 1021 CTAGTGGTGGTGTCTGCTGCTGCTCTGTTTATCATGATAGCTCTTACAGCTTCAATGTC 1080
Db 1088 CTAGTGGTGGTGTCTGCTGCTGCTCTGTTTATCATGATAGCTCTTACAGCTTCAATGTC 1147
Oy 1081 TTCCGAATGCAAGGGCGCTTCCGCAAGTCTCAGAGCAAACTTCGAGTGGCGGTG 1140
```


Unpublished (2001)
 On May 8, 2003 this sequence version replaced gi:30454945.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6632.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas-CS0D1065CD08QPl&c=6632.r.
 FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1065YH15"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN

	Query Match	54.7%	Score 793;	DB 5;	Length 1092;
	Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0; Gaps 0;
	Matches 793;	Conservative 0;			
Qy	1	ATGGCGTCTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG	60		
Db	79	ATGGGCTCTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACAGCCATGGAATGAG	138		
Qy	61	CCCCAGTAATCTCTCATGGTCAATCTCAGCCCTTACTTTTCTACATGGGATGCCAGGC	120		
Db	139	CCCCAGTAATCTCTCATGGTCAATCTCAGCCCTTACTTTTCTACATGGGATGCCAGGC	198		
Qy	121	AATGGGCTGGTGTGGTGGCTGGCTGGAAGATGACGGGACAGTGAACACAAATTTGG	180		
Db	199	AATGGGCTGGTGTGGTGGCTGGCTGGAAGATGACGGGACAGTGAACACAAATTTGG	258		
Qy	181	TTCTCTCCACCTCACTTGTGGGGACCTCTCTGTGCTCTCTCTTGGCCCTTCTCGCTGGCT	240		
Db	259	TTCTCTCCACCTCACTTGTGGGGACCTCTCTGTGCTCTCTCTTGGCCCTTCTCGCTGGCT	318		
Qy	241	CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC	300		
Db	319	CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC	378		
Qy	301	ATCAATTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATAGCCATTAGCTGGATCGC	360		
Db	379	ATCAATTGCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGTCATAGCCATTAGCTGGATCGC	438		
Qy	361	TGCTCTGTGGTATTCAAGCCCAATCTGTGTGTCAGAAATCATGCAATGTAGGGATGGCTTCG	420		
Db	439	TGCTCTGTGGTATTCAAGCCCAATCTGTGTGTCAGAAATCATGCAATGTAGGGATGGCTTCG	498		
Qy	421	TCTATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTGTGTTCGTGTAC	480		
Db	499	TCTATCTGTGGATGTATCTGGGTGGTGGCTTTTGTGATGTGCAATCTGTGTTCGTGTAC	558		
Qy	481	CGGGAAATCTTCACTACAGACAAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	540		
Db	559	CGGGAAATCTTCACTACAGACAAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC	618		
Qy	541	TCATTAGATTATCCAGACTTTTATGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT	600		
Db	619	TCATTAGATTATCCAGACTTTTATGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT	678		
Qy	601	GTTCAGCGCCCTGGGAAATGAATGATAGTTAGATCCTTCTCTTCTTCCAAACAAATGAT	660		

Db 679 GTTCAGCGCGCTGGAGAAATGAATAGTGGTAGATCCTTCTCTTTCCAAACAATGAT 738
Qy 661 CATCTCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAAGACCTTCTGCAGAT 720
Db 739 CATCTCTTGGACAGTCCCACTGTCTTCCAACTCAACATTTCAAAGACCTTCTGCAGAT 798
Qy 721 TCACCTCCCTAGGGTCTCGCTAGGTTAACAGTCAAAATCTGTAATCTTAATGATTTTAA 780
Db 799 TCACCTCCCTAGGGTCTCGCTAGGTTAACAGTCAAAATCTGTAATCTTAATGATTTTAA 858
Qy 781 CCTGCTGATGTGG 793
Db 859 CTGCTGATGTGG 871

RESULT 9
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LOCUS
DEFINITION BX095575 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGP998D01374 ; IMAGE:196176, mRNA sequence.
ACCESSION BX095575
VERSION 1
KEYWORDS BX095575.1 GI:27827777
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Human Unigeneset - RZPD3
COMMENT Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998D01374.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 {RZPDLIB No.972}
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

FEATURES
source
1..797
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACACTATGAC.
Location/Qualifiers
1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998D01374 ; IMAGE:196176"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5, AACTGGAAGATAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 53.8%; Score 779; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 779; Conservative 0; Mismatches 0; Indels 0; Gaps

574 CTAGAAACAGGCTCTTCAAAACATTTGTTACGCCCTGGAGAAATGAATGATAGGTTA 633
 17 CTAGAAACAGGCTCTTGAACAAATGTTTCAGCGCTGGAGAAATGAATGATAGGTTA 76
 634 GATCCTCTCTCTTTCAAAACAAATGATCATCTTCGACAGTCCCACTGTCTTCCAACT 693
 77 GATCCTCTCTCTTTCAAAACAAATGATCATCTTCGACAGTCCCACTGTCTTCCAACT 136
 694 CAAACATTTCAAGACCTTCTGCAGATTCATCTCCCTAGGGGTTCTGCTAGGTTTCAAACT 753
 137 CAAACATTTCAAGACCTTCTGCAGATTCATCTCCCTAGGGGTTCTGCTAGGTTTCAAACT 196
 754 CAAACATTTCAAGATTTTAAACCTGCTGATGTTGCTCACTCACTAAATCCCACT 813
 197 CAAACATTTCAAGATTTTAAACCTGCTGATGTTGCTCACTCACTAAATCCCACT 256
 814 GGGTTCTCTATTAAGATCAGAAACACGACCTGATGATCTGATGCTTTTCTCTCT 873
 257 GGGTTCTCTATTAAGATCAGAAACACGACCTGATGATCTGATGCTTTTCTCTCT 316
 874 ACTGATTTAAAGCTTTCCCTAGGCTTCTAGCAATTCCTTCTAGGATCTGAGTACCA 933
 317 ACTGATTTAAAGCTTTCCCTAGGCTTCTAGCAATTCCTTCTAGGATCTGAGTACCA 376
 934 CAAAGTTTCCAGGATTTATTAATTTAGGCCAAATTCACAGATGACGATCAAGTGCCACA 993
 377 CAAAGTTTCCAGGATTTATTAATTTAGGCCAAATTCACAGATGACGATCAAGTGCCACA 436
 994 CCCCTCTGCGCAATTAACGATCACTAGGCTAGTGGGTTTCTGCTGCCCTCTGTTATC 1053
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 1054 ATGATAGCTCTTACAGCTTCATTTGCTTCGCAATGCAAGGGGCGGTTTCCCAAGTCT 1113
 497 ATGATAGCTCTTACAGCTTCATTTGCTTCGCAATGCAAGGGGCGGTTTCCCAAGTCT 556
 1114 CAGAGCAAAACCTTTTCAGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 557 CAGAGCAAAACCTTTTCAGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 616
 1174 CCATACGACATTTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
 617 CCATACGACATTTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 676
 1234 ACTCTGATGCTCTGGGATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1293
 677 ACTCTGATGCTCTGGGATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
 1294 CCCTTCTCTTATGCCCTCTTGGGAAAGATTTTGGGAAAGCAAGGAGTCCATTTCA 1352
 737 CCCTTCTCTTATGCCCTCTTGGGAAAGATTTTGGGAAAGCAAGGAGTCCATTTCA 795

RESULT 10
 BX337391
 LOCUS
 DEFINITION BX337391 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1041Y11 5-PRIME, mRNA sequence.
 ACCESSION BX337391
 VERSION BX337391.2 GI:46283013
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 934)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30346958.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6632.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CS0D1041AA06QPI&c=6632.r.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1041Y11"
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6
 vector. Library was normalized."

ORIGIN

Query Match 53.6%; Score 776; DB 5; Length 934;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCGCTTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 60
 Db 79 ATGGCGCTTTTCTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCATGGAATGAG 138
 Qy 61 CCCCAGCTAAATTCCTCCATGGTCAATTCAGCCTTACTTTTCTGCGGATGCCAGGC 120
 Db 139 CCCCAGCTAAATTCCTCCATGGTCAATTCAGCCTTACTTTTCTGCGGATGCCAGGC 198
 Qy 121 AATGGCTGTGCTGCTGGTGGCTGAGATGAGGACAGTGAACACAAATTTGG 180
 Db 199 AATGGCTGTGCTGCTGGTGGCTGAGATGAGGACAGTGAACACAAATTTGG 258
 Qy 181 TTCTTCCACCTCACTTGGCGGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 259 TTCTTCCACCTCACTTGGCGGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
 Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTACGGAGGTTCTATGCAAGCTCATCCCCCTCC 300
 Db 319 CACTTGGCTCTCCAGGACAGTGGCCCTACGGAGGTTCTATGCAAGCTCATCCCCCTCC 378
 Qy 301 ATCAATTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTGATGCGC 360
 Db 379 ATCAATTCCTCAACATGTTTGGCAGTGTCTTCTGCTTACTGCTTACTGCTGATGCGC 438
 Qy 361 TGCTTGTGTTTCAAGCCAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 439 TGCTTGTGTTTCAAGCCAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
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 Qy 481 CGGGAATCTTCACTCAGACCAACCAATTAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
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 Qy 541 TCATTAGATTTACAGACTTTTATGGAGTCCACTAGAAACAGGCTCTCTTGAACAACTT 600
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 Qy 601 GTTCAGCGCGCTGGAGAAATGAATGATAGTGTAGATCTTCTCTTCCAAACAAATGAT 660
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 Qy 661 CATCTTGGACAGTCCCACTGCTTCCAACTCAAACTTCAAAAGACCTTCTTGCAGAT 720


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Db 739 CATCTTGGACAGTCCCACTGCTTCCAACTTCAAAACATTTCAAGACCTTCTCAGAT 798
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Qy 721 TCATCCCTAGGGTTCGTAGGTTAAACAAGTCAAAATCTGTATTCTAAATGATT 776
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Db 799 TCATCCCTAGGGTTCGTAGGTTAAACAAGTCAAAATCTGTATTCTAAATGATT 854
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|
|
RESULT 11
BX395616 1122 bp mRNA linear EST 29-APR-2004
LOCUS BX395616 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI003YE01 5-PRIME, mRNA sequence.
ACCESSION BX395616
VERSION BX395616.2 GI:46874469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1122)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30616746.
Contact: Genoscope
Genoscope - Centre National de Sequencage.
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: secrefegenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6632_r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0DI003AC01Q1&c=6632.r.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="CS0DI003YE01"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 52.7%; Score 763; DB 5; Length 1122;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 883; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ATGGCGTCTTCTGCTGAGACCAATTCACATGACCTACTCTCAGCCATGGAATGAG 60
Db 69 ATGGCGTCTTCTGCTGAGACCAATTCACATGACCTACTCTCAGCCATGGAATGAG 128
Qy 61 CCCCAGTAATTTCTCCATGCTCATTTCTCAGCCTTACTTTTACTGGGATGCCAGC 120
Db 129 CCCCAGTAATTTCTCCATGCTCATTTCTCAGCCTTACTTTTACTGGGATGCCAGC 188
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Db 189 AATGGCTGGTGTGGGTGGTGGCTGAAGATGCAGGACAGTGAACAATTTGG 248
Qy 181 TTCTCCACCTCACCTTGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 240
Db 249 TTCTCCACCTCACCTTGCGGACCTCTCTGCTGCTCTCTGCTGCTCTCTGCTGCT 308
Qy 241 CACTTGGCTCTCAGGACAGTGGCCCTCAGGAGGTTCCTATGCAAGCTCATCCCTCC 300
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Db 369 ATCATTTGCTCAACATGTTTGGCCAGTGTCTTCTGCTTACTGCAATAGCTGATGCG 428
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Db 549 CGGAAATCTTCACTACAGACAACCAATATAGATGTGGCTACAAATTTGGTCTCTCCAGC 608
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Db 609 TCATTAGATTATCCAGACTTTTATGGAGATCCACTAGAAAACAGCTCTCTTCAAAACATT 668
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Qy 601 GTTCAGCCGCTCGAGAAATGAATGATAGGTTAGATCCTTCTCTTTCCAAACAAATGAT 660
|
|
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Db 669 GTTCAGCCGCTCGAGAAATGAATGATAGGTTAGATCCTTCTCTTTCCAAACAAATGAT 728
|
|
|
Qy 661 CATCTTGGACAGTCCCACTGTCTTCAACCTCAAACTTCAAGACCTTCTGAGAT 720
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|
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Db 729 CATCTTGGACAGT-CCCACTGTCTTCAACCTCAAACTTCAAGACCTTCTGAGAT 787
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Qy 721 TCATCTCCCTAGGGTTCGTAGGTTAAACAAGTCAAAATCTGTATTCTTAATGATTAAA 780
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Db 788 TCATCTCCCTAGGGTTCGTAGGTTAAACAAGTCAAAATCTGTATTCTTAATGATTAAA 847
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|
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Qy 781 CTGCTGATGTGGTCTCACCTAAAATCCCAAGTGGGTTTCTTATTGAAGATCAGAAACC 840
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|
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Qy 841 AGCCCACTGGATACTGATGCTGCTTCTCTACTCATTTAAA 884
|
|
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Db 908 AGCCCACTGGATACTGATGCTGCTTCTCTACTCATTTAAA 951
|
|
|
RESULT 12
BM562131 1112 bp mRNA linear EST 20-FEB-2002
LOCUS BM562131
DEFINITION AGENCOURT_6562000 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5745461
5' mRNA sequence.
ACCESSION BM562131
VERSION BM562131.1 GI:18807958
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1112)
NIH-MGC http://mgi.cni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (NLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/NLNL at:
http://image.llnl.gov
Plate: LLAM12768 row: h column: 06
High quality sequence start: 11
High quality sequence stop: 686.
FEATURES
Location/Qualifiers
1..1112
source
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QY 421 TCTATCTGTGGATCTATCTGGTGGTCTTTCTGTGATGTCATCTCCTGTGTTCTGCTGAC 480
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 Db 717 CATCTTTGGACAGTCCCACTGTCTTC 743

RESULT 14
 BM920604
 LOCUS
 DEFINITION AGENCOURT 6709588 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750634
 5', mRNA sequence.

ACCESSION
 VERSION BM920604.1 GI:19370983

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1093)

AUTHORS
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

JOURNAL
 Contact: Robert Strausberg, Ph.D.

COMMENT
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 688.

Location/Qualifiers

1..1093

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5750634"

/lab_host="DH10B"

/clone_lib="NIH_MGC_122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;

Site 1: NotI; Site 2: EcoRV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female

spleen, and 20-22 week male spleens. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note:

this is a NIH_MGC Library."

Db 72 ATGGCGTCTTCTCTGCTGAGACCAATCAATCACTGACCTACTCTCAGACCAATGAATGAG 131
 QY 61 CCCCCAGTAATCTCTCCATGTCATCTCAGCCTTACTTTTTTATCTGGGATGCCAGGC 120
 Db 132 CCCCCAGTAATCTCTCCATGTCATCTCAGCCTTACTTTTTTATCTGGGATGCCAGGC 191
 QY 121 AATGGGCTGCTGCTGGGCTGGGCTGAAGTCAGCGGACAGTGACACACAAATTTGG 180
 Db 192 AATGGGCTGCTGCTGGGCTGGGCTGAAGTCAGCGGACAGTGACACAAATTTGG 251
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 Db 372 ATCATTTGCTCAACATGTTTGGCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
 QY 361 TGTCTTGTGTTTCAAGCCAACTCTGCTGTCAGAAATCATCGCAATGTAGGATGCCCTGC 420
 Db 432 TGTCTTGTGTTTCAAGCCAACTCTGCTGTCAGAAATCATCGCAATGTAGGATGCCCTGC 491
 QY 421 TCTATCTGTGGATGATCTCTGGTGGTGGCTTTTGTGATGTCATCTCTGCTGCTGCTGCTG 480
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 Db 552 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 611
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 Db 612 TCATTAGATATCCAGACTTTTATGGAGATCCACTAGAAAACAGGTCTCTTGAACAAATT 671
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 Db 672 GTTCAGCGCTGGAGAAATGAATGATAGTTAGATCTTCTCTTCCAAACAAATGAT 731
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RESULT 15

BM546347

LOCUS

DEFINITION AGENCOURT 6498674 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722907

5', mRNA sequence.

ACCESSION

BM546347

VERSION

BM546347.1 GI:18779232

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1124)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM12709 row: 1 column: 12

High quality sequence start: 9

High quality sequence stop: 688.

FEATURES

source

location/Qualifiers

1..1124

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5722907"

/lab_host="DH10B"

/clone_lib="NIH MGC 125"

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

ORIGIN

Query Match 44.9%; Score 651; DB 4; Length 1124;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||
Qy 99 ATGGCGTCTTTCTGCTGAGACCAATTCAACTGACCTACTCTCACGCCCATGGAATGAG 158
Db |||
Qy 61 CCCCGAGTAATCTCTCCATGGTCAATCTCAGCCCTACTTTTTTACTGGGATTGCCAGGC 120
Db |||
Qy 159 CCCCGAGTAATCTCTCCATGGTCAATCTCAGCCCTACTTTTTTACTGGGATTGCCAGGC 218
Db |||
Qy 121 AATGGCGTGGTCTGCTGGGCTGGCTGAAGATGACGGCAGCAGTGAACACAAATTGG 180
Db |||
Qy 219 AATGGCGTGGTCTGCTGGGCTGGCTGAAGATGACGGCAGCAGTGAACACAAATTGG 278
Db |||
Qy 181 TTCTCTCACTCACCTTGGCGGACCTCTCTGCTGCCCTCTCTTGGCCCTCTCGCTGGCT 240
Db |||
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Db |||
Qy 241 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 300
Db |||
Qy 339 CACTTGGCTCTCCAGGACAGTGGCCCTTACGGCAGGTTCTTATGCAAGCTCATCCCTCC 398
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Db |||
Qy 361 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGAGAAATCATCGCAATGTAGGATGGCCTGC 420
Db |||
Qy 459 TGTCTTGTGGTATTCAAGCCCAATCTGGTGTGAGAAATCATCGCAATGTAGGATGGCCTGC 518
Db |||
Qy 421 TCTATCTGTGATGATGATCTGGTGGTGGCTTTTGTGATGTCATCTCTGTCTGTGTAC 480
Db |||
Qy 519 TCTATCTGTGATGATGATCTGGTGGTGGCTTTTGTGATGTCATCTCTGTCTGTGTAC 578
Db |||
Qy 481 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 540
Db |||
Qy 579 CGGGAATCTTCACTACAGACCAACATAATAGATGTGGCTACAAATTTGGTCTCTCCAGC 638
Db |||
Qy 541 TCATTAGATATCAGACTTTTATGGAGATCCACTAGAAAAACAGTCTCTTTGAAAAACATT 600
Db |||
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Db |||
Qy 601 GTTCAGCGCCTGGAGAAATGAATAGTAGTATCTTCTCTTTCCAA 651
Db |||
Qy 699 GTTCAGCGCCTGGAGAAATGAATAGTAGTATCTTCTCTTTCCAA 749
Db |||
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Search completed: April 11, 2005, 14:11:57

Job time : 5253 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2005, 09:28:16 ; Search time 174 Seconds

(without alignment)

1071.371 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 2552

Sequence: 1 MASFSAEINSDLLSQPWNE.....TRSTHCPNNVIERNSTTV 482

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2552	100.0	482	AAW42376	Homo sapi
2	2552	100.0	482	AAU99102	Human ana
3	2552	100.0	482	ABU79122	Chemoatr
4	2552	100.0	482	ABP81797	Human com
5	2552	100.0	482	ADC86209	Human GPC
6	2552	100.0	482	ADf43378	Chemoatr
7	2552	100.0	482	ADR05360	Human ana
8	2544	99.7	482	AAW02151	Human G-p
9	2544	99.7	482	ABU62861	Putative
10	2544	99.7	482	ADL22832	Human C3a
11	2543	99.6	482	ADQ19275	Human sof
12	2543	99.6	482	AAW23367	Novel G-p
13	2543	99.6	482	ADD46294	Human Pro
14	2543	99.6	482	ADO29203	Human GPC
15	2543	99.6	482	ADS09204	Complemen
16	2539	99.5	485	AAW58319	Lung canc
17	2535	99.3	482	ABB56336	Non-endog
18	2532	99.2	482	AAW06540	C5a-like
19	2145.5	84.1	415	AAW83496	Human dia
20	1565.5	61.3	477	AAW72389	Mouse C3a
21	1565.5	61.3	477	AAU75166	Mouse ana
22	1565.5	61.3	477	ADL22834	Murine C3
23	1565.5	61.3	477	ADO29204	Mouse GPC
24	1565.5	61.3	477	ADR05368	Mouse ana
25	1426.5	55.9	473	ADD46292	Rat Prote

26	551.5	21.6	350	6	ABU09503	Human C5a
27	551.5	21.6	350	6	ABP81798	Human com
28	551.5	21.6	350	7	ABU62862	Human C3a
29	551.5	21.6	350	7	ABR63913	Human C5a
30	551.5	21.6	350	7	ADJ68582	Human hea
31	551.5	21.6	350	8	ADO29205	Human GPC
32	551.5	21.6	350	8	ADQ19520	Human sof
33	551.5	21.6	350	8	ADR05362	Human ana
34	551.5	21.6	350	8	ADR67242	Human C3a
35	551.5	21.6	350	8	ADS15321	Human com
36	549.5	21.5	351	8	ADH58986	Mouse GPC
37	549.5	21.5	351	8	ADI53333	Mouse FPR
38	549.5	21.5	351	8	ADO29714	Mouse GPC
39	549.5	21.5	351	8	ADO57850	Mouse for
40	548.5	21.5	350	4	ABB56337	Non-endog
41	545.5	21.4	333	8	ADR05370	Mouse ana
42	545.5	21.4	347	8	ADO29206	Mouse GPC
43	543.5	21.3	371	6	ABJ38617	Mouse TIG
44	543.5	21.3	371	8	ADO29260	Mouse GPC
45	543.5	21.3	371	8	ADS74160	Mouse Res

ALIGNMENTS

RESULT 1

AAW42376

ID AAW42376 standard; protein; 482 AA.

XX AC AAW42376;

XX AC AAW42376;

DT 08-JUN-1998 (first entry)

XX DE Homo sapiens C3a receptor.

XX KW C3a receptor; treatment; diagnosis; atherosclerosis; chronic;

XX KW polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's;

XX KW disease; acute inflammatory disease; Crohn's disease; food; allergies;

XX KW non-bronchial allergies; osteoarthritis; osteoporosis; thyroid disease;

XX KW coronary heart disease.

XX OS Homo sapiens.

XX PN EP814158-A2.

XX PD 29-DEC-1997.

XX PF 17-JUN-1997; 97EP-00304250.

XX PR 17-JUN-1996; 96US-0019627P.

XX PA (SMIK) SMITHLINE BEECHAM CORP.

XX PI Ames RS, Bergsma DJ, Foley JJ, Kumar C, Sarau HM;

XX DR WPI; 1998-044336/05.

XX DR N-PSDB; AAU03250.

XX PT C3a receptor agonists, antibodies and antagonists - useful for diagnosis

XX PT of disease related to expression of C3a receptor, e.g. acute inflammatory

XX PT disease, atherosclerosis, chronic polyarthritis, etc.

XX PS Disclosure; Fig 1; 43pp; English.

XX CC The sequence is that of the C3a receptor. It can be used in a process for

XX CC diagnosing a disease or susceptibility to a disease related to expression

XX CC of the C3a receptor. This process involves analysing for the presence of

XX CC such a disease. C3a receptor-related diseases that can be detected by

XX CC this method comprise acute inflammatory disease, atherosclerosis, chronic

XX CC polyarthritis, systemic vasculitis, multiple sclerosis, Alzheimer's

XX CC disease, CNS inflammatory disease, Crohn's Disease, food allergies, non-

XX CC bronchial allergies, osteoarthritis, osteoporosis, thyroid disease,

CC coronary heart disease, Systemic Lupus Erythematosus SLE-associated
 CC nephritis, membranoproliferative GN, membranous nephritis, rheumatoid
 CC arthritis, Behcet's syndrome, juvenile rheumatoid arthritis, Sjogren's
 CC syndrome, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome,
 CC pemphigus/pemphigoid, phototoxic reactions, vasculitis, post-bypass
 CC syndrome, catheter reactions, sepsis, ARDS, anaphylaxis, transplant
 CC rejection, pre-eclampsia, atheroma, bowel inflammation, thyroiditis,
 CC infertility, susceptibility to pyogenic infections, glomerulonephritis,
 CC susceptibility to neisserial infections, recurrent subcutaneous swelling
 CC and mucosal oedema, and recurrent episodes of thrombosis/haemolysis. C3a
 CC receptor agonists, antagonists and antibodies can be used in the
 CC treatment of patients having need to inhibit or activate a C3a receptor
 XX
 SQ Sequence 482 AA;

Query Match 100.0%; Score 2552; DB 2; Length 482;
 Best Local Similarity 100.0%; Pred. No. 7.6e-252;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MASFSAEATNSTDLLSQPNWPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60

QY 61 FLHLTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLTAISLDR 120
 DB 61 FLHLTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLTAISLDR 120

QY 121 CLVVFKEPIWQCNHRNVGMACISGCIWVAFVFCIPVYREIFTDNNHRCGKFGLS 180
 DB 121 CLVVFKEPIWQCNHRNVGMACISGCIWVAFVFCIPVYREIFTDNNHRCGKFGLS 180

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QY 241 SLPRGSARLTQNLNYSNVFKPADVVPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
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QY 361 FRMQRGFPAKSQSTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 DB 361 FRMQRGFPAKSQSTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

QY 421 IALASANSFNPFLYALLGKDFRKARQSIQIGILEAAFSBELTRSTHCPNSNVISERNST 480
 DB 421 IALASANSFNPFLYALLGKDFRKARQSIQIGILEAAFSBELTRSTHCPNSNVISERNST 480

QY 481 TV 482
 DB 481 TV 482

RESULT 2
 AAU99102
 ID AAU99102 standard; protein; 482 AA.
 XX
 AC AAU99102;
 XX
 DT 04-SEP-2002 (first entry)
 XX Human anaphylotoxin C3a receptor.
 DE Human; C3a; receptor; nootropic; neuroprotective; antiparkinsonian;
 XX G protein-coupled receptor; GPCR; anaphylotoxin C3a receptor; AR;
 KW Alzheimer's disease; Parkinson's disease; cell signalling; proliferation;
 KW differentiation; leukocyte migration; gene transcription; vision; smell;
 KW neurotransmission; hormonal response; ulcerative colitis; diabetes;
 KW myocardial infarction; hypertension; asthma; bronchitis; pneumonia;
 KW Crohn's disease; rheumatoid arthritis; Hodgkin's disease; glioblastoma;

KW neurodegenerative disorder.
 XX Homo sapiens.
 XX WO200244737-A2.
 FN 06-JUN-2002.
 XX 29-NOV-2001; 2001WO-US045220.
 XX 29-NOV-2000; 2000US-0250251P.
 PR 30-NOV-2000; 2000US-0250452P.
 PR 17-OCT-2001; 2001US-0330036P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA Brown JP, Burmer GC, Roush CL, Morningstar DA;
 XX WPI; 2002-508526/54.
 DR N-PSDB; ABK86860.
 XX Isolated and purified composition useful for manufacture of medicament
 PT for inhibiting, preventing or treating Alzheimer's or Parkinson's
 PT disease, comprises G protein-coupled receptor anaphylotoxin C3a receptor.
 XX Disclosure; Fig 1; 112pp; English.

CC The invention discloses an isolated and purified composition including
 CC the G protein-coupled receptor (GPCR) anaphylotoxin C3a receptor (AR) and
 CC a pharmaceutically acceptable carrier for use in the manufacture of a
 CC medicament for inhibiting, preventing or treating Alzheimer's disease or
 CC Parkinson's disease. G protein-coupled receptors are involved in cell
 CC signalling and play key roles in cell proliferation, differentiation,
 CC leukocyte migration, gene transcription, vision, smell, neurotransmission
 CC and hormonal response. Compositions relating to the anaphylotoxin C3a
 CC receptor can also be used against ulcerative colitis, diabetes,
 CC myocardial infarction, hypertension, asthma, bronchitis, pneumonia,
 CC Crohn's disease, rheumatoid arthritis, Hodgkin's lymphoma, glioblastomas
 CC and other neurodegenerative disorders. The compositions include
 CC antibodies, agonists, antagonists, probes, antisense and gene therapies.
 CC The anaphylotoxin C3a receptor sequence can be used to manufacture
 CC medicaments able to reduce symptoms associated with Alzheimer's or
 CC Parkinson's disease in a human patient, by combining a pharmaceutically
 CC effective amount of an AR agonist or antagonist, a pharmaceutically
 CC acceptable carrier, adjuvant, excipient, buffer and diluent, and for
 CC detecting an increased possibility of Alzheimer's or Parkinson's disease.
 CC The sequence presented is the human anaphylotoxin C3a receptor

SQ Sequence 482 AA;

Query Match 100.0%; Score 2552; DB 5; Length 482;
 Best Local Similarity 100.0%; Pred. No. 7.6e-252;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASFSAEATNSTDLLSQPNWPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60
 DB 1 MASFSAEATNSTDLLSQPNWPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60

QY 61 FLHLTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLTAISLDR 120
 DB 61 FLHLTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLTAISLDR 120

QY 121 CLVVFKEPIWQCNHRNVGMACISGCIWVAFVFCIPVYREIFTDNNHRCGKFGLS 180
 DB 121 CLVVFKEPIWQCNHRNVGMACISGCIWVAFVFCIPVYREIFTDNNHRCGKFGLS 180

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 DB 241 SLPRGSARLTQNLNYSNVFKPADVVPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300

Qy 301 SSNSFYSELPGQFDYNYLQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
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 Qy 361 FRMQRGRPAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
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 Qy 421 IALASANSFNPFLYALGKDFRKKARQSIQGIILEAFSEELTRSTHCPSNNVIERNST 480
 Db 421 IALASANSFNPFLYALGKDFRKKARQSIQGIILEAFSEELTRSTHCPSNNVIERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 3

ABU79122 ID ABU79122 standard; protein; 482 AA.

AC ABU79122;

DT 18-JUN-2003 (first entry)

DE Chemoattractant protein.

KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.

OS Unidentified.

PN US2002177551-A1.

PD 28-NOV-2002.

PF 30-MAY-2001; 2001US-00870759.

PR 31-MAY-2000; 2000US-0208128P.

PA (TERM/) Terman D S.

PI Terman DS;

PP WPI; 2003-361759/34.

DR N-FSDB; ACA64730.

PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.

PS Example 2; Page; 167pp; English.

SS The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing

CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX SQ Sequence 482 AA;

Query Match 100.0%; Score 2552; DB 6; Length 482;
 Best Local Similarity 100.0%; Pred. No. 7.6e-252;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFSAEITNSTDLLSQPNNEPVLISVILSLTFLGLPGNGLVWVAGLKKQRTVNTIW 60
 Db 1 MASFSAEITNSTDLLSQPNNEPVLISVILSLTFLGLPGNGLVWVAGLKKQRTVNTIW 60
 Qy 61 FLHLLTADLLCCLSLPFLSLAHLAQOGMPYGRFLCKLIPSIIVLNMFASVLLTAISLDR 120
 Db 61 FLHLLTADLLCCLSLPFLSLAHLAQOGMPYGRFLCKLIPSIIVLNMFASVLLTAISLDR 120
 Qy 121 CLVVFKPIWCONHRNVGMACSIICGIWVAFVWCIPVYVREIFTDNHRCGYKFLSS 180
 Db 121 CLVVFKPIWCONHRNVGMACSIICGIWVAFVWCIPVYVREIFTDNHRCGYKFLSS 180
 Qy 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHPHTVPTVFPQTFORPSAD 240
 Db 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHPHTVPTVFPQTFORPSAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSXKIPSGFPIEDHETSPLDNSDAFLSLKLFPSA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSXKIPSGFPIEDHETSPLDNSDAFLSLKLFPSA 300
 Qy 301 SSNSFYSELPGQFDYNYLQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
 Db 301 SSNSFYSELPGQFDYNYLQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
 Qy 361 FRMQRGRPAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRPAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALGKDFRKKARQSIQGIILEAFSEELTRSTHCPSNNVIERNST 480
 Db 421 IALASANSFNPFLYALGKDFRKKARQSIQGIILEAFSEELTRSTHCPSNNVIERNST 480
 Qy 481 TV 482
 ||


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DR WPI; 2003-315783/31.
XX N-PSDB; ADF43378.
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 2; SEQ ID NO 662; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADF43378-ADP43378 represent GPCR's of the invention.
XX
XX Sequence 482 AA;
XX
XX Query Match 100.0%; Score 2552; DB 7; Length 482;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-252;
XX Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MASPSAETNSTDLISQPNWPPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60
XX |
XX 1 MASPSAETNSTDLISQPNWPPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60
XX |
XX 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
XX |
XX 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
XX |
XX 121 CLVVPKPIWCONHNRNVGMACISGCIWVAFVWVCIPVYVREIETTONHNRGKYGFLSS 180
XX |
XX 121 CLVVPKPIWCONHNRNVGMACISGCIWVAFVWVCIPVYVREIETTONHNRGKYGFLSS 180
XX |
XX 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVPTVFQQTQRPSPAD 240
XX |
XX 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVPTVFQQTQRPSPAD 240
XX |
XX 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGPFPIEDHETSPLDNDSDAFLSTHLKLPSPA 300
XX |
XX 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGPFPIEDHETSPLDNDSDAFLSTHLKLPSPA 300
XX |
XX 301 SSNSFYSESELPGQFDYNYLQGTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
XX |
XX 301 SSNSFYSESELPGQFDYNYLQGTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
XX |
XX 361 FMORGRPAKSQSKTFRVAVVAVFLVWVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
XX |
XX 361 FMORGRPAKSQSKTFRVAVVAVFLVWVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
XX |
XX 421 IALASANSFCNFPFLYALGKDFRKKARQSIQGLEAFAFSEBLTSTHCPSSNNVISERNST 480
XX |
XX 421 IALASANSFCNFPFLYALGKDFRKKARQSIQGLEAFAFSEBLTSTHCPSSNNVISERNST 480
XX |
XX 481 TV 482
XX
XX 481 TV 482
XX
XX RESULT 6
XX ADF43378
XX ID ADF43378 standard; protein; 482 AA.
XX
XX AC ADF43378;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX Chemoattractant polypeptide seq id 98.
XX
XX receptor; lipid-based tumour associated antigen; cytostatic;
XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
XX infectious disease; chemoattractant.

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XX Unidentified.
XX US2003157113-A1.
XX 21-AUG-2003.
XX
XX 28-DEC-2000; 2000US-00751708.
XX
XX 28-DEC-1999; 99US-0173371P.
XX (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 2003-787326/74.
XX N-PSDB; ADF43377.
XX
XX New receptor in a mammalian cell that inhibits regular activation by
XX receptors specific for lipid-based tumor associated antigens, useful for
XX treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 98; 151pp; English.
XX
XX The invention describes a receptor in a mammalian cell that inhibits
XX regular activation by receptors specific for lipid-based tumour
XX associated antigen. The receptor has cytostatic and antimicrobial
XX properties and is suitable for use in gene therapy. The receptors,
XX methods and compositions are useful for treating a neoplastic disease or
XX tumour (cancer), and infectious diseases. This sequence represents a
XX chemoattractant polypeptide, a cell surface moiety, the DNA of which can
XX be transfected into a cell with superantigen DNA to generate antitumour
XX immunity.
XX
XX Sequence 482 AA;
XX
XX Query Match 100.0%; Score 2552; DB 7; Length 482;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-252;
XX Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MASPSAETNSTDLISQPNWPPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60
XX |
XX 1 MASPSAETNSTDLISQPNWPPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60
XX |
XX 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
XX |
XX 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
XX |
XX 121 CLVVPKPIWCONHNRNVGMACISGCIWVAFVWVCIPVYVREIETTONHNRGKYGFLSS 180
XX |
XX 121 CLVVPKPIWCONHNRNVGMACISGCIWVAFVWVCIPVYVREIETTONHNRGKYGFLSS 180
XX |
XX 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVPTVFQQTQRPSPAD 240
XX |
XX 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVPTVFQQTQRPSPAD 240
XX |
XX 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGPFPIEDHETSPLDNDSDAFLSTHLKLPSPA 300
XX |
XX 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGPFPIEDHETSPLDNDSDAFLSTHLKLPSPA 300
XX |
XX 301 SSNSFYSESELPGQFDYNYLQGTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
XX |
XX 301 SSNSFYSESELPGQFDYNYLQGTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
XX |
XX 361 FMORGRPAKSQSKTFRVAVVAVFLVWVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
XX |
XX 361 FMORGRPAKSQSKTFRVAVVAVFLVWVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
XX |
XX 421 IALASANSFCNFPFLYALGKDFRKKARQSIQGLEAFAFSEBLTSTHCPSSNNVISERNST 480
XX |
XX 421 IALASANSFCNFPFLYALGKDFRKKARQSIQGLEAFAFSEBLTSTHCPSSNNVISERNST 480
XX |
XX 481 TV 482
XX
XX 481 TV 482
XX
XX RESULT 6
XX ADF43378
XX ID ADF43378 standard; protein; 482 AA.
XX
XX AC ADF43378;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX Chemoattractant polypeptide seq id 98.
XX
XX receptor; lipid-based tumour associated antigen; cytostatic;
XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
XX infectious disease; chemoattractant.

```

Db 481 TV 482

RESULT 7

ADRO5360

ID ADRO5360 standard; protein; 482 AA.

AC ADRO5360;

XX 04-NOV-2004 (first entry)

XX Human anaphylatoxin receptor C3aR.

DE Human; receptor; anaphylatoxin receptor; C3aR; white adipose tissue;

XX non-insulin dependent diabetes mellitus; obesity; metabolic disorder;

KW diabetes; endocrine abnormality; triglyceride storage disease;

KW Bardet-Biedl syndrome; Lawrence-Moon syndrome;

KW Prader-Labhart-Willi syndrome; lipid metabolism disorder; OPN; HAP;

KW MCP-1; osteopontin; haptoglobin; monocyte chemoattractant protein-1;

XX C3aR.

OS Homo sapiens.

XX US2004157253-A1.

XX 12-AUG-2004.

XX 26-JAN-2004; 2004US-00764649.

XX 07-FEB-2003; 2003US-0446041P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Xu H, Chen H, Barnes G;

XX WPI; 2004-614754/59.

XX N-PSDB; ADRO5359.

XX Identifying a nucleic acid molecule/polypeptide associated with a

XX metabolic disorder for use in treating obesity, comprises contacting a

XX sample with a compound that binds to anaphylatoxin receptor.

XX Claim 1; SEQ ID NO 2; 59pp; English.

XX The invention relates to identifying (M1) a nucleic acid molecule or

XX polypeptide associated with a metabolic disorder, comprises contacting a

XX sample with a compound which binds to the nucleic acids or their encoded

XX proteins representing human anaphylatoxin receptors C3aR and C5aR,

XX osteopontin (OPN), haptoglobin (HAP) or monocyte chemoattractant protein

XX (MCP-1) and detecting the presence of a nucleic acid molecule or protein

XX in the sample that binds to the compound. OPN, HAP and MCP 1 are all

XX modulated by C3aR and C5aR (both expressed in the white adipose tissue).

XX Also included are identifying (M2) a subject having a metabolic

XX disorder/at risk for developing a metabolic disorder (involving

XX contacting a sample obtained from the subject comprising nucleic acid

XX molecules or polypeptides with the above identified compound, and

XX detecting the presence of a nucleic acid molecule or polypeptide in the

XX sample that binds to the compound, where detection of a nucleic acid

XX molecule or polypeptide chosen from anaphylatoxin receptors C3aR, C5aR,

XX HAP, OPN or MCP-1, identifying (M3) a compound capable of treating a

XX metabolic disorder (involving assaying the ability of a compound to

XX modulate anaphylatoxin receptor C3aR or C5aR nucleic acid expression or

XX anaphylatoxin receptor C3aR or C5aR polypeptide activity, and identifying

XX the compound), identifying (M4) a compound capable of modulating an

XX anaphylatoxin receptor mediated metabolic activity (involving contacting

XX a composition comprising anaphylatoxin receptor with a test compound, and

XX assaying the ability of the test compound to modulate the expression of a

XX anaphylatoxin receptor nucleic acid or the activity of a anaphylatoxin

XX receptor polypeptide, thus identifying a compound capable of modulating

XX anaphylatoxin receptor mediated metabolic activity, where the

XX anaphylatoxin receptor comprises C3aR or C5aR) and modulating (M5) an

XX anaphylatoxin receptor mediated metabolic activity (involving contacting

CC a cell or a tissue expressing the anaphylatoxin receptor with a

CC anaphylatoxin receptor modulator, thus modulating the anaphylatoxin

CC receptor mediated metabolic activity, where the anaphylatoxin receptor is

CC C3aR or C5aR). (M1) is useful for identifying a nucleic acid molecule or

CC polypeptide associated with a metabolic disorder. (M2) is useful for

CC identifying subject having metabolic disorder, for detecting mRNA and

CC genomic DNA in the sample. (M3) is useful for identifying a compound

CC capable of treating a metabolic disorder such as obesity, diabetes

CC (especially non-insulin dependent), or insulin resistance. The metabolic

CC disorders treated by the compound include endocrine abnormalities,

CC triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon

CC syndrome, Prader-Labhart-Willi syndrome and disorders of lipid

CC metabolism. The present sequence represents human C3aR.

XX Sequence 482 AA;

Qy Query Match 100.0%; Score 2552; DB 8; Length 482;

Db Best Local Similarity 100.0%; Pred. No. 7.6e-252;

Qy Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MASFSATNSTDLSSQPNNEPPVILSNVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60

Qy 61 FLHLTLADLLCCLSLPFLSLAHLALQGGQPYGRFLCKLIPSIIVLNMFAFVLLTAISLDR 120

Db 61 FLHLTLADLLCCLSLPFLSLAHLALQGGQPYGRFLCKLIPSIIVLNMFAFVLLTAISLDR 120

Qy 121 CLVVFKEIWCQNHRNVGMACISICGCIWVAFVVCIPVFVYREIPTTNNHRCGKFGLS 180

Db 121 CLVVFKEIWCQNHRNVGMACISICGCIWVAFVVCIPVFVYREIPTTNNHRCGKFGLS 180

Qy 181 SLDPDFYGDPLENRSLENIIVQPPGEMNDRLDPSSFCOTNDHPWTVTFQPTQRPESAD 240

Db 181 SLDPDFYGDPLENRSLENIIVQPPGEMNDRLDPSSFCOTNDHPWTVTFQPTQRPESAD 240

Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSPGPIEDHETSPDLNDSDAFLSTHLKLPESA 300

Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSPGPIEDHETSPDLNDSDAFLSTHLKLPESA 300

Qy 301 SSNSFYSELPOGFODYNNIGQTTDDDDVPTPLVAITITLTVGFLPLPSVIMACYSFIV 360

Db 301 SSNSFYSELPOGFODYNNIGQTTDDDDVPTPLVAITITLTVGFLPLPSVIMACYSFIV 360

Qy 361 FRMQGRFAKSSQKTFERVAVVAVFLVCMTPYVHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Db 361 FRMQGRFAKSSQKTFERVAVVAVFLVCMTPYVHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Qy 421 IALASANSFNPFYALLGKDFRKKARQSQIQGILEAAFSBELTRSTHCPSSNNVISERNST 480

Db 421 IALASANSFNPFYALLGKDFRKKARQSQIQGILEAAFSBELTRSTHCPSSNNVISERNST 480

Qy 481 TV 482

Db 481 TV 482

RESULT 8

AAW02151

ID AAW02151 standard; protein; 482 AA.

XX AAW02151;

XX 08-DEC-1996 (first entry)

XX Human G-protein coupled receptor.

XX G-coupled receptor; asthma; transplant rejection; immunodeficiency;

XX severe infection; membrane protein.

XX Homo sapiens.

XX W09625432-A1.

XX PD 22-AUG-1996.
XX PF 17-FEB-1995; 95WO-US001992.
XX PR 17-FEB-1995; 95WO-US001992.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Li Y, Rosen CA;
XX DR WPI; 1996-393343/39.
XX DR N-PSDB; AAT36375.
XX DNA encoding G-protein coupled receptor - and antagonists and agonists,
PT useful to treat asthma and transplant rejection, and immunodeficiency and
PT severe infections, respectively.
XX
XX
PS Claim 1; Page 45-48; 63pp; English.
XX
XX This sequence of a human G-protein coupled receptor may be expressed in a
CC host cell using a vector, for production of the recombinant protein. An
CC antagonist of this G-protein coupled receptor (GPCR) can be used to
CC inhibit GPCR, to treat conditions relating to over-expression of the
CC receptor, e.g. asthma, SLE, transplant rejection and abnormal cell
CC growth. The agonist of GPCR can be used to stimulate GPCR, to treat
CC conditions relating to under-expression of the receptor, e.g.
CC immunodeficiency and severe infections, and for the prophylaxis of
CC bacteril and viral infections, and Csa immunoregulatory effect
CC stimulation
XX
XX Sequence 482 AA;

Query Match 99.7%; Score 2544; DB 2; Length 482;
Best Local Similarity 99.8%; Pred. No. 5e-251;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MASFSAEATNSTDLISQPNNEPVLISWVLSITLGLPGNGLVWAGLQKQRTVNTIW 60
Db 1 MASFSAEATNSTDLISQPNNEPVLISWVLSITLGLPGNGLVWAGLQKQRTVNTIW 60
Qy 61 FLHLTLADLLCLSLPFLSLAHALQGWYGRFLCKLPSIIVLNMPASVFLTLAISLDR 120
Db 61 FLHLTLADLLCLSLPFLSLAHALQGWYGRFLCKLPSIIVLNMPASVFLTLAISLDR 120
Qy 121 CLVVFKEPIWQNHNVGMACSIQGCIIWVAFVVCIPVYVYREIPTDNNHRCGYKFGLS 180
Db 121 CLVVFKEPIWQNHNVGMACSIQGCIIWVAFVVCIPVYVYREIPTDNNHRCGYKFGLS 180
Qy 181 SLDPYDFYGDPLENRSLENIQPGEMNDRLDPSFQNDHPVTVVTFQPTQRPASD 240
Db 181 SLDPYDFYGDPLENRSLENIQPGEMNDRLDPSFQNDHPVTVVTFQPTQRPASD 240
Qy 241 SLPGSARLTSONLYSNVFKADVVSPKIPSGFPTEDHETSPLONSDAFLSTHLKLPPSA 300
Db 241 SLPGSARLTSONLYSNVFKADVVSPKIPSGFPTEDHETSPLONSDAFLSTHLKLPPSA 300
Qy 301 SSNGFYSELPQGFQDYNNLQFTDDQVPTPLVAITITRLVWGLFLLPSVIMACYSPV 360
Db 301 SSNGFYSELPQGFQDYNNLQFTDDQVPTPLVAITITRLVWGLFLLPSVIMACYSPV 360
Qy 361 FMQGRFAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLITDPETPLGKTLMSWDHVC 420
Db 361 FMQGRFAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLITDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPLFYALLGKDFRKKAROSIQGLEAFAFSEBLTRSTHCPNNVISERNST 480
Db 421 IALASANSFNPLFYALLGKDFRKKAROSIQGLEAFAFSEBLTRSTHCPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 9
ABU62861
ID ABU62861 standard; protein; 482 AA.
XX
XX AC ABU62861;
XX
XX DT 11-SEP-2003 (first entry)
XX DE Putative mature human G protein coupled receptor.
XX KW G protein coupled receptor; GPCR; human; infection;
XX KW immunodeficiency disease; asthma; bronchial allergy;
XX KW chronic inflammation; systemic lupus erythematosus; gout;
XX KW transplant rejection; hypertension; abnormal cell growth;
XX KW neurological disease; receptor.
XX OS Homo sapiens.
XX
XX PN US2003022310-A1.
XX PD 30-JAN-2003.
XX PF 30-SEP-2002; 2002US-00259521.
XX PR 17-FEB-1995; 95WO-US001992.
XX PR 05-JUN-1995; 95US-00462314.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Li Y, Rosen CA;
XX
XX DR WPI; 2003-531445/50.
XX DR N-PSDB; ACD26620.
XX
XX PT New G-protein coupled receptor polypeptides and polynucleotide, useful
XX for screening receptor agonists and/or antagonists and/or receptor
XX ligands, in chromosome identification, and in for producing antibodies.
XX
XX PS Claim 1; Fig 1A-D; 26pp; English.

The invention describes an isolated polynucleotide (I) comprising a
sequence which: (a) encodes a polypeptide having a sequence of 482 amino
acids (II) given in the specification; (b) encodes a mature polypeptide
(c) is capable of hybridising to and which is at least 70% identical to
(a) or (b); or (d) a fragment of (a), (b) or (c). The G-protein coupled
receptors (GPCR) are useful for screening receptor agonists and/or
antagonists and/or receptor ligands. GPCR agonists are useful for
stimulating GPCR for the treatment of conditions related to the under-
expression of GPCR, e.g. bacterial or viral infection, immunodeficiency
diseases and severe infections. GPCR antagonists are useful for
inhibiting the action of GPCR for treating conditions associated with
over-expression of the GPCR, e.g. asthma, bronchial allergy, chronic
inflammation, systemic lupus erythematosus, gout, transplant rejection,
hypertension, abnormal cell growth, and neurological diseases. The GPCR
genes are also useful in diagnostic assays for detecting diseases or
susceptibility to diseases related to the presence of mutations in the
GPCR genes. These may also be used in chromosome identification. This is
polypeptides are useful as immunogens for producing antibodies. This is
the amino acid sequence of a putative mature human G protein coupled
receptor

Query Match 99.7%; Score 2544; DB 7; Length 482;
Best Local Similarity 99.8%; Pred. No. 5e-251;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MASFSAEATNSTDLISQPNNEPVLISWVLSITLGLPGNGLVWAGLQKQRTVNTIW 60
Db 1 MASFSAEATNSTDLISQPNNEPVLISWVLSITLGLPGNGLVWAGLQKQRTVNTIW 60

Qy 61 FLHLTLADLLCCLSLPFLSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
 Db 61 FLHLTLADLLCCLSLPFLSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
 Qy 121 CLVVFKEPIWQNHNVGMACSIQCGIIVVAFVVCIPVVFVREIFTTNDHNRCCGYKFLGSS 180
 Db 121 CLVVFKEPIWQNHNVGMACSIQCGIIVVAFVVCIPVVFVREIFTTNDHNRCCGYKFLGSS 180
 Qy 181 SLDPYDFYGDPLENRSLENIQVPGEMNDRLDPSSFCOTNDHPWTPTVFPQTQRPESAD 240
 Db 181 SLDPYDFYGDPLENRSLENIQVPGEMNDRLDPSSFCOTNDHPWTPTVFPQTQRPESAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGFPPIEDHETSPLDNDSDAFLSTHLKLPFSA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGFPPIEDHETSPLDNDSDAFLSTHLKLPFSA 300
 Qy 301 SSNSFYSELPGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
 Db 301 SSNSFYSELPGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
 Qy 361 FRMQRGFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPSSNNVISERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPSSNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 10

ID ADL22832 standard; protein; 482 AA.
 XX ADL22832;
 AC ADL22832;
 XX 20-MAY-2004 (first entry)
 XX Human C3a receptor.
 XX human; C3a receptor; antiasthmatic; antiallergic; cardiovascular;
 KW antiinflammatory; antiarthritic; receptor; antirheumatic; dermatological;
 KW immunosuppressive; vulnerary; antimicrobial; cytostatic.
 XX Homo sapiens.
 XX WO2004013287-A2.
 XX 12-FEB-2004.
 XX 31-JUL-2003; 2003WO-US023826.
 XX 02-AUG-2002; 2002US-0400057P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA;
 XX WPI; 2004-169327/16.
 DR N-PSDB; ADL22831.
 XX New isolated antibody that specifically binds C3a Receptor, useful for
 PT preventing, detecting, diagnosing, treating or ameliorating asthma,
 PT allergy, rheumatoid arthritis, systemic lupus erythematosus, arthritis or
 PT proliferative disorders.
 XX Claim 5; Page 178-180; 199pp; English.
 PS The present invention relates to an isolated antibody that specifically
 CC binds the C3a Receptor, and which is shown in the specification. The

CC antibody is useful for preventing, detecting, diagnosing, treating or
 CC ameliorating asthma, allergy, inflammatory or immune disorders. It is
 CC also useful for treating, preventing or ameliorating rheumatoid
 CC arthritis, systemic lupus erythematosus, arthritis, immunological
 CC hypersensitivities, physical trauma, organ transplant rejection,
 CC infectious diseases, cardiovascular disorders or proliferative disorders.
 CC The present sequence is the human C3a receptor.
 XX
 SQ Sequence 482 AA;

Query Match 99.7%; Score 2544; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 5e-251;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASFSASNTSTDLISQWNPFPVILSNVILSLFLLPGNGLVWVAGLKMORTVNTIW 60
 Db 1 MASFSASNTSTDLISQWNPFPVILSNVILSLFLLPGNGLVWVAGLKMORTVNTIW 60
 Qy 61 FLHLTLADLLCCLSLPFLSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
 Db 61 FLHLTLADLLCCLSLPFLSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
 Qy 121 CLVVFKEPIWQNHNVGMACSIQCGIIVVAFVVCIPVVFVREIFTTNDHNRCCGYKFLGSS 180
 Db 121 CLVVFKEPIWQNHNVGMACSIQCGIIVVAFVVCIPVVFVREIFTTNDHNRCCGYKFLGSS 180
 Qy 181 SLDPYDFYGDPLENRSLENIQVPGEMNDRLDPSSFCOTNDHPWTPTVFPQTQRPESAD 240
 Db 181 SLDPYDFYGDPLENRSLENIQVPGEMNDRLDPSSFCOTNDHPWTPTVFPQTQRPESAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGFPPIEDHETSPLDNDSDAFLSTHLKLPFSA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGFPPIEDHETSPLDNDSDAFLSTHLKLPFSA 300
 Qy 301 SSNSFYSELPGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
 Db 301 SSNSFYSELPGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
 Qy 361 FRMQRGFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPSSNNVISERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPSSNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 11

ADQ19275
 ID ADQ19275 standard; protein; 482 AA.
 XX ADQ19275;
 AC ADQ19275;
 XX 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2094.
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 XX Homo sapiens.
 XX WO2004048938-A2.
 XX 10-JUN-2004.
 XX 26-NOV-2003; 2003WO-US038193.
 XX 26-NOV-2002; 2002US-0429739P.
 XX

(PROT-) PROTEIN DESIGN LABS INC.

Aziz N, Ginsburg WM, Zlotnik A;

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 2094; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 482 AA;

Query Match 99.7%; Score 2544; DB 8; Length 482;

Best Local Similarity 99.8%; Pred. No. 5e-251;

Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASPSAETNSDLSQPNNEPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60

Db 1 MASPSAETNSDLSQPNNEPVILSMVILSLTFLGLPGNGLVWAGLQKQRTVNTIW 60

Qy 61 FLHITLADLLCCLSLPFLSLAHLAQGPYGRFLCKLIPSIIVLNMFAVFLTLAISLDR 120

Db 61 FLHITLADLLCCLSLPFLSLAHLAQGPYGRFLCKLIPSIIVLNMFAVFLTLAISLDR 120

Qy 121 CLVVFKEPIWQHNHNVGACISGCIWVAFVVCIPVYVREIETDHNRCYKFGLS 180

Db 121 CLVVFKEPIWQHNHNVGACISGCIWVAFVVCIPVYVREIETDHNRCYKFGLS 180

Qy 181 SLDPDFYDGPDLNRSLENIQPPGEMNDRLDPSFQTNHPTVPTVFQPTQFSPSAD 240

Db 181 SLDPDFYDGPDLNRSLENIQPPGEMNDRLDPSFQTNHPTVPTVFQPTQFSPSAD 240

Qy 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPIDHETSPIDNSDAFLSTHLKLPFA 300

Db 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPIDHETSPIDNSDAFLSTHLKLPFA 300

Qy 301 SSNPFYSELSFQGDYNYLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYSFIV 360

Db 301 SSNPFYSELSFQGDYNYLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYSFIV 360

Qy 361 FMQGRFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Db 361 FMQGRFAKQSQTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Qy 421 IALASANSFNPFYALLGKDFRKARQSIQIGILEAAFSBELTSTHCPSNNVLSERNST 480

Db 421 IALASANSFNPFYALLGKDFRKARQSIQIGILEAAFSBELTSTHCPSNNVLSERNST 480

Qy 481 TV 482

Db 481 TV 482

RESULT 12

AAW23367

ID AAW23367 standard; protein; 482 AA.

XX AC

XX DT

XX DE

XX KW

XX KW

XX OS

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AAW23367;

30-MAR-1998 (first entry)

Novel G-protein coupled receptor with an enlarged extracellular domain.

G-protein coupled receptor; enlarged extracellular loop;

inflammatory disease; asthma; chronic obstructive pulmonary disease;

cystic fibrosis; multiple sclerosis; antibody.

Homo sapiens.

Key Location/Qualifiers

Modified-site 9

Domain /note= "predicted N-glycosylation site"

Domain /note= "putative transmembrane domain"

Domain /note= "enlarged extracellular loop"

Modified-site 194

Domain /note= "predicted N-glycosylation site"

Domain /note= "putative transmembrane domain"

W09728188-A1.

07-AUG-1997.

30-JAN-1997; 97MO-US001736.

30-JAN-1996; 96US-0010808P.

(SCRI) SCRIPPS RES INST.

Ye RD;

WPI; 1997-402552/37.

N-PSDB; AAT64946.

G-protein-coupled receptor with enlarged extracellular domain - between fourth and fifth transmembrane domains, also nucleic acid and antibodies useful for treating inflammation and neurological disease.

Claim 4; Fig 1; 54pp; English.

The present sequence represents a novel G-protein coupled receptor that has an enlarged extracellular loop between the fourth and fifth transmembrane domains. Antibodies generated against the present protein revealed expression in a variety of tissues, including heart, lung and placenta. Diseases or conditions mediated by the G-protein coupled receptor can be treated by administering reagents such as the present sequence, antisense nucleic acid or antibodies generated against the receptor. Reagents may comprise a molecule binding to the receptor but not transmitting a signal across the cell membrane or reducing effectiveness of binding of the natural ligand. The reagent may also alter the interaction of the receptor with the G-protein with which it naturally reacts e.g. by altering phosphorylation sites in intracellular domains of the receptor. Inflammatory diseases or conditions mediated by the novel receptor which can be treated include e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, multiple sclerosis. The antibody can also be used to diagnose these diseases e.g. in brain tissue from patients with suspected neurological disease, especially Alzheimer's, in skin samples especially from patients with a suspected inflammatory disease or in haematopoietic cells. The nucleic acids are also useful in screening for compounds modulating gene expression by standard assays

Sequence 482 AA;

Query Match 99.6%; Score 2543; DB 2; Length 482;

Best Local Similarity 99.8%; Pred. No. 6.3e-251;

Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLSSOPWNEPPVILSWILSLTLLGLPGNGLVWVAGLKMORTVNTI 60
 Db 1 MASFAETNSTDLSSOPWNEPPVILSWILSLTLLGLPGNGLVWVAGLKMORTVNTI 60
 QY 61 FLHLLTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120
 Db 61 FLHLLTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120
 QY 121 CLVVFKEPIWQNHNVGMACSGICGCIWVAVFVWCIPVYVREIFTTDNHNRGKYGFLSS 180
 Db 121 CLVVFKEPIWQNHNVGMACSGICGCIWVAVFVWCIPVYVREIFTTDNHNRGKYGFLSS 180
 QY 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPTVPTVQPTQRPASD 240
 Db 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPTVPTVQPTQRPASD 240
 QY 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPESA 300
 QY 301 SSNSFYSELPGQFQDYNLGQFTDDOVPPLVAITITRLVVGFLPLSPVIMACYSFIV 360
 Db 301 SSNSFYSELPGQFQDYNLGQFTDDOVPPLVAITITRLVVGFLPLSPVIMACYSFIV 360
 QY 361 FRMQRGRFAKSQSKTRFVAVVAVFLVWCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTRFVAVVAVFLVWCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSFCNPFYALLGKDFRKARQSIQIGILEAAFPSEELTRSTHCPSNNVISERNST 480
 Db 421 IALASANSFCNPFYALLGKDFRKARQSIQIGILEAAFPSEELTRSTHCPSNNVISERNST 480
 QY 481 TV 482
 Db 481 TV 482
 RESULT 13
 ID ADD46294 standard; protein; 482 AA.
 AC ADD46294;
 DT 29-JAN-2004 (first entry)
 XX Human Protein Q16581, SEQ ID NO 11969.
 DE Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WO2003016475-A2.
 PN 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; Q16581.
 XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 482 AA;

Query Match 99.6%; Score 2543; DB 7; Length 482;
 Best Local Similarity 99.8%; Pred. No. 6.3e-251;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASFAETNSTDLSSOPWNEPPVILSWILSLTLLGLPGNGLVWVAGLKMORTVNTI 60
 Db 1 MASFAETNSTDLSSOPWNEPPVILSWILSLTLLGLPGNGLVWVAGLKMORTVNTI 60
 QY 61 FLHLLTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120
 Db 61 FLHLLTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120
 QY 121 CLVVFKEPIWQNHNVGMACSGICGCIWVAVFVWCIPVYVREIFTTDNHNRGKYGFLSS 180
 Db 121 CLVVFKEPIWQNHNVGMACSGICGCIWVAVFVWCIPVYVREIFTTDNHNRGKYGFLSS 180
 QY 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPTVPTVQPTQRPASD 240
 Db 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPTVPTVQPTQRPASD 240
 QY 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPESA 300
 QY 301 SSNSFYSELPGQFQDYNLGQFTDDOVPPLVAITITRLVVGFLPLSPVIMACYSFIV 360
 Db 301 SSNSFYSELPGQFQDYNLGQFTDDOVPPLVAITITRLVVGFLPLSPVIMACYSFIV 360
 QY 361 FRMQRGRFAKSQSKTRFVAVVAVFLVWCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTRFVAVVAVFLVWCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSFCNPFYALLGKDFRKARQSIQIGILEAAFPSEELTRSTHCPSNNVISERNST 480
 Db 421 IALASANSFCNPFYALLGKDFRKARQSIQIGILEAAFPSEELTRSTHCPSNNVISERNST 480
 QY 481 TV 482
 Db 481 TV 482

RESULT 14
 ID ADO29203
 XX ADO29203 standard; protein; 482 AA.
 AC ADO29203;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human GPCR C3AR1, SEQ ID NO:304.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2004/0000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028226.
 XX
 PR 09-SEP-2003; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461323P.
 XX
 PA (PRIM-) PRIMAL INC.
 XX
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 DR WPI; 2004-390329/36.
 DR N-PSDB; ADO29820.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 304; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or

CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 482 AA;

Query Match 99.6%; Score 2543; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 6.3e-251;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASFSATNSTDLISQPNWEPVILSMVLSITFLGLPGNGLVWVAGLKMQRVTWIIW 60
 DB 1 MASFSATNSTDLISQPNWEPVILSMVLSITFLGLPGNGLVWVAGLKMQRVTWIIW 60
 QY 61 FLHLLTADLLCCLSLPFLSLAHLAQGGQWPGYGRFLCKLIPSIIVLNMFPASVFLLTALSIDR 120
 DB 61 FLHLLTADLLCCLSLPFLSLAHLAQGGQWPGYGRFLCKLIPSIIVLNMFPASVFLLTALSIDR 120
 QY 121 CLVVFKEPIWQNHNVGMACISICGCIWVAFVVCIPFVYREIFTTDNHRCGYKFGGLSS 180
 DB 121 CLVVFKEPIWQNHNVGMACISICGCIWVAFVVCIPFVYREIFTTDNHRCGYKFGGLSS 180
 QY 181 SLDYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPHWVTVTFQPTFORPSAD 240
 DB 181 SLDYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPHWVTVTFQPTFORPSAD 240
 QY 241 SLPRGSARLTSONLYSNVFKPADVVSPKIPSGFPEDHETSPLDNDSDAFLSLTHLKLFPSPA 300
 DB 241 SLPRGSARLTSONLYSNVFKPADVVSPKIPSGFPEDHETSPLDNDSDAFLSLTHLKLFPSPA 300
 QY 301 SSNSFYSELSPQGFQDYNNLGQFTDDQVTPPLVAITITRLVWGFLPSVIMIACYSTIV 360
 DB 301 SSNSFYSELSPQGFQDYNNLGQFTDDQVTPPLVAITITRLVWGFLPSVIMIACYSTIV 360
 QY 361 FRMQRGRFAKQSQTFRVAVVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 DB 361 FRMQRGRFAKQSQTFRVAVVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSCEFNPFLYALLGKDFRKKARQSIQIGILEAAFPSELTSTHCPSSNNVISERNST 480
 DB 421 IALASANSCEFNPFLYALLGKDFRKKARQSIQIGILEAAFPSELTSTHCPSSNNVISERNST 480
 QY 481 TV 482
 DB 481 TV 482

RESULT 15
 ADO29204
 ID ADO29204 standard; protein; 482 AA.

XX ADO29204;

DT 16-DEC-2004 (first entry)

DE Complement component 3a receptor 1, C3AR1, SEQ ID 2.

XX Antianemic; Antiinflammatory; Cardiovascular; Gastrointestinal;
 KW Hepatotropic; Neuroprotective; Respiratory; Gene therapy;
 KW cardiovascular disease; Gastrointestinal disease; liver disease;
 KW inflammatory disease; hematological disease; respiratory disease;
 KW neurological disease; complement component 3a receptor 1; C3AR1;
 KW C3a anaphylatoxin receptor; G protein coupled receptor; human.

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 203 /note= "Encoded by CCG"
 FT
 XX WO2004082566-A2.
 XX 30-SEP-2004.
 XX PD
 XX PF 04-MAR-2004; 2004WO-EP002173.
 XX PR 17-MAR-2003; 2003EP-00005468.
 XX PA (FARB) BAYER HEALTHCARE AG.
 XX PI Golz S, Brueggemeier U, Summer H;
 XX DR WPI; 2004-690917/67.
 XX DR N-PSDB; ADS09203.
 XX PT Screening for agents for treating e.g., cardiovascular, liver, or
 PT neurological diseases, comprises detecting agents which modulate the
 PT expression or activity of the G protein coupled receptor C3AR1
 PT (complement component 3a receptor 1).
 XX PS Disclosure; SEQ ID NO 2; 121bp; English.
 XX

Search completed: April 13, 2005, 09:43:19
 Job time : 178 secs

The present invention relates to a method (M1) for screening for
 therapeutic agents for treating a cardiovascular, gastrointestinal,
 liver, inflammatory, hematological, respiratory or neurological disease
 in a mammal. The method comprises detecting binding of a test compound to
 a complement component 3a receptor 1 (C3AR1) polypeptide (ADS09204) or
 polynucleotide (ADS09203), or detecting an affect on C3AR1 activity.
 C3AR1 (also known as C3a anaphylatoxin receptor, is a seven transmembrane
 G protein coupled receptor. Compositions comprising agents identified by
 M1 or C3AR1 polynucleotides and polypeptides are useful for treating the
 diseases. The present sequence is human C3AR1, used in the method of the
 invention.

SQ Sequence 482 AA;

Query Match 99.6%; Score 2543; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 6.3e-251;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 MAFSAETNSTDLISQPNBPPVILSMVILSLTLLGPGNLVWVAGLKMQRVTNTIW 60
 1 MAFSAETNSTDLISQPNBPPVILSMVILSLTLLGPGNLVWVAGLKMQRVTNTIW 60
 61 FLHITLADLCCLSLPSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTLAISLDR 120
 61 FLHITLADLCCLSLPSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTLAISLDR 120
 121 CLVVFKEIWCQNHNHNVGACISGCIWVAFVVCIPVYVREIPTTDNHNRCGYKFGLS 180
 121 CLVVFKEIWCQNHNHNVGACISGCIWVAFVVCIPVYVREIPTTDNHNRCGYKFGLS 180
 181 SLDPYDFYGPDLNRSLENIQVPGEMNDRLDSSQFOTNDHPWTVPTVQPTQFORSAD 240
 181 SLDPYDFYGPDLNRSLENIQVPGEMNDRLDSSQFOTNDHPWTVPTVQPTQFORSAD 240
 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGPIEDHETSPLDSDAFSLTKLPFSA 300
 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGPIEDHETSPLDSDAFSLTKLPFSA 300
 301 SSNSFYSESLPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 301 SSNSFYSESLPQGFQDYINLQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPVPHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPVPHIFGVLSLLTDPETPLGKTLMSWDHVC 420

QY 421 IALASANSCEFNPFLYALLGKDFRKARQSIQIGILEAAAFSEELTRSTHCPSPNNVISERNST 480
 DB 421 IALASANSCEFNPFLYALLGKDFRKARQSIQIGILEAAAFSEELTRSTHCPSPNNVISERNST 480
 QY 481 TV 482
 DB 481 TV 482

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 09:39:42 ; Search time 43 Seconds
(without alignments)
836.764 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 2552

Sequence: 1 MASFSASTNTDLSQPNW.....TRSTHCPNNVNSRSTTV 482

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2544	99.7	482	2	US-08-876-874-2
2	2543	99.6	482	4	US-09-117-440-2
3	2535	99.3	482	4	US-09-826-509-465
4	551.5	21.6	350	2	US-08-458-970A-9
5	548.5	21.5	350	4	US-09-826-509-467
6	510.5	20.0	304	1	US-08-118-270-35
7	510.5	20.0	304	5	PCT-US93-08528-35
8	509.5	20.0	351	4	US-09-944-807-2
9	508.5	19.9	364	2	US-08-458-970A-10
10	508.5	19.8	351	4	US-09-826-509-501
11	477.5	18.7	350	3	US-07-759-568-3
12	475.5	18.6	350	3	US-08-430-286A-8
13	475.5	18.6	350	4	US-09-826-509-499
14	449.5	17.6	355	4	US-09-170-496D-2
15	446.5	17.5	355	4	US-09-170-496D-164
16	444	17.4	395	3	US-08-981-825-6
17	444	17.4	395	3	US-09-480-784-6
18	434	17.0	315	1	US-08-118-270-34
19	434	17.0	315	5	PCT-US93-08528-34
20	422.5	16.6	337	4	US-09-693-242-2
21	419.5	16.4	337	4	US-09-786-442B-2
22	387.5	15.2	356	4	US-09-170-496D-246
23	386.5	15.1	356	4	US-09-170-496D-270
24	372.5	14.6	355	2	US-08-458-970A-2
25	371.5	14.6	400	3	US-08-889-108-8
26	371.5	14.6	400	5	PCT-US94-10358-8
27	370	14.5	392	4	US-09-826-509-547

28	370	14.5	400	3	US-09-351-198-2	Sequence 2, Appli
29	370	14.5	400	3	US-09-113-426-2	Sequence 2, Appli
30	370	14.5	400	4	US-09-826-509-545	Sequence 545, App
31	370	14.5	415	4	US-08-405-271A-20	Sequence 20, Appli
32	368	14.4	400	3	US-08-188-275A-2	Sequence 2, Appli
33	364	14.3	391	2	US-08-454-549-3	Sequence 3, Appli
34	364	14.3	391	3	US-08-454-552-3	Sequence 3, Appli
35	364	14.3	398	1	US-08-149-093A-5	Sequence 5, Appli
36	364	14.3	398	2	US-08-911-245-5	Sequence 5, Appli
37	364	14.3	398	3	US-08-889-108-2	Sequence 2, Appli
38	364	14.3	398	3	US-08-120-601B-2	Sequence 2, Appli
39	364	14.3	398	3	US-08-188-275A-3	Sequence 3, Appli
40	364	14.3	398	3	US-08-387-707-16	Sequence 16, Appli
41	364	14.3	398	3	US-09-510-473-5	Sequence 5, Appli
42	364	14.3	398	3	US-09-351-198-3	Sequence 3, Appli
43	364	14.3	398	3	US-09-113-426-3	Sequence 3, Appli
44	364	14.3	398	4	US-08-405-271A-16	Sequence 16, Appli
45	364	14.3	398	5	PCT-US94-10358-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-876-874-2
; Sequence 2, Application US/08876874
; Patent No. 5942405
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert
; APPLICANT: Bergsma, Derk
; APPLICANT: Foley, James
; APPLICANT: Kumar, Chandrika
; APPLICANT: Sarau, Henry
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
; TITLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/876,874
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,627
; FILING DATE: 16-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: P50501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-876-874-2

Query Match 99.7%; Score 2544; DB 2; Length 482;

Best Local Similarity 99.8%; Pred. No. 2.4e-209;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60
DB 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60

QY 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120
DB 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120

QY 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180
DB 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180

QY 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240
DB 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240

QY 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPFSA 300
DB 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPFSA 300

QY 301 SSNSFYSELPOGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLSPVIMIACTSYFIV 360
DB 301 SSNSFYSELPOGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLSPVIMIACTSYFIV 360

QY 361 FRMORGRFAKSQSKTFVAVVAVFVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
DB 361 FRMORGRFAKSQSKTFVAVVAVFVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

QY 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEELTRSTHCPSSNNVISERNST 480
DB 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEELTRSTHCPSSNNVISERNST 480

QY 481 TV 482
DB 481 TV 482

RESULT 2
US-09-117-440-2
; Sequence 2, Application US/09117440
; Patent No. 6521418
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; FILE REFERENCE: SCR20418
; CURRENT APPLICATION NUMBER: US/09/117,440
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: PCT/US97/01736
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: 60/010,808
; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Human
US-09-117-440-2

Query Match 99.6%; Score 2543; DB 4; Length 482;
Best Local Similarity 99.8%; Pred. No. 2.9e-209;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60
DB 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60

QY 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120
DB 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120

DB 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120
QY 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180
DB 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180

QY 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240
DB 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240

QY 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPFSA 300
DB 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPFSA 300

QY 301 SSNSFYSELPOGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLSPVIMIACTSYFIV 360
DB 301 SSNSFYSELPOGQDYNNLQFTDDDDQVPTPLVAITITRLVVGFLPLSPVIMIACTSYFIV 360

QY 361 FRMORGRFAKSQSKTFVAVVAVFVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
DB 361 FRMORGRFAKSQSKTFVAVVAVFVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

QY 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEELTRSTHCPSSNNVISERNST 480
DB 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEELTRSTHCPSSNNVISERNST 480

QY 481 TV 482
DB 481 TV 482

RESULT 3
US-09-826-509-465
; Sequence 465, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: Aken-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 465
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-465

Query Match 99.3%; Score 2535; DB 4; Length 482;
Best Local Similarity 99.6%; Pred. No. 1.4e-208;
Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60
DB 1 MASFAETNSTDLLSQPNNEPPIVLSWILSTFLGLPGNGLVWVAGLKMORTVNTIW 60

QY 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120
DB 61 FLHLLTADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTLAISLDR 120

QY 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180
DB 121 CLVVFKEPIWQNHNRVGMACSGICGCIWVAVFVVCIPVYVREIFTTNDHNRCCGKFGGLSS 180

QY 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240
DB 181 SLDPDFDVGDDPLENRSLENIQVPPGEMNDRLDPSFQTNHDPWTVPTVFPQTFORPSAD 240

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Db 181 SLIDYDFYGDPLENRSLENIYVQPGEMDRDLPSSFQNDHPWTVTFQOTQORPSAD 240
Qy 241 SLPRGSARLTONLYSNVFKPADVVSPKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Db 241 SLPRGSARLTONLYSNVFKPADVVSPKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Qy 301 SSNSFYSELPGFQDYNNLGOFTDDDDQVPTPLVAITITRLVVGGLPSVIMIACTSYIV 360
Db 301 SSNSFYSELPGFQDYNNLGOFTDDDDQVPTPLVAITITRLVVGGLPSVIMIACTSYIV 360
Qy 361 FRMQRGFAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FRMQRGFAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFLYALGKDFRKAQSIQCIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFLYALGKDFRKAQSIQCIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

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RESULT 4

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US-08-458-970A-9
; Sequence 9, Application US/08458970A
; Patent No. 5861272
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: C5a Receptor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-970A-9

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Query Match 21.6%; Score 551.5; DB 2; Length 350;
Best Local Similarity 27.4%; Pred. No. 3.8e-39;
Matches 124; Conservative 60; Mismatches 112; Indels 157; Gaps 6;

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Qy 22 PVILSMVLSLTFLLGLPGNLVWVAGLKMQRVTNTWFLHLTLADLLCCLSLPFSLAH 81

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Db 36 PDILALVIFAVFLVGLGNALVWVVTAFEAQRITINAIWFLNLAVADFLSCALPILPTS 95
Qy 82 LALQGMYPGRFLCKLIPSIIVLNMFAVFLTLTAISLDRCLVWFKPIWQCNHRNVGMACS 141
Db 96 IVQHHWPFPGGAACSIILPSLILNMYASILLATISADRFLLVFKPIWQCNFRAGLAWI 155
Qy 142 ICGCIWVAVFVWCIPVFVYREIFTTDNHNRGKFGLSLSSLDYDFYGDPLENRSLENI 201
Db 156 ACAVANGALLLTIPSLYR----- 175
Qy 202 QPGEMDRDLPSSFQNDHPWTVTFQOTQORPSADSPLRGSARLTONLYSNVFKP 261
Db 176 -----VREYF----- 182
Qy 262 ADVVSPKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSASSNPYSESELPGFQDYNNLG 321
Db 183 ----PPKVLGV-----LTRST 466
Qy 322 QFTDDQVPTPLVAITITRLVVGGLPSVIMIACTSYIVFMQRGFAKQSKTFRVAVV 381
Db 191 DYSHDKRER---AVAIIVLVLGLFWPLLTITICTYITILLRTWSRRATRS-TKTLKVVA 246
Qy 382 VVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFLYALGKD 441
Db 247 VVASFPFVLPYQVTGIMSFLEPSSPTFLLNKLKLSLCVSPAYINCCINFIIVVAGQG 306
Qy 442 FRKARQSIQCIIEAFAFSE-----LTRST 466
Db 307 FQGRLRKSLPILLNVLTEESVVRKSKSFTRST 339

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RESULT 5

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US-09-826-509-467
; Sequence 467, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 467
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-467

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Query Match 21.5%; Score 548.5; DB 4; Length 350;
Best Local Similarity 27.4%; Pred. No. 6.9e-39;
Matches 124; Conservative 60; Mismatches 112; Indels 157; Gaps 6;

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Qy 22 PVILSMVLSLTFLLGLPGNLVWVAGLKMQRVTNTWFLHLTLADLLCCLSLPFSLAH 81
Db 36 PDILALVIFAVFLVGLGNALVWVVTAFEAQRITINAIWFLNLAVADFLSCALPILPTS 95
Qy 82 LALQGMYPGRFLCKLIPSIIVLNMFAVFLTLTAISLDRCLVWFKPIWQCNHRNVGMACS 141
Db 96 IVQHHWPFPGGAACSIILPSLILNMYASILLATISADRFLLVFKPIWQCNFRAGLAWI 155
Qy 142 ICGCIWVAVFVWCIPVFVYREIFTTDNHNRGKFGLSLSSLDYDFYGDPLENRSLENI 201
Db 156 ACAVANGALLLTIPSLYR----- 175

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QY 202 OPPGEMNDRLDPSPTQNDHPWTVTFQPOQTFORPSADSLPRGSARLTSONLYSNVFKP 261
 Db 176 -----VREEYF----- 182
 QY 262 ADVSPKIPSPPIEDHETSPLDNSDAFLSTHLKLPSPASSNSFYSELPOGFQDYNNLG 321
 Db 183 -----PPKVLGV----- 190
 QY 322 OPTDDOQVPTPLVAITITRLVVGFLPLSPVIMACYSFIVFMRQGRFAKSQSKTRVAVV 381
 Db 191 DYSHDKRER---AVALVRLVGLFWPLLTITCYTFILLRTWSRRATRS-TKTKKVVVA 246
 QY 382 VVAVFLVCTWPHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFLYALLGKD 441
 Db 247 VVASFFIWLFPYQVTGIMMSFLEPSSPTFLLLNKLDLSLVCVSFAYINCCINPIIYVWAGQ 306
 QY 442 FRKAROSIQIGILEAAFSSE-----LTRST 466
 Db 307 FGRLRKLSPSLRLNVLTEESVVRRESKSFTRST 339

RESULT 6
 US-08-118-270-35
 ; Sequence 35, Application US/08118270
 ; Patent No. 5508384
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Randall B.
 ; APPLICANT: Schuster, David I.
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/118,270
 ; FILING DATE: 09-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,236
 ; FILING DATE: 10-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Townsend, Kevin G.
 ; REGISTRATION NUMBER: 34,033
 ; REFERENCE/DOCKET NUMBER: MURPHY=2A
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 304 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-118-270-35

Query Match 20.0%; Score 510.5; DB 1; Length 304;
 Best Local Similarity 25.9%; Pred. No. 1e-35;
 Matches 117; Conservative 59; Mismatches 107; Indels 169; Gaps 7;
 QY 24 ILSNVLSTLFLGLPGNGLVWVAGLKMORTVNTIWLHLTLADLCLSLPFLSLAHLA 83
 Db 2 ILALVFAVFLVGLGNALVWVWTAFAEAKRTINAIWFLNIAVADFLSLALPILFTSIV 61

QY 84 LQOQPYGRFLCKLPSIIIVLNMFAVPELLFAISLDRLCLVVKPITWQNHNVGMACSTIC 143
 Db 62 QHHWPFPGGAACSLPSLLILNMYASILLATISADRELLVFKPITWQNFAGLAWIAC 121
 QY 144 GCIWVAFMVICPVFVYREIFTTDNHNRCYKFGLSLSDYDFDYGDPLENRSLENIQV 203
 Db 122 AVANGIALLLTIPFLYR----- 139
 QY 204 PGEMNDRLDPSPTQNDHPWTVTFQPOQTFORPSADSLPRGSARLTSONLYSNVFKPAD 263
 Db 140 -----VREEYF----- 146
 QY 264 VVSPKIPSGPIEDHETSPLDNSDAFLSTHLKLPSPASSNSFYSELPOGFQDYNNLGQF 323
 Db 147 --PPKVLGC-----LTRST 466
 QY 324 TDDQVPTPLVAITITRLVVGFLPLSPVIMACYSFIVFMRQGRFAKSQSKTRVAVV 383
 Db 157 SHDKRER---AVALVRLVGLFWPLLTITCYT-----TRSTKLVVAVV 201
 QY 384 AVFLVCTWPHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFLYALLGK-DF 442
 Db 202 ASFFIWLFPYQVTGIMMSFLEPSSPTFLLLNKLDLSLVCVSFAYINCCINPIIYVWAGQ 261
 QY 443 RKAROSIQIGILEAAFSSE-----LTRST 466
 Db 262 QGRRLKSLPLRLNVLTEESVVRRESKSFTRST 293

RESULT 7
 PCT-US93-08528-35
 ; Sequence 35, Application PC/TUS9308528
 ; GENERAL INFORMATION:
 ; APPLICANT: New York University
 ; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 ; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 ; NUMBER OF SEQUENCES: 348
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/08528
 ; FILING DATE: 09-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/943,236
 ; FILING DATE: 10-SEP-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Townsend, Kevin G.
 ; REGISTRATION NUMBER: 34,033
 ; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 304 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT-US93-08528-35

D	b	118	FIALDR	CIVLHPWAQNHRTVSLAMKVI	GVPWILALVLPLVFLTVITPI	PNGDTYCT	177
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Q	y	174	YKFG	LSSLDYPDFGDPLENR	SLENIVQPCEMNDRLDPSFQTNDHPWTVTVF	QPOPT	233
			:			-SW-	
D	b	178	FNEA	-----			183
Q	y	234	FORP	ADSLPRGSARLTSONLYSNVFKPADVVSPKI	PGFPIDHETSPLONSDAFLSTH	293	
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D	b	184	-----		--GGTPEE--		R 190
Q	y	294	LKLPPS	ASSNSFYEBELPQGFDYYNLGQFTDDQVPTPLVAITITRLVVGFLLP	SVMI	353	
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D	b	191	LKV	-----	---ATMLTARGIIRFVIGFSLPMSIVA	218	
Q	y	354	ACYSFI	VFRMQRGRFAKSQKTFRVAVVAVLVLCWTPYHI	-----	F 396	
			::	::	::	::	::
D	b	219	ICYGLIAAKITHKGMIKS-SRPKEVLTA	VASFICWFPPQIVALLGTVMWKEMLFYGYK	277		
Q	y	397	GVL	SLLTDPTPLGKTLMSDHWCI	ALASANCENPFYALLGKDFRKAQRSIQIGILEA	456	
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D	b	278	KIIDLVNPTS	-----	---SLAFFNSCLNPMLYVVFVGQDFRELRHTLSPTS	323	
Q	y	457	AFSEELTRTHCPSNNVISERN	S 479			
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D	b	324	ALS	ED-----	SAPTNDTAANSAS	341	

RESULT 11
US-07-759-568-3
; Sequence 3, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murby, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 861 3000

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/ TELEFAX: 202-822-0944
/
/ TELEX: 6714627 CUSH
/
/ INFORMATION FOR SEQ ID NO: 3:
/
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 350 amino acids
/   TYPE: AMINO ACID
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: peptide
/
US-07-759-568-3

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; LENGTH: 350
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-826-509-499
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Query Match 18.6%; Score 475.5; DB 4; Length 350;
Best Local Similarity 25.1%; Pred. No. 1.2e-32;
Matches 122; Conservative 73; Mismatches 125; Indels 167; Gaps 10;

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Db 58 TVTITISYLNLAADFCTSTLTFPFWRKAMCGHWPFGWFLCKFTFTIVDLNLFSGVFLIA 117
QY 115 AISLDRCLVFKPIWCQHNHNVGMACISGCIGWYVAFVMCIPFVYREIFTTNDHNRCGY 174
Db 118 LIALDRCCVCLHPVWTOHRTVSLAKKVIITGPWVMAILLTLPLVII-----162
QY 175 KFGLSLSDLPDFYGDPLENRSLENIYQPPCEMNDRLDPSPFOINDHPWTVPTVFPQPTF 234
Db 163 -----RVTVVPK-----170
QY 235 QRSADSLPGSARLTSONLYSNVFKPADVVPKIPSGFTIEDHETSFLDNSDAFLSTHL 294
Db 171 -----TGTVACT-----177
QY 295 KLFPASASSNFYESELPOGQDYVNLGQTTD--DOVPTPLVAIT---ITRLVVGFLPLPS 349
Db 178 -----FNPSWTDNPKERINVAAMLTVRGILFRFIIGFSAPM 214
QY 350 VIMACYSFIVRMORGRFAKOSKTPRVAVVVVAVELVCWTPYPIHFGVLSLLTDPSTPL 409
Db 215 SIVAVSYGLIATIKHKQGLIKS--SRPKVLVSFAAAFFLCWSYQVVALLIATVRIRELLQ 273
QY 410 G--KTLMSDHWDCIALASANSFCNPELYALLGDKDFRKARQSTQGLEAAFSBELTRSTH 467
Db 274 GMYKETGIADVTSALAFNFNSCLNPMPLYFMWGQDFRERLIHALPASLERALTEDSTQTS 333
QY 468 CPNSNNVI 474
Db 334 TATNSTL 340

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RESULT 14
US-09-170-496D-2
; Sequence 2, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-2

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Db	100	NIHWPFGIWLCKANSFTQALNNFASVPLTWSLDRYIHLHPVL	159
QY	145	CIWVAVFWCITPVFYRIEFTTDNNHRCGYKGLSSLDYDFYGDPL	204
Db	160	FIWLLASLIGGFALYFRDTEVFNHNLTC	187
QY	205	GEMNDRLDPPSSFOQNDHPWTVPTVFPQTFORPSSADSLPRGSAR	264
Db	188	YNNFQKHDPDLTL	200
QY	265	VSPKIPSGFPDIEDHETSPDNDSDAFLSTHLKLPFSASSNSFY	324
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QY	325	DDQVPTPLVAITITRLVVGELLPSVIMIACTVIFRMQGRFRAKS	384
Db	205	VLTWKVIIGYLPFLTMSICYCLCIFKVK-RITVLISSRFHTLIVV	253
QY	385	VFLVCWTPYHIFGVLSLLTOPETPLGKTLMSDWCVIALASANS	444
Db	254	AFVVCWTPYHLFSIWELTTHNSYSHVMQAGIPLSTGLAFLNS	313
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Db	314	RFRSSVAEILKYTLWE-----VSC--SGTVSEOLRNSET	345

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US-09-170-496D-164
; Sequence 164, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endog
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-164

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Query Match	17.5%	Score 446.5;	DB 4;	Length 355;
Best Local Similarity	24.4%;	Pred. No. 3.7e-30;		
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Db	100	NFHWPFGIWLCKANSFTAQLNMFASVFFLTIVISLDHYIHLHPVLSHRHTLKNLSLIVII	159	
QY	145	CIWVAFVVCIPVVFVREIFTTNDHNRCKGKGLSSSLDYPDFVGDPLENRSLENIQVP	204	
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Db      205  -----VLTWVKFIIGYLFPLLTMSICVLCIFKVKKRTVLISRRHKWTILVVVVA 254
Qy      385  VFLVCWTEPHLFGVLSLLTDPETPLGKTLMSWDHVCIALASANCFNPPLYALLGKDPK 444
Db      255  -FVVCWTEPHLFSIWELTHHNSYSHVWQAGIPLSTGLAFNLSCINPILYVLISKFOA 313
Qy      445  KAROSIQGLEAAFPSEELTRSTHCPSNNVISE--RNSTT 481
Db      314  RFRSSVAELKXYLWE-----VSC--SGTVSEQLNSET 345

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 Job time : 45 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2005, 09:46:38 ; Search time 135 Seconds
(without alignments)
1186.686 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 2552

Sequence: 1 MASFSAEINSTDLLSQPWE.....TRSTHCFSPNNVSRNSTTV 482

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Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2552	100.0	482	9	US-09-870-759-98
2	2552	100.0	482	10	US-09-751-708A-98
3	2552	100.0	482	14	US-10-225-567A-78
4	2552	100.0	482	14	US-10-206-395B-2
5	2552	100.0	482	15	US-10-292-798-662
6	2552	100.0	482	16	US-10-764-649-2
7	2544	99.7	482	8	US-08-462-314-2
8	2544	99.7	482	14	US-10-259-521-2
9	2543	99.6	482	14	US-10-367-035-2
10	2539	99.5	485	9	US-09-925-302-657
11	2539	99.5	485	10	US-09-925-302-657
12	2535	99.3	482	10	US-09-836-509-465
13	2535	99.3	482	17	US-10-925-095-465

14	2009	78.7	390	14	US-10-017-161-760	Sequence 760, App
15	1585.5	61.3	477	9	US-09-892-206-2	Sequence 2, Appli
16	1585.5	61.3	477	16	US-10-764-649-10	Sequence 10, Appl
17	551.5	21.6	350	9	US-09-867-569-10	Sequence 10, Appl
18	551.5	21.6	350	18	US-09-893-512-15	Sequence 15, Appl
19	551.5	21.6	350	13	US-10-025-335-3	Sequence 3, Appli
20	551.5	21.6	350	14	US-10-218-574-10	Sequence 10, Appl
21	551.5	21.6	350	14	US-10-259-521-9	Sequence 9, Appli
22	551.5	21.6	350	14	US-10-425-567A-80	Sequence 80, Appl
23	551.5	21.6	350	16	US-10-408-765A-388	Sequence 388, App
24	551.5	21.6	350	16	US-10-764-649-4	Sequence 4, Appli
25	548.5	21.5	350	10	US-09-826-509-467	Sequence 467, App
26	548.5	21.5	350	17	US-10-925-095-467	Sequence 467, App
27	545.5	21.4	333	16	US-10-764-649-12	Sequence 12, Appl
28	543.5	21.3	371	10	US-09-905-253A-4	Sequence 4, Appli
29	543.5	21.3	371	14	US-10-201-187-4	Sequence 4, Appli
30	543.5	21.3	371	15	US-10-603-566-4	Sequence 2, Appli
31	530	20.8	371	10	US-09-905-253A-2	Sequence 2, Appli
32	530	20.8	371	14	US-10-201-187-2	Sequence 235, App
33	530	20.8	371	14	US-10-225-567A-235	Sequence 664, App
34	530	20.8	371	15	US-10-292-798-664	Sequence 2, Appli
35	530	20.8	371	15	US-10-603-566-2	Sequence 128, App
36	530	20.8	371	17	US-10-753-267-128	Sequence 6, Appli
37	516	20.2	371	10	US-09-905-253A-6	Sequence 6, Appli
38	516	20.2	371	14	US-10-201-187-6	Sequence 6, Appli
39	516	20.2	371	15	US-10-603-566-6	Sequence 633, App
40	514	20.1	353	14	US-10-225-567A-633	Sequence 218, App
41	514	20.1	353	15	US-10-116-275-218	Sequence 12, Appl
42	514	20.1	353	16	US-10-789-241-12	Sequence 8, Appli
43	513	20.1	349	14	US-10-305-555-8	Sequence 2, Appli
44	509.5	20.0	351	9	US-09-944-807-2	Sequence 120, App
45	509.5	20.0	351	14	US-10-225-567A-120	

ALIGNMENTS

RESULT 1

US-09-870-759-98
; Sequence 98, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-870-759-98

Query Match	100.0%	Score	2552;	DB	9;	Length	482;
Best Local Similarity	100.0%	Pred. No.	2.5e-223;				
Matches	482;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MASFSAEINSTDLLSQPWEPPVILSWILSTFLGLPGNGLVWVAGLKMORTVNTIW	60				
Qy	61	FLHTLADLLCCLSLPFFSLAHALQGPYGRFLCKLIPSIIVLNMVAFVLLTAISLDR	120				
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Qy	121	CLVWFKPIWCQNRHNVGMACISGCGIWWVAFVMCIPIVFVYREIFTTDNNHRCGYKFLSS	180				
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Db 301 SSNSFYSESELPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
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Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 2
US-09-751-708A-98
; Sequence 98, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-98

Query Match 100.0%; Score 2552; DB 10; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.5e-223;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 FLHLTLADLLCCLSLPSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
Db 61 FLHLTLADLLCCLSLPSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
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Db 301 SSNSFYSESELPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
Qy 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482
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Qy 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 3
US-10-225-567A-78
; Sequence 78, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glemma C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-78

Query Match 100.0%; Score 2552; DB 14; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.5e-223;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASFSAETNSTDLLSQPWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60
Db 1 MASFSAETNSTDLLSQPWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60
Qy 61 FLHLTLADLLCCLSLPSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
Db 61 FLHLTLADLLCCLSLPSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTLTAISLDR 120
Qy 121 CLVVFKPIWQNHNRNVGMACSIQCIWVAFVVCIPVVFYREIFTTNDHNRGKYGKGLSS 180
Db 121 CLVVFKPIWQNHNRNVGMACSIQCIWVAFVVCIPVVFYREIFTTNDHNRGKYGKGLSS 180
Qy 181 SLDPDYGDPLENSLENIQPPGEMNDRDLPSSFQNDHPWTVPTVFQPTQRPSPAD 240
Db 181 SLDPDYGDPLENSLENIQPPGEMNDRDLPSSFQNDHPWTVPTVFQPTQRPSPAD 240
Qy 241 SLPRGSARLTQNLVSNVFKPADVVSPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
Db 241 SLPRGSARLTQNLVSNVFKPADVVSPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
Qy 301 SSNSFYSESELPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
Db 301 SSNSFYSESELPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPLPSVIMIACTYFIV 360
Qy 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFCNPFYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
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; APPLICANT: Chen, Hong
 ; APPLICANT: Barnes, Glenn
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
 ; TITLE OF INVENTION: INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
 ; TITLE OF INVENTION: METABOLIC DISORDERS
 ; FILE REFERENCE: MPI2003-025PIRNM
 ; CURRENT FILING DATE: 2004-01-26
 ; PRIOR FILING DATE: 2004-01-26
 ; PRIOR FILING DATE: 2003-02-07
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: human
 US-10-764-649-2

Query Match 100.0%; Score 2552; DB 16; Length 482;
 Best Local Similarity 100.0%; Pred. No. 2.5e-223;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFSATNSTDLISQPNNEPVLISWVILSLTLLGLPGNGLVWAGLKMORTVNTI 60
 Db 1 MASFSATNSTDLISQPNNEPVLISWVILSLTLLGLPGNGLVWAGLKMORTVNTI 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLLTALSIDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLLTALSIDR 120
 Qy 121 CLVVFKPIWCQNHNRNVGMACISICGCIWVAFVVCIPVVFYREIFTTDNHNRCGYKFGLS 180
 Db 121 CLVVFKPIWCQNHNRNVGMACISICGCIWVAFVVCIPVVFYREIFTTDNHNRCGYKFGLS 180
 Qy 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRDPSFQTNHDPWTVPTVFQPTQRPESAD 240
 Db 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRDPSFQTNHDPWTVPTVFQPTQRPESAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Qy 301 SSNSFYSELPGQFDQYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMIAICYFIV 360
 Db 301 SSNSFYSELPGQFDQYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMIAICYFIV 360
 Qy 361 FRMQRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 7
 US-08-462-314-2
 ; Sequence 2, Application US/08462314
 ; Publication No. US20030027245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, ET AL.
 ; TITLE OF INVENTION: Human G-protein coupled Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY

; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,314
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01992
 ; FILING DATE: 17 FEB 95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-382
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 482 AMINO ACIDS
 ; TYPE: AMINO ACID
 ; STRANDEDNESS:
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: PROTEIN
 US-08-462-314-2

Query Match 99.7%; Score 2544; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 1.3e-222;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MASFSATNSTDLISQPNNEPVLISWVILSLTLLGLPGNGLVWAGLKMORTVNTI 60
 Db 1 MASFSATNSTDLISQPNNEPVLISWVILSLTLLGLPGNGLVWAGLKMORTVNTI 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLLTALSIDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFASVFLLTALSIDR 120
 Qy 121 CLVVFKPIWCQNHNRNVGMACISICGCIWVAFVVCIPVVFYREIFTTDNHNRCGYKFGLS 180
 Db 121 CLVVFKPIWCQNHNRNVGMACISICGCIWVAFVVCIPVVFYREIFTTDNHNRCGYKFGLS 180
 Qy 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRDPSFQTNHDPWTVPTVFQPTQRPESAD 240
 Db 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRDPSFQTNHDPWTVPTVFQPTQRPESAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Qy 301 SSNSFYSELPGQFDQYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMIAICYFIV 360
 Db 301 SSNSFYSELPGQFDQYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMIAICYFIV 360
 Qy 361 FRMQRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 8
 US-10-259-521-2

```
; Sequence 2, Application US/10259521
; Publication No. US20030022310A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/259,521
; FILING DATE: 30-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,314
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: PCT/US95/01992
; FILING DATE: 17 FEB 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-382 (PF159)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-259-521-2

Query Match 99.7%; Score 2544; DB 14; Length 482;
Best Local Similarity 99.8%; Pred. No. 1.3e-222;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLISQPNNEPPVILSMVILSLTFLGLPGNGLVLMVAGLKMORTVNTIW 60
Db 1 MASPSAETNSTDLISQPNNEPPVILSMVILSLTFLGLPGNGLVLMVAGLKMORTVNTIW 60
Qy 61 FLHUTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
Db 61 FLHUTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
Qy 121 CLVFKPIWCQNHRNVGMACISGCIWVAVFVVCIPVYREIFFTDNNHRCGYKFGLS 180
Db 121 CLVFKPIWCQNHRNVGMACISGCIWVAVFVVCIPVYREIFFTDNNHRCGYKFGLS 180
Qy 181 SLDPYDFDGLPDLNRSLENIQPPGEMNDRDLPSSFQTNHDPHTVPTVFQPTORPSAD 240
Db 181 SLDPYDFDGLPDLNRSLENIQPPGEMNDRDLPSSFQTNHDPHTVPTVFQPTORPSAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPDNDSDAFLSTHLKLPESA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPDNDSDAFLSTHLKLPESA 300
Qy 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIACYSPV 360
Db 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIACYSPV 360
Qy 361 FMORGFAKSOKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMORGFAKSOKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAAFSEELTRSTHCPSSNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAAFSEELTRSTHCPSSNNVISERNST 480

; Sequence 2, Application US/10367035
; Publication No. US20030187244A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; TITLE OF INVENTION: EXTRACELLULAR DOMAIN
; FILE REFERENCE: TSRI 511.1D1
; CURRENT APPLICATION NUMBER: US/10/367,035
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/117,440
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: PCT/US97/01736
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 60/010,808
; PRIOR FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Human
; US-10-367-035-2

Query Match 99.6%; Score 2543; DB 14; Length 482;
Best Local Similarity 99.8%; Pred. No. 1.7e-222;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLISQPNNEPPVILSMVILSLTFLGLPGNGLVLMVAGLKMORTVNTIW 60
Db 1 MASPSAETNSTDLISQPNNEPPVILSMVILSLTFLGLPGNGLVLMVAGLKMORTVNTIW 60
Qy 61 FLHUTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
Db 61 FLHUTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
Qy 121 CLVFKPIWCQNHRNVGMACISGCIWVAVFVVCIPVYREIFFTDNNHRCGYKFGLS 180
Db 121 CLVFKPIWCQNHRNVGMACISGCIWVAVFVVCIPVYREIFFTDNNHRCGYKFGLS 180
Qy 181 SLDPYDFDGLPDLNRSLENIQPPGEMNDRDLPSSFQTNHDPHTVPTVFQPTORPSAD 240
Db 181 SLDPYDFDGLPDLNRSLENIQPPGEMNDRDLPSSFQTNHDPHTVPTVFQPTORPSAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPDNDSDAFLSTHLKLPESA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPDNDSDAFLSTHLKLPESA 300
Qy 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIACYSPV 360
Db 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIACYSPV 360
Qy 361 FMORGFAKSOKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMORGFAKSOKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAAFSEELTRSTHCPSSNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAAFSEELTRSTHCPSSNNVISERNST 480
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Qy 481 TV 482
Db 481 TV 482

RESULT 10

US-09-925-302-657
; Sequence 657, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 657
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-657

Query Match 99.5%; Score 2539; DB 9; Length 485;
Best Local Similarity 99.6%; Pred. No. 3.9e-222;
Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MASFAETNSTDL	LSQPNNEP	SVILSL	TLFLGLPGNGLV	LVWAGL	KMQRTV	NTI	60
Db	4	MASFAETNSTDL	LSQPNNEP	SVILSL	TLFLGLPGNGLV	LVWAGL	KMQRTV	NTI	63
Qy	61	FLHUTLADLLCCL	SLP	SLPSLA	HLALQGW	PGYGRFLCK	LIP	SIIVLNM	FASVFL
Db	64	FLHUTLADLLCCL	SLP	SLPSLA	HLALQGW	PGYGRFLCK	LIP	SIIVLNM	FASVFL
Qy	121	CLVVFKEPIW	QNHNRNV	GMACS	ICGCIW	VAFV	MCIPV	FVYREI	FTT
Db	124	CLVVFKEPIW	QNHNRNV	GMACS	ICGCIW	VAFV	MCIPV	FVYREI	FTT
Qy	181	SLDYPDFY	GDPLEN	SRLENI	VQPPGEM	NDR	LDPS	SFQ	TNDHP
Db	184	SLDYPDFY	GDPLEN	SRLENI	VQPPGEM	NDR	LDPS	SFQ	TNDHP
Qy	241	SLPGSARLT	SONLYSN	VFKAD	VVSPKI	PSGF	PIEDHETS	PLD	NSDAFL
Db	244	SLPGSARLT	SONLYSN	VFKAD	VVSPKI	PSGF	PIEDHETS	PLD	NSDAFL
Qy	301	SSNSFY	SESEL	PQGFQ	DYNNLG	QFTD	DDQV	PTPL	VAITIT
Db	304	SSNSFY	SESEL	PQGFQ	DYNNLG	QFTD	DDQV	PTPL	VAITIT
Qy	361	FRMQRG	FAK	SQSKT	FRVAVV	VAV	FLV	CV	TPYH
Db	364	FRMQRG	FAK	SQSKT	FRVAVV	VAV	FLV	CV	TPYH
Qy	421	IALASANS	CNFP	LYAL	LGKDFR	KARQ	SIQ	IGILEA	AFSE
Db	424	IALASANS	CNFP	LYAL	LGKDFR	KARQ	SIQ	IGILEA	AFSE
Qy	481	TV	482						
Db	484	TV	485						

RESULT 12

US-09-925-509-465
; Sequence 465, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin

RESULT 11

US-09-925-302-657
; Sequence 657, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 657
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-657

Query Match 99.5%; Score 2539; DB 10; Length 485;
Best Local Similarity 99.6%; Pred. No. 3.9e-222;
Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MASFAETNSTDL	LSQPNNEP	SVILSL	TLFLGLPGNGLV	LVWAGL	KMQRTV	NTI	60
Db	4	MASFAETNSTDL	LSQPNNEP	SVILSL	TLFLGLPGNGLV	LVWAGL	KMQRTV	NTI	63
Qy	61	FLHUTLADLLCCL	SLP	SLPSLA	HLALQGW	PGYGRFLCK	LIP	SIIVLNM	FASVFL
Db	64	FLHUTLADLLCCL	SLP	SLPSLA	HLALQGW	PGYGRFLCK	LIP	SIIVLNM	FASVFL
Qy	121	CLVVFKEPIW	QNHNRNV	GMACS	ICGCIW	VAFV	MCIPV	FVYREI	FTT
Db	124	CLVVFKEPIW	QNHNRNV	GMACS	ICGCIW	VAFV	MCIPV	FVYREI	FTT
Qy	181	SLDYPDFY	GDPLEN	SRLENI	VQPPGEM	NDR	LDPS	SFQ	TNDHP
Db	184	SLDYPDFY	GDPLEN	SRLENI	VQPPGEM	NDR	LDPS	SFQ	TNDHP
Qy	241	SLPGSARLT	SONLYSN	VFKAD	VVSPKI	PSGF	PIEDHETS	PLD	NSDAFL
Db	244	SLPGSARLT	SONLYSN	VFKAD	VVSPKI	PSGF	PIEDHETS	PLD	NSDAFL
Qy	301	SSNSFY	SESEL	PQGFQ	DYNNLG	QFTD	DDQV	PTPL	VAITIT
Db	304	SSNSFY	SESEL	PQGFQ	DYNNLG	QFTD	DDQV	PTPL	VAITIT
Qy	361	FRMQRG	FAK	SQSKT	FRVAVV	VAV	FLV	CV	TPYH
Db	364	FRMQRG	FAK	SQSKT	FRVAVV	VAV	FLV	CV	TPYH
Qy	421	IALASANS	CNFP	LYAL	LGKDFR	KARQ	SIQ	IGILEA	AFSE
Db	424	IALASANS	CNFP	LYAL	LGKDFR	KARQ	SIQ	IGILEA	AFSE
Qy	481	TV	482						
Db	484	TV	485						

RESULT 12

US-09-925-509-465
; Sequence 465, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin

Matches 311; Conservative 50; Mismatches 108; Indels 13; Gaps 6;

Qy 1 MASFAETNSTDLISOPWNEPPVILSMVILSLTFLGLPGNGLVWAGLKMORTVNTI 60
 Db 1 MESFDADTNTDLSRPLFOFQDIAWVILGLLGLNGLVWAGLKMORTVNTI 60

Qy 61 FLHUTLADLCLLSLPSLAHLALQGWPGYGRFLCKLIPSIILNMFASVFLTLAISLDR 120
 Db 61 FLHUTLADLCLLSLPSLAHLALQGWPGYGRFLCKLIPSIILNMFASVFLTLAISLDR 120

Qy 121 CLVVFKEPIWQNHNRNMGACISICGCIWVAFVWCIPVYVREIFTTNDHNRCCGYKGLSS 180
 Db 121 CLVVFKEPIWQNHNRNMGACISICGCIWVAFVWCIPVYVREIFTTNDHNRCCGYKGLSS 180

Qy 181 SLDYPDFGDPLENSLENIVQPGEMNDRLDPSSFQTNHDPWTVPTVFQOTFORP 237
 Db 181 SYDIWDVYKLSLPESNSTDNSTAQLTGHMNDRASSVQARDYFWTVTTALOSQPELTS 240

Qy 238 SADSPLRGSA RLTSQNLVSNVFKPADVVPKIPSGFPEDHETSPLDNSDAFLSTHLKLF 297
 Db 241 PEDSFLDSA--NQOPHYGG--KPPNVLTAAVSPGFPVEDRKSNTL--NADAFLSAHTFL 295

Qy 298 PSASSNSFYSESELPOGFQDYNNLQOFTDDQVTPPLVAITITRLVVGFLPLSPVIMIA 357
 Db 296 PTASSGHLV----PYDFQGDY--VDQFTYDNHVPPLMAITITRLVVGFLPLSPVIMIA 350

Qy 358 FIVRMORGRFAKQSOKTFRVAVVAVFLVCWTPYHIFGVLSLITDPETPLGKTLMSWD 417
 Db 351 LIVRMKKTFTKSRNKTFRVAVVAVVTVFFICWTPHLVGVLLITDPESLGEAVMSWD 410

Qy 418 HVCIALASANSFCNPFYALLGKDFRKKAROSIQGILEAAAFSEBELTSTHCPSNVVISER 477
 Db 411 HMSIALASANSFCNPFYALLGKDFRKKAROSIQGILEAAAFSEBELTSTHCPSNVVISER 470

Qy 478 NS 479
 Db 471 NN 472

Search completed: April 13, 2005, 09:59:16
 Job time : 137 secs

LENGTH: 390
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-017-161-760

Query Match 78.7%; Score 2009; DB 14; Length 390;
 Best Local Similarity 80.9%; Pred. No. 4.9e-174;
 Matches 390; Conservative 0; Mismatches 0; Indels 92; Gaps 1;

Qy 1 MASFAETNSTDLISOPWNEPPVILSMVILSLTFLGLPGNGLVWAGLKMORTVNTI 60
 Db 1 MASFAETNSTDLISOPWNEPPVILSMVILSLTFLGLPGNGLVWAGLKMORTVNTI 60

Qy 61 FLHUTLADLCLLSLPSLAHLALQGWPGYGRFLCKLIPSIILNMFASVFLTLAISLDR 120
 Db 61 FLHUTLADLCLLSLPSLAHLALQGWPGYGRFLCKLIPSIILNMFASVFLTLAISLDR 120

Qy 121 CLVVFKEPIWQNHNRNMGACISICGCIWVAFVWCIPVYVREIFTTNDHNRCCGYKGLSS 180
 Db 121 CLVVFKEPIWQNHNRNMGACISICGCIWVAFVWCIPVYVREIFTTNDHNRCCGYKGLSS 180

Qy 181 SLDYPDFGDPLENSLENIVQPGEMNDRLDPSSFQTNHDPWTVPTVFQOTFORPSAD 240
 Db 181 SLDYPDFGDPLENSLENIVQPGEMND----- 209

Qy 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSGFPEDHETSPLDNSDAFLSTHLKLFPSA 300
 Db 210 ----- 209

Qy 301 SSNSFYSESELPOGFQDYNNLQOFTDDQVTPPLVAITITRLVVGFLPLSPVIMIA 360
 Db 210 -SNSFYSESELPOGFQDYNNLQOFTDDQVTPPLVAITITRLVVGFLPLSPVIMIA 268

Qy 361 FMORGRFAKQSOKTFRVAVVAVFLVCWTPYHIFGVLSLITDPETPLGKTLMSWDHVC 420
 Db 269 FMORGRFAKQSOKTFRVAVVAVVAVFLVCWTPYHIFGVLSLITDPETPLGKTLMSWDHVC 328

Qy 421 IALASANSFCNPFYALLGKDFRKKAROSIQGILEAAAFSEBELTSTHCPSNVVISERNST 480
 Db 329 IALASANSFCNPFYALLGKDFRKKAROSIQGILEAAAFSEBELTSTHCPSNVVISERNST 388

Qy 481 TV 482
 Db 389 TV 390

RESULT 15
 US-09-892-206-2
 ; Sequence 2, Application US/09892206
 ; Patent No. US2002012712A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brennan, Thomas J.
 ; APPLICANT: Matthews, William
 ; APPLICANT: Moore, Mark
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING ANAPHYLATOXIN
 ; FILE REFERENCE: R-171
 ; CURRENT APPLICATION NUMBER: US/09/892,206
 ; CURRENT FILING DATE: 2001-08-26
 ; PRIOR APPLICATION NUMBER: US 60/215,467
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 60/244,083
 ; PRIOR FILING DATE: 2000-10-26
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 477
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-892-206-2

Query Match 61.3%; Score 1565.5; DB 9; Length 477;
 Best Local Similarity 64.5%; Pred. No. 1.5e-133;

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: April 13, 2005, 09:37:22 ; Search time 46 Seconds

(without alignments)
1008.184 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 2552

Sequence: 1 MASFSATNSTDLLSQPWNE.....TRSTHCFPSNNVIERNSTTV 482

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2543	99.6	482	2 S65766	G protein-coupled
2	1426.5	55.9	473	2 JC5835	anaphylatoxin C3a
3	551.5	21.6	350	1 A37963	complement C5a ana
4	549	21.5	352	1 S27357	complement C5a ana
5	545.5	21.4	351	1 A46525	complement C5a ana
6	543.5	21.3	371	2 JC5498	G protein-coupled
7	516	20.2	371	2 JC5796	probable chemoatr
8	515	20.2	352	2 A46520	N-formyl peptide r
9	514	20.1	353	2 C42009	FMLP-related recep
10	509.5	20.0	351	2 B42009	FMLP-related recep
11	508.5	19.9	364	2 A49542	N-formyl peptide c
12	479.5	18.8	350	2 A42009	N-formyl peptide r
13	449.5	17.6	355	2 A55733	G protein-coupled
14	427	16.7	353	2 JC2492	G protein-coupled
15	372.5	14.6	392	2 S65693	opioid receptor mu
16	371.5	14.6	400	2 I56553	mu opiate receptor
17	368	14.4	362	2 JN0694	angiotensin II rec
18	364.5	14.3	359	2 I51372	angiotensin II rec
19	364	14.3	351	2 JC7096	leukotriene B4 rec
20	364	14.3	398	2 I56517	mu opioid receptor
21	362	14.2	398	2 I56504	mu opioid receptor
22	359	14.1	398	2 A57510	mu opioid receptor
23	348	13.6	369	2 JC2083	somatostatin recep
24	344.5	13.5	369	2 B41795	somatostatin recep
25	344	13.5	372	2 S26667	G protein-coupled
26	342	13.4	369	2 D41795	somatostatin recep
27	341.5	13.4	359	2 S15403	angiotensin II rec
28	340	13.3	369	2 A45291	somatostatin recep
29	339.5	13.3	380	2 I38435	angiotensin recep

30	338.5	13.3	359	2 A42656	angiotensin II rec
31	337.5	13.2	359	2 JC1104	angiotensin II rec
32	337.5	13.2	359	2 A48857	angiotensin II rec
33	337	13.2	327	2 S56162	MDCR15 protein - h
34	334.5	13.1	359	2 JQ1516	angiotensin II rec
35	333.5	13.1	359	2 S44425	angiotensin II rec
36	332.5	13.0	359	2 JH0621	angiotensin II rec
37	332.5	13.0	359	2 JC2134	angiotensin II rec
38	331.5	13.0	333	2 I38974	G protein-coupled
39	330	12.9	353	2 S28787	neuropeptide Y/pep
40	329	12.9	352	2 A45747	neuropeptide Y/pep
41	329	12.9	380	2 S36143	kappa opioid recep
42	328.5	12.9	345	2 S29248	sonatostatin recep
43	327.5	12.8	363	2 I57940	sonatostatin recep
44	327	12.8	380	2 JC2338	kappa opioid recep
45	327	12.8	380	2 A48227	kappa opioid recep

ALIGNMENTS

RESULT 1

S65766

G protein-coupled receptor (clone AZ3B) - human

C:Species: Homo sapiens (man)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S65766

R:RoGlic, A.; Prossnitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.

Biochim. Biophys. Acta 1305, 39-43, 1996

A:Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular 1

A:Reference number: S65766; MUID:96180983; PMID:8605247

A:Accession: S65766

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-482 <ROG>

A:Cross-references: UNIPROT:Q16581; EMBL:U28488; NID:g1199577; PIDN:AAC50374.1; PID:g119

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match	99.6%	Score	2543	DB 2	Length	482			
Best Local Similarity	99.8%	Pred. No.	1.2e-196						
Matches	481	Conservative	0	Mismatches	1	Indels	0	Gaps	0
Qy	1	MASFSATNSTDLLSQPWNEPVL	SVILSLTFLGLPGNGLVLA	GLVLA	GLVLA	GLVLA	GLVLA	GLVLA	GLVLA
Db	1	MASFSATNSTDLLSQPWNEPVL	SVILSLTFLGLPGNGLVLA	GLVLA	GLVLA	GLVLA	GLVLA	GLVLA	GLVLA
Qy	61	FLHLLADLLCCLSLPFLSLA	LALQGGWPYGRFLCKLIPS	IIVLNMPASV	FLLTALSLDR	120			
Db	61	FLHLLADLLCCLSLPFLSLA	LALQGGWPYGRFLCKLIPS	IIVLNMPASV	FLLTALSLDR	120			
Qy	121	CLVVFKEPTWCQHRNVGMACS	ICGCIWVAFVVCIPFVYREI	FTTDNHNRCG	YKFGGLSS	180			
Db	121	CLVVFKEPTWCQHRNVGMACS	ICGCIWVAFVVCIPFVYREI	FTTDNHNRCG	YKFGGLSS	180			
Qy	181	SLDVPDFGDDPLENRSLENI	VQPPGEMNDRLDPSFQND	HPHTWPTVPQPT	FORPSAD	240			
Db	181	SLDVPDFGDDPLENRSLENI	VQPPGEMNDRLDPSFQND	HPHTWPTVPQPT	FORPSAD	240			
Qy	241	SLRGSARLTQNLVSNVFKPAD	VVSPKIPSGFPTEHETS	PLDNDSDAFSL	THLKLFP	300			
Db	241	SLRGSARLTQNLVSNVFKPAD	VVSPKIPSGFPTEHETS	PLDNDSDAFSL	THLKLFP	300			
Qy	301	SSNSFYSESELPGQDYNNL	QGFDDDDQVTPPLVAIT	ITRLVVGFLPS	VIMACYSFIV	360			
Db	301	SSNSFYSESELPGQDYNNL	QGFDDDDQVTPPLVAIT	ITRLVVGFLPS	VIMACYSFIV	360			
Qy	361	FRMQRGRPAKSQSKTFR	VAVVAVFLVCWTPYHIFG	VLSTLTDDET	PLGKTLMSD	420			
Db	361	FRMQRGRPAKSQSKTFR	VAVVAVFLVCWTPYHIFG	VLSTLTDDET	PLGKTLMSD	420			
Qy	421	IALLSANSCTFPFLYALL	GKFRKKAROSIOGILEA	AFSEELTRSTH	CFSPNNVIER	480			

Qy	142	ICGCIWVAVFVCIPVFYVRIBFTTDNHNRCYGKLGSSLDYPDYGDBPLENRLENIIV	201
		: : : :	
Db	156	ACAVAGLALLTTPSFLYR	175
		: : : :	
Qy	202	QPPEMDRLDPSSFQNDHWPVTVPQOTFORPSADSLPRGSARLTSONLYSNVPKP	261
		: : : :	
Db	176	-----VVREYF-----	182
		: : : :	
Qy	262	ADVSPKIPSGPIEDHETSPLDNSDAFLSTHLKLPPSASSNPYESELPOGFQDYINLG	321
		: : : :	
Db	183	----PPKVLCGV-----	190
		: : : :	
Qy	322	QFTDDQVPTPLVAITTRLVVGLLPSPVIMTACYSPVFRMQRFPAKSQSKTRFAVV	381
		: : : : : : : : : : :	
Db	191	DYSHDKRRER---AVAIVRVLGFLPWLPLTLTCYTFILLRTWSRRATRS-TKTILKVVA	246
		: : : : : : : : : :	
Qy	382	WAVFLVCWTPIHFGVLSLLTDPTPLGKTLMSWDHYCIAALASANSFCNPFYALLGKD	441
		: : : : : : : : : :	
Db	247	VVASFFFWLBYQTGIMWSELEBSSPTFELLNKLDLSICVSFAYINCINPIYVVVGQG	306
		: : : : : : : : : :	
Qy	442	FRKKAROSIQGILEAAAFSEE-----LTRST	466
		: : : : : : : : : :	
Db	307	FOGRLRKSPLSLRNVLTEBSVWRESKSFTRAST	339

RESULT 4
S27357
complement C5a anaphylatoxin receptor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S27357
R:Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A:Title: Cloning and functional expression of the canine anaphylatoxin C5a receptor. Evi
A:Reference number: S27357; MUID:93111969; PMID:1472004
A:Accession: S27357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352 <PER>
A:Cross-references: UNIPROT:P30992; EMBL:X65860; NID:9878; PIDN:CAA46690.1; PID:9879
C:Function:
A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F:1-38/Domain: extracellular #status predicted <EX1>
F:39-62/Domain: transmembrane #status predicted <TM1>
F:63-72/Domain: intracellular #status predicted <IN1>
F:73-95/Domain: transmembrane #status predicted <TM2>
F:96-111/Domain: extracellular #status predicted <EX2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:134-150/Domain: intracellular #status predicted <IN2>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:176-208/Domain: extracellular #status predicted <EX3>
F:209-229/Domain: transmembrane #status predicted <TM5>
F:230-244/Domain: intracellular #status predicted <IN3>
F:245-266/Domain: transmembrane #status predicted <TM6>
F:267-285/Domain: extracellular #status predicted <EX4>
F:286-309/Domain: transmembrane #status predicted <TM7>
F:310-352/Domain: intracellular #status predicted <IN4>
F:5/Binding site: carbonydrate (Asn) (covalent) #status predicted

	Query Match	21.5%	Score 549;	DB 1;	Length 352;
	Best Local Similarity	27.0%;	Pred. No. 1.6e-36;		
	Matches 121;	Conservative 64;	Mismatches 115;	Indels 148;	Gaps 5
Qy	14	LSQPNNEPVLISVMSILSTFLGLHPGNGLVLAAGLKMQRTWTITWFLHLTLADLLCL	73		
Db	29	LNTPKLSVPMIALVIFVMVFLGVPGHFLVVMVTGVFEVRRINATWFLNLAVADLLSCL	88		
Qy	74	SLPFSLAHLAQGWOPYGRFLCKLIPSIIVLNMFAVSFLITATISLDRCLVWPFKPIWQNH	133		

Db	89	ALPILFSSIVQOGVWPFGNACRILPSLILNMTVASILLTTTISADRFLVFNPNWQCY	148
Qy	134	RNVGMAGSICGCIWVAWFCIPVVFVREIETTNNHRCYKFGLSLSDYDFYCDPLE	193
Db	149	RGQLAWAACSVAVALLTVSPFIRGVHT-----EYFPF-----	185
Qy	194	NRSLENTVPPGEMNDRDLPSSFTQNDHPWTVTVFQPQTFQRPASDLSLPRGSARLTSON	253
Db	186	-----WMTCGV-----	191
Qy	254	LYSNVFXPADVVSPKIFSGPPIEDHETSPLDNSDAFLSTHLKLPPSASSNSFYSESLPOG	313
Db	192	-----	191
Qy	314	FQDYNNLGQFTDDQVPTPLVAITITRLVAGFLLPSVIMIACYSFIVPMRQGRFAKSOS	373
Db	192	--DYSGGVGLVER-----GVALRLUMGFLGLVLILSCYTFELLRTW-SRKATRT	240
Qy	374	KTRFVAVVAVFVLCVCTPVHIFGVLSLTDPETPLGKTLMSWDVCIALASANSFCNPF	433
Db	241	KTLKVVAVVVVSFFVLWLPQVQTGMMAFLFYKHSESFRVRSLDSLCAVAVAINCCINPI	300
Qy	434	LYALLGKDPRKARQSIQGILEAAFSSES	461
Db	301	IYVLAAGCFHSRFLKSLPARUOVLAEE	328

RESULT 5
A46525
complement C5a anaphylatoxin receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A46525
R/Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
J. Immunol. 149, 2600-2606, 1992
A/Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled
A/Reference number: A46525; MUID:93017861; PMID:1401897
A/Accession: A46525
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-351 <GER>
A/Cross-references: GB:I46665; GB:L05630; NID:Q257519; PIDN:AAB97774.1; PID:G257520
A/Experimental source: BALB/C
A/Note: sequence extracted from NCBI backbone (NCBIP:116075)
C/Function:

- Query Match	21.4%	Score 545.5;	DB 1;	Length 351;
Best Local Similarity	26.7%;	Pred. No. 3.le-36;		
Matches 127; Conservative	58;	Mismatches 135;	Indels 155;	Gaps 5;
Qy	12	DLLSQPNNEPPEVLISMVILSITLFLGPGRGGLVWAGLVKQKRVNTIWFHLTLADLLC	71	
		: : : : : :		
		: : : : : :		
		: : : : : :		
Db	26	DGHLPKRPQGDVAALIIYSVFVGVEGNALVVMTAFAPDGPSSNAIFNLAVADLLS	85	
		: : : : : :		
		: : : : : :		
		: : : : : :		

Db 322 -KKPKVALFGRNLVAUSEDTGPSSY-PSHRSFTQMSS 356

RESULT 8

A46520

N-formyl peptide receptor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A46520

R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.

J. Immunol. 150, 1383-1394, 1993

A/Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and

A/Reference number: A46520; MUID:93163563; PMID:8432984

A/Accession: A46520

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-352 <YEL>

A/Cross-references: UNIPROT:Q05394; GB:M94549; NID:g165027; PID:AAA31254.1; PID:g165028

A/Experimental source: NZW, neutrophils

A/Note: sequence extracted from NCBI backbone (NCBIP:124908)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.2%; Score 515; DB 2; Length 352;

Best local Similarity 29.6%; Pred. No. 8.9e-34;

Matches 135; Conservative 55; Mismatches 120; Indels 146; Gaps 11;

Qy 24 ILSNVILSLFLGLPGNGVLVWAGLKMQRVTNTWFLHTLADLLCCLSLSPSLAHLA 83

Db 27 VFSYLLILVVTFLVGLVNGVLVWTFGRMTHVTITSYLNALALADFSTLTLPFFIVTKA 86

Qy 84 LQGWPPYGRFLCKLIPGIIIVLNNFASVFLTLAISDRCLVVPKPIWQNHNNVGMACSIC 143

Db 87 LGGHWPGFELCKFPVTIVDINLFGSVFLIALALDEICVLPHPVAQNHNNVSLAKVI 146

Qy 144 GCIVVAVFVVCIPVYVREIFTDNNHRCGYKFGLSLLDPDFYGDPLENRSLENIVQP 203

Db 147 VGPWICALLTLPVIR---VTTLSHPR--- 172

Qy 204 PGENVDRLDSSFGTDNDHPHTVTVTFQFPQSPADSLSRGSARLTSONLYSNVFKPAD 263

Db 173 PGRVACTFDWS-----PWT----- 186

Qy 264 VSPKIPSGPIEDHETSPLDNSDAPLSTHLKLPSSASSNFYSESLPQGFQDYVNLGQF 323

Db 187 -----ED-----PAEK---LKVLSHF-----MVRG----- 204

Qy 324 TDDQVPTPLVAITITLVVGFLLPSPVIMIACYSFIVFRMQRGRFAKQSKTFRVAVVV 383

Db 205 -----IIRFIIGFSPMSIVAVCYGLIATKTHRQGLIKS-SRPLRVLSFVV 249

Qy 384 AVFLVCTPPIHIFGVLSLLTDPETPL--GKTLMSWDHVCIALASANSFCNPFYIALLGKD 441

Db 250 ASFLLCWSPYQIAALIAVTAIRELLGMGKDLRLVLDVTSFVAFNFSCLNPMPLYVFMGQD 309

Qy 442 FRKKAROSIQGILEAAPSSEL-----TRSTHCPs 470

Db 310 FRERLIHSLPASLRALESQAQTSDTGTNSTSAPA 345

RESULT 9

C42009

FMPLP-related receptor 2 - human

N/Alternate names: FMPLP-related receptor I; probable chemotactic receptor FPRH2

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: C42009

R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A/Title: Mapping of genes for the human C5a receptor (C5AR), human FMPLP receptor (FPR),

A/Reference number: A42009; MUID:92307681; PMID:1612600

A/Accession: C42009

[illegible]

— — — — —

Db 259 AAPFLCHPCFOVVALISTIQVRELRKNTPGIVTALK---ITSPLAFNSCLNPLMLVFM 315
Qy 439 GKDFRKKAROSIQGLEAFSEELTRSTHCPNNVIBERNSTTV 482
Db 316 GQDFRERLIHSLPASLERALTEDSAQTSDDTGTN---LGTNSTSL 356

RESULT 12
A42009
N-formyl peptide receptor - human
N;Alternate names: FMLP receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: J02014; A36309; A35495; A42009; I52414
R;Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.
Gene 133, 285-290, 1993
A;Title: Sequence and organization of the human N-formyl peptide receptor-encoding gene.
A;Reference number: J02014; MUID:94040825; PMID:8224916
A;Accession: J02014
A;Molecule type: mRNA
A;Residues: 1-350 <MUR>
A;Cross-references: UNIPROT:P21462; GB:L10820; NID:g182739; PIDN:AAA16863.1; PID:g182740
A;Note: 192-Aan was also found
R;Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochemistry 29, 11123-11133, 1990
A;Title: The human N-formylpeptide receptor. Characterization of two cDNA isolates and e
A;Reference number: A36309; MUID:91105045; PMID:2176894
A;Accession: A36309
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-191, 'N', 193-345, 'E', 347-350 <BOU1>
A;Cross-references: GB:M60627; GB:M33538; NID:g182664; PIDN:AAA35847.1; PID:g182665
R;Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.
Biochem. Biophys. Res. Commun. 168, 1103-1109, 1990
A;Title: Synthesis and use of a novel N-formyl peptide derivative to isolate a human N-f
A;Reference number: A35495; MUID:90267449; PMID:2161213
A;Accession: A35495
A;Molecule type: mRNA
A;Residues: 1-100, 'L', 102-191, 'N', 193-350 <BOU2>
A;Cross-references: GB:M37128; NID:g189183
A;Note: the sequence in GenBank entry HUNNFP, release 112.0, (PIDN:AAA36362.1) has the
R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A;Reference number: A42009; MUID:92307681; PMID:1612600
A;Accession: A42009
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1, 'G', 3-28, 30-100, 'L', 102-104, 106-112, FLIA', 115-176, 178-182, 184-191, 'N', 194
R;Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.
Biochemistry 31, 11595-11599, 1992
A;Title: Cloning of the gene coding for a human receptor for formyl peptides. Characteri
A;Reference number: I52414; MUID:93075765; PMID:1445895
A;Accession: I52414
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5 <PER>
A;Cross-references: GB:S49810; NID:g260832; PIDN:AAD14906.1; PID:g4262758
C;Genetics:
A;Gene: GDB:FPRI
A;Cross-references: GDB:127999; OMIM:136537
A;Map position: 19q13.4-19q13.4
A;Introns: #status absent
A;Note: entire coding region is found in exon 3; alternatively spliced mRNA transcripts
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein;
F;27-53/Domain: transmembrane #status predicted <TM1>
F;59-83/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;145-169/Domain: transmembrane #status predicted <TM4>
F;206-225/Domain: transmembrane #status predicted <TM5>
F;242-266/Domain: transmembrane #status predicted <TM6>
F;279-304/Domain: transmembrane #status predicted <TM7>

F;4,10/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;98-176/Disulfide bonds: #status predicted

Query Match 18.8%; Score 479.5; DB 2; Length 350;
Best Local Similarity 25.1%; Pred. No. 6.3e-31;
Matches 122; Conservative 73; Mismatches 125; Indels 167; Gaps 10;

Qy 7 ETNSTDLLSQPNW---BPPV-----ILSNWLSLTFLGLPGNGLVWVAGLKMQR 54
Db 2 ETNS-----SLPTNISGGTPAVSAGYLFIDITLYLVFAVTFVLGNGLVWVAGFRMTH 57
Qy 55 TVNTWFLHLTADLLCCLSLPFLSLAHALQOGWPYGRFLCKLIPSIIVLNMFAVFLIT 114
Db 58 TVTITSYLANAVADFCTSTLTPFFWVKAMGHPFGFLCKFVFTIVDINLFGSVFLIA 117
Qy 115 AISLDRCLVVPKPIWCQNHRNVGMACISGCIWVAVFVVCIPFVYRIFFTDNNRCGY 174
Db 118 LIALDRCCVCLHPVMTQNHRTVSLAKKVIIGPWVWALLLTLPVII-----162
Qy 175 KFLGSSSLDYPDFDYGDDPLENRSLENIYQPPGEMMDRLDPSSFQTNHDHPTVTVFPQPTF 234
Db 163 -----RVTTVPCK-----170
Qy 235 QRPSADSLPRGSARLTSONLYSNVFKPADVSPKIPSGFPEDHETSPLDNDAPLSTHL 294
Db 171 -----TGTACT-----177
Qy 295 KLPPSASSNSFYSELPQGFQDYYNLQGTDD--DQVPTPLVAIT---ITRLVVGFLPLS 349
Db 178 -----ENFSPWTNDPKERIKVAVAMLTVRGIIIRFIIGFSAPM 214
Qy 350 VIMTACTSYFIVRMQRGRFAKQSKTRFVAVVAVFVLCVTPPHIFGVLSLTDPEPL 409
Db 215 SIVAVSGLIATKTHKGLIKS--SRPLRVLSFVAAPFLCWSFYQVVALIATVIRELLQ 273
Qy 410 G--KTLMSWDHVCITALASNCENPFLYALGKDFRKKAROSIQGLEAFSEELTRSTH 467
Db 274 GMYKEIGIADVTSALAFFNSCLNPLMLYVFMGQDFRRLIHALPASLERALTEDSTQTS 333
Qy 468 CPSNNVI 474
Db 334 TATNSTL 340

RESULT 13

A55733

G protein-coupled receptor GPR1 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C;Accession: A55733

R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tauti, L.

Genomics 23, 609-618, 1994

A;Title: Cloning of human genes encoding novel G protein-coupled receptors.

A;Reference number: A55733; MUID:95154831; PMID:7851889

A;Accession: A55733

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-355 <MAR>

A;Cross-references: UNIPROT:P46091; GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g577413

C;Genetics:

A;Gene: GDB:GPR1

A;Cross-references: GDB:371707; OMIM:600239

A;Map position: 15q25-15q26.1

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 17.6%; Score 449.5; DB 2; Length 355;

Best Local Similarity 24.4%; Pred. No. 1.7e-28;

Matches 112; Conservative 65; Mismatches 127; Indels 155; Gaps 7;

Qy 25 LSMVLSLTFLGLPGNGLVWVAGLKMQRVTNTWFLHLTADLLCCLSLPFLSLAHAL 84

Db 40 VSLVLYCLAFVIGIPGNIVWFTGLKWKKTVTTLWFLNLALADFIPLFLPLYSIVAM 99

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Qy 85 QGQMPYGRFLCKLPSIIIVLNMEASVFLITSLDRCLVWFKPIWQCNHRNVGMACSICG 144
Db 100 NFHPFGIWLCKANSFQAQNNFASVFLTVISLDHYIHLHPVLSHRHRTLKNLSLVII 159
Qy 145 CIWVAVFMCIPFVYREIFTDNNRCGYKFGSLSSLDYDFYCDPLENRSLENIVQPP 204
Db 160 FIWLLASLIGGPALYFRDVFENHTLC----- 187
Qy 205 GEMDRDLPSPQNDHPWTVTFQPTFORPSADSLPRGSARLTSONLYSNVFKPADV 264
Db 188 -----YNNFQKHDPDLTL----- 200
Qy 265 VSPKIPSGFPEDHETSPLDNSDAFLSHLKLFPSSASSNSFYSELPOGFODYNLGQFT 324
Db 201 -----IRHH----- 204
Qy 325 DDDQVPTPLV---AITTRLVVGFLPSVIMIACYSFIVFMQRGRFAKOSKTRFVAVV 384
Db 205 -----VLTWVKFIIGVFLPFLTWMSICYCLIFKVKK-RTVLSSRHFWILVVVV 253
Qy 385 VFLVCTWPTPYHFLGVLSLLTDPETPLGKTLMSDWHVCIALASANGCFNPFYALLGKDRK 444
Db 254 AFVVCWTPPYHLFSIWEIHTHNSYSHHVQAGIPLSTGLAFINSLNPLVILYSKRFQA 313
Qy 445 KAROSIQOILEAAFEELTRSTHCPNNVISE--RNSTT 481
Db 314 RFRSVAEILKYITWE-----VSC--SGTVSEQLRNSET 345

RESULT 14
JC2492
G protein-coupled receptor 1 - rat
N:Alternate names: GPR-1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: JC2492
R:Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.R.
Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994
A:Title: Mapping studies of two G protein-coupled receptor genes: An amino acid differ
A:Reference number: JC2492; MUID:95110347; PMID:7811287
A:Accession: JC2492
A:Molecule type: mRNA
A:Residues: 1-353 <MAR>
A:Cross-references: UNIPROT:P46090; GB:S74702; NID:G786483; PIDN:AAB32978.1; PID:G786484
C:Superfamily: vertebrate rhodopsin
F:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; trans
F:74-94/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:134-135/Region: DR motif
F:155-175/Domain: transmembrane #status predicted <TM4>
F:209-229/Domain: transmembrane #status predicted <TM5>
F:246-266/Domain: transmembrane #status predicted <TM6>
F:295-306/Domain: transmembrane #status predicted <TM7>
F:14,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict
F:330/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 15.7%; Score 427; DB 2; Length 353;
Best Local Similarity 23.2%; Pred. No. 1.1e-26;
Matches 102; Conservative 66; Mismatches 117; Indels 154; Gaps 5;

Qy 25 LSMVLSLITFLGLPGNGLVWAGLQKQRTVNTIWFHLTLADLLCCLSLPFSIAHLAL 84
Db 40 ISLLLYALAVLGIPIGNAIVWFGKWKKTIVTLFNLALAIADFIVFLFPLYSIVAL 99
Qy 85 QGQMPYGRFLCKLPSIIIVLNMEASVFLITSLDRCLVWFKPIWQCNHRNVGMACSICG 144
Db 100 SFHWPFGRLCKLSNFQAQNNFASVFLTVISLDHYIHLHPVLSHRHRTLKNLSLVII 159
Qy 145 CIWVAVFMCIPFVYREIFTDNNRCGYKFGSLSSLDYDFYCDPLENRSLENIVQPP 204
Db 160 FVWLLASLIGGPTLYFRDVFENNRITC----- 187
```

```
Qy 205 GEMDRDLPSPQNDHPWTVTFQPTFORPSADSLPRGSARLTSONLYSNVFKPADV 264
Db 188 -----YNN----- 190
Qy 265 VSPKIPSGFPEDHETSPLDNSDAFLSHLKLFPSSASSNSFYSELPOGFODYNLGQFT 324
Db 191 -----FOEY----- 194
Qy 325 DDDQVPTPLV---AITTRLVVGFLPSVIMIACYSFIVFMQRGRFAKOSKTRFVAVV 381
Db 195 -----ELTLRHRHVLTVWKFGLGYLLPLLTWSSCYCLIFKTKKQNTLISLKKMLWSV 249
Qy 382 VVAVFLVCTWPTPYHFLGVLSLLTDPETPLGKTLMSDWHVCIALASANGCFNPFYALLGKD 441
Db 250 VIA-FMVCWTPPYHLFSIWEIHTHNSYSHHVQAGIPLSTGLAFINSLNPLVILYSK 308
Qy 442 FRKAROSIQOILEAAFE 460
Db 309 FOARFRASVAEVLKRSWE 327

RESULT 15
S65693
opioid receptor mu variant MOR1A - human
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: S65693; S51216
R:Bare, L.A.; Mansson, E.; Yang, D.
submitted to the EMBL Data Library, July 1994
A:Description: Expression of two variants of the human mu opioid receptor mRNA in SK-N-S
A:Reference number: S65693
A:Accession: S65693
A:Molecule type: mRNA
A:Residues: 1-392 <BAR>
A:Cross-references: EMBL:U12569; NID:G607911; PIDN:AAB60354.1; PID:G607912
R:Bare, L.A.; Mansson, E.; Yang, D.
FEBS Lett. 354, 213-216, 1994
A:Title: Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cell
A:Reference number: S51215; MUID:95046336; PMID:7957926
A:Accession: S51216
A:Molecule type: mRNA
A:Residues: 387-392 <BAW>
C:Superfamily: vertebrate rhodopsin
```

```
Query Match 14.6%; Score 372.5; DB 2; Length 392;
Best Local Similarity 24.3%; Pred. No. 2.9e-22;
Matches 120; Conservative 64; Mismatches 118; Indels 191; Gaps 18;

Qy 9 NSTDL-----LSQFWNEPPVILSMVIL---SLTFLLGLPGNGLVWV-AGLKMORTVNTI 59
Db 48 NRITDLGGRDSLCPTGSPSMITAITINALYSIVCVGLFGNFLVMYVIVRYTKMKATNI 107
Qy 60 WFLHLTLADLLCCLSLPFSIAHLALQGWYGRPLCKLIPSIIVLNMFASVFLITSLD 119
Db 108 YIFNLALADALATSLTPFQSVNY-LMGTWDPFTGLKIVISIDYNNMFTSFTLCTMSVD 166
Qy 120 RCLVVFKEPIWQCNHRNVGMACSICGCIWVAVFVYREIFTDNNRCGYKFGSL 179
Db 167 RYAVCHPVKALDFTTRPNAKIINVNCNWLSSAIGLWVF---IATTK-----YRQ-- 215
Qy 180 SSLDYPDFYCDPLENRSLENIVQPPGEMDRDLPSPSQNDHP-WTVPTVFPQPTFORPS 238
Db 216 -SID-----CTLTFSHPTW----- 228
Qy 239 ADSLPRGSARLTSONLYSNVFKPADVWVVKIPSGFPEDHETSPLDNSDAFLSHLKLFP 298
Db 229 -----YWENLLK----- 235
Qy 299 SASSNSFYSELPOGFODYNLGQFTDDQVTPPLVAITITRLVVGFLPSVIMIACYSF 358
Db 236 -----ICVFIFAIMPVLLITVCYGL 256
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Search completed: April 13, 2005, 09:47:20
Job time : 49 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2005, 09:29:06 ; Search time 184 Seconds
(without alignments)
1341.425 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 2552

Sequence: 1 MASFSAEINSTDLSQPWNE.....TRSTHCPNNVISERNSTTV 482

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2552	100.0	482	1 C3AR HUMAN	Q16581 homo sapien
2	2231.5	87.4	481	2 Q6TAC8	Q6tac8 macaca fasc
3	1565.5	61.3	477	1 C3AR MOUSE	O09047 mus musculus
4	1551.5	60.8	477	2 Q8C6R2	Q8C6r2 mus musculus
5	1456.5	57.1	475	1 C3AR CAVPO	O88680 cavia porce
6	1426.5	55.9	473	1 C3AR RAT	O55197 rattus norv
7	583	22.8	350	1 CSAR RABIT	Q9tuel oryctolagus
8	553.5	21.7	340	1 CSAR PANTR	P79240 pan troglod
9	551.5	21.6	340	1 CSAR GORGO	P79175 gorilla gor
10	551.5	21.6	350	1 CSAR HUMAN	P21730 homo sapien
11	549.5	21.5	351	2 O88536	O88536 mus musculus
12	549	21.5	352	1 CSAR CANFA	P30992 canis famil
13	545.5	21.4	347	1 CSAR MOUSE	P30993 mus musculus
14	544.5	21.3	340	1 CSAR PONPY	P79234 pongo pygma
15	543.5	21.3	371	1 CML1 MOUSE	P79468 mus musculus
16	541	21.2	352	1 CSAR RAT	P97520 rattus norv
17	536.5	21.0	340	1 CSAR MACMU	P79188 macaca mula
18	530	20.8	373	1 CML1 HUMAN	Q93788 homo sapien
19	521	20.4	349	1 FML2 PANTR	P79243 pan troglod
20	518	20.3	349	1 FML2 GORGO	P79178 gorilla gor
21	516	20.2	371	1 CML1 RAT	O35786 rattus norv
22	515	20.2	352	1 FMLR RABIT	Q05394 oryctolagus
23	514	20.1	349	1 FML2 MACMU	P79191 macaca mula
24	514	20.1	353	1 FML2 HUMAN	P25089 homo sapien
25	513	20.1	349	1 FML2 PONPY	P79237 pongo pygma
26	511.5	20.0	352	2 Q673L2	Q673l2 bos taurus
27	510.5	20.0	348	1 FML1 PONPY	P79236 pongo pygma
28	509.5	20.0	348	1 FML1 MACMU	P79190 macaca mula
29	509.5	20.0	351	1 FML1 HUMAN	P25090 homo sapien
30	509	19.9	351	1 FML1 MOUSE	O08790 mus musculus
31	508.5	19.9	348	1 FML1 GORGO	P79177 gorilla gor

32	508.5	19.9	364	1 FMLR MOUSE	P33766 mus musculus
33	504.5	19.8	345	1 CSAR_CAVPO	O70129 cavia porce
34	503.5	19.7	346	2 Q6T3R0	Q6t3r0 oncorhynch
35	503.5	19.7	350	2 Q6UNA4	Q6una4 oncorhynch
36	501.5	19.7	348	1 FML1 PANTR	P79242 pan troglod
37	493	19.3	347	2 O88535	O88535 mus musculus
38	483.5	18.9	346	1 FMLR PONPY	P79235 pongo pygma
39	478.5	18.8	339	2 O71ME8	O71mr8 mus musculus
40	477.5	18.7	350	1 FMLR HUMAN	P21462 homo sapien
41	476.5	18.7	346	1 FMLR GORGO	P79176 gorilla gor
42	473	18.5	343	2 O88537	O88537 mus musculus
43	472.5	18.5	346	1 FMLR MACMU	P79189 macaca mula
44	470.5	18.4	338	2 O71MR7	O71mr7 mus musculus
45	470.5	18.4	345	1 FMLR PANTR	P79241 pan troglod

ALIGNMENTS

RESULT 1

ID	C3AR HUMAN	STANDARD;	PRT;	482 AA.
AC	Q16581; O43771; Q92868;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).			
GN	Name=C3AR1; Synonyms=AZ3B, C3R1, HNFAG09;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96180983; PubMed=8605247; DOI=10.1016/0167-4781(95)00209-X;			
RA	Roglic A., Prossnitz E.R., Cavanagh S.L., Pan Z., Zou A., Ye R.D.;			
RT	"cDNA cloning of a novel G protein-coupled receptor with a large extracellular loop structure.";			
RL	Biochim. Biophys. Acta 1305:39-43(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96350520; PubMed=8765043;			
RA	Crass T., Raffetseeder U., Martin U., Grove M., Klos A., Koehl J.,			
RT	Bautsch W.;			
RT	"Expression cloning of the human C3a anaphylatoxin receptor (C3AR) from differentiated U-937 cells.";			
RL	Eur. J. Immunol. 26:1944-1950(1996).			
RN	[3]			
RP	REVISONS.			
RA	Bautsch W.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96355342; PubMed=8702752; DOI=10.1074/jbc.271.34.20231;			
RA	Ames R.S., Li Y., Sarau H.M., Nuthallaganti P., Foley J.J., Ellis C.,			
RA	Zeng Z., Su K., Jurewicz A.J., Hertzberg R.P., Bergsma D.J., Kumar C.;			
RT	"Molecular cloning and characterization of the human anaphylatoxin C3a receptor.";			
RL	J. Biol. Chem. 271:20231-20234(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix receptor genes.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction sequenced by the Guchrie cDNA resource center (www.cdna.org).";			
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
RN	[7]			

SEQUENCE FROM N.A., AND VARIANT ALA-136.
 RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi Q., Nickerson D.A.; and the EMBL/GenBank/DBJ databases.
 RT "SeattleSNPs: NHLBI HLB682 program for genomic applications, UW-
 RT FHRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RP [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.F., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marinova K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [9]
 RP SULFATION.
 RX PubMed=12871936; DOI=10.1074/jbc.M306061200;
 RA Gao J., Choe H., Bota D., Wright P.L., Gerard C., Gerard N.P.;
 RA "Sulfation of tyrosine 174 in the human C3a receptor is essential for
 RT binding of C3a anaphylatoxin.";
 RL J. Biol. Chem. 278:37902-37908(2003).
 CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 CC anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
 CC enzyme release and superoxide anion production.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed in several differentiated
 CC hematopoietic cell lines, in the lung, spleen, ovary, placenta,
 CC small intestine, throughout the brain, heart, and endothelial
 CC cells. Mostly expressed in lymphoid tissues.
 CC -!- PTM: Among the sulfation sites Tyr-174 is essential for binding of
 CC C3a anaphylatoxin.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; U28488; AAC50374.1; -;
 DR EMBL; Z73157; CAA97504.1; -;
 DR EMBL; U62027; AAC50657.1; -;
 DR EMBL; AB065870; BAC06088.1; -;
 DR EMBL; AY268431; AAR23198.1; -;
 DR EMBL; AY455929; AAR13862.1; -;
 DR EMBL; BC020742; AAB30742.1; -;
 DR PIR; S65766; S65766;
 DR Genbank; HGNC:1319; C3AR1.
 DR H-invDB; HIX0010402; -;
 DR MIM; 605246; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004943; F: C3a anaphylatoxin receptor activity; TAS.
 DR GO; GO:0004876; F: complement component C3a receptor activity; TAS.
 DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 DR GO; GO:0004435; F: phosphoinositide phospholipase C activity; TAS.

DR GO; GO:0008015; P: circulation; TAS.
 DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; TAS.
 DR GO; GO:0006954; P: inflammatory response; TAS.
 DR InterPro; IPR002334; Anaphylx receptor.
 DR InterPro; IPR001644; C3Aantx receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1104; ANPHYLATXNR.
 DR PRINTS; PRO1060; C3ANPHYLXNR.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Polymorphism;
 KW Sulfation; Transmembrane.
 FT DOMAIN 1 23 Extracellular (Potential).
 FT TRANSMEM 24 46 1 (Potential).
 FT DOMAIN 47 57 Cytoplasmic (Potential).
 FT TRANSMEM 58 80 2 (Potential).
 FT DOMAIN 81 96 Extracellular (Potential).
 FT TRANSMEM 97 118 3 (Potential).
 FT DOMAIN 119 139 Cytoplasmic (Potential).
 FT TRANSMEM 140 160 4 (Potential).
 FT DOMAIN 161 340 Extracellular (Potential).
 FT TRANSMEM 341 360 5 (Potential).
 FT DOMAIN 361 377 Cytoplasmic (Potential).
 FT TRANSMEM 378 400 6 (Potential).
 FT DOMAIN 401 417 Extracellular (Potential).
 FT TRANSMEM 418 438 7 (Potential).
 FT DOMAIN 439 482 Cytoplasmic (Potential).
 FT MOD RES 174 174 Sulfotyrosine.
 FT MOD RES 184 184 Sulfotyrosine.
 FT MOD RES 318 318 Sulfotyrosine.
 FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 194 194 N-linked (GlcNAc...) (Potential).
 FT DISULFID 95 172 By similarity.
 FT VARIANT 136 136 V -> A.
 FT CONFLICT 151 151 /FTID=VAR_019164.
 FT CONFLICT 203 203 P -> C (in Ref. 4).
 FT CONFLICT 482 AA; 53864 MW; 287E219D98CED203 CRC64;
 SQ SEQUENCE 482 AA; 53864 MW; 287E219D98CED203 CRC64;
 Query Match 100.0%; Score 2552; DB 1; Length 482;
 Best Local Similarity 100.0%; Pred. No. 3e-173;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFAETNTDLSQPNWPPVLTSMVLSLFLGLPGNGLVWAGLQWQRTVNTI 60
 Db 1 MASFAETNTDLSQPNWPPVLTSMVLSLFLGLPGNGLVWAGLQWQRTVNTI 60
 Qy 61 FLHLTLADLLCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
 Db 61 FLHLTLADLLCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
 Qy 121 CLVVFKPIWQNHQNVGACISGCIWVAFVWCIPVYVREIFTTNNHRCGKFGLS 180
 Db 121 CLVVFKPIWQNHQNVGACISGCIWVAFVWCIPVYVREIFTTNNHRCGKFGLS 180
 Qy 181 SLDPYDFVGDPLENRSLENIVPPGEMNDRLDPSSFOINDHPVTVPVFPOTQPSAD 240
 Db 181 SLDPYDFVGDPLENRSLENIVPPGEMNDRLDPSSFOINDHPVTVPVFPOTQPSAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFPEDHETSPLDNSDAFLSTHLKLPFA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFPEDHETSPLDNSDAFLSTHLKLPFA 300
 Qy 301 SSNSFYSESLPQGFQDYINLGOFTDDDDQVTPVLAITITRLVVGFLPSPVIMACYFIV 360
 Db 301 SSNSFYSESLPQGFQDYINLGOFTDDDDQVTPVLAITITRLVVGFLPSPVIMACYFIV 360
 Qy 361 FRMORGRFAKSSQKTFRRVAVVAVFLVCMVTPVPHIFGLVSLTLDPETPLGKTLMSWDHVC 420
 Db 361 FRMORGRFAKSSQKTFRRVAVVAVFLVCMVTPVPHIFGLVSLTLDPETPLGKTLMSWDHVC 420

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Qy 421 IALASANSFNPFYALLGKDFRKAROSIQGILEAAFSBELTRSTHCPSSNNVFSERNST 480
Db 421 IALASANSFNPFYALLGKDFRKAROSIQGILEAAFSBELTRSTHCPSSNNVFSERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 2
Q6TAC8
ID Q6TAC8 PRELIMINARY; PRT; 481 AA.
AC Q6TAC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Anaphylatoxin C3a receptor.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Therien A.G., Gervais F.G.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426336; AAR06214.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004943; F: C3a anaphylatoxin receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0006935; P: chemotaxis; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002234; Anphylx receptor.
DR InterPro; IPR001644; C3aantx_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1104; ANPHYLATOXNR.
DR PRINTS; PRO1060; C3ANPHYLTXNR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ
SEQUENCE 481 AA; 53577 MW; 4C64DCB8006BA4F CRC64;

Query Match 87.4%; Score 2231.5; DB 2; Length 481;
Best Local Similarity 88.6%; Pred. No. 1.8e-150;
Matches 429; Conservative 13; Mismatches 37; Indels 5; Gaps 2;

Qy 1 MASFSAEITNDLLSQPNNEPVLISMLVLSITFLGLPGNGLVWVAGLRKQRTVNTIW 60
Db 1 MAPFSAEITNDLLSQPNNEPVLISMLVLSITFLGLPGNGLVWVAGLRKQRTVNTIW 60

Qy 61 FLHITLADLLCLSLPFLSLAHALOGQWPYGRFLCKLIPSIIVLNMFPASVFLITSLDR 120
Db 61 FLHITLADLLCLSLPFLSLAHALOGQWPYGRFLCKLIPSIIVLNMFPASVFLITSLDR 120

Qy 121 CLVVPKPTWCQNRHNVGACISCGIIVVAFVVCIPVYVREIFTDNNHRCGVKFGLS 180
Db 121 CLVVPKPTWCQNRHNVGACISCGIIVVAFVVCIPVYVREIFTDNNHRCGVKFGLS 180

Qy 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHPTVPTVFPQTQFQPSAD 240
Db 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHPTVPTVFPQTQFQPSAD 240

Qy 241 SLRPGSARLTQNLVSNVFKPADVVPKIPSGFPDIEDHETPLDNSDAFLSTHLKLPSPA 300
Db 241 SLRPGSARLTQNLVSNVFKPADVVPKIPSGFPDIEDHETPLDNSDAFLSTHLKLPSPA 300

Qy 297 SLRPGSARLTQNLVSNVFKPADVVPKIPSGFPDIEDHETPLDNSDAFLSTHLKLPSPA 297
Db 297 SLRPGSARLTQNLVSNVFKPADVVPKIPSGFPDIEDHETPLDNSDAFLSTHLKLPSPA 297

Qy 301 SSNSPSESLPQGFODYINLQFTDDQVPLVAITITRLVVGFLPSVIMIACYSTIV 360
Db 301 SSNSPSESLPQGFODYINLQFTDDQVPLVAITITRLVVGFLPSVIMIACYSTIV 360

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Db 298 ASNSLYVELPQDFQDYVSLGQFTYDQVSTPLVAITITRLVVGFLPSVIMIACYSTIV 357
Qy 361 FRMQRGPAKSGKSTFRVAVVVAVFLVCTWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 358 LRMQRGPAKSGKSTFRVAVVVAVFLVCTWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 417
Qy 421 IALASANSFNPFYALLGKDFRKAROSIQGILEAAFSBELTRSTHCPSSNNVFSERN-- 478
Db 418 TALASANSFNPFYALLGKDFRKAROSIQGILEAAFSBELTRSTHCPSSNNVFSERN-- 477
Qy 479 STTV 482
Db 478 STTV 481

RESULT 3
C3AR MOUSE
ID C3AR MOUSE STANDARD; PRT; 477 AA.
AC 009047; 035951;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR) (Complement component 3a receptor 1).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ, and C57BL/6; TISSUE=Brain;
RX MEDLINE=97307604; PubMed=9164946;
RA Tornetta M.A., Foley J.J., Sarau H.M., Ames R.S.;
RT "The mouse anaphylatoxin C3a receptor: molecular cloning, genomic organization, and functional expression.";
RL J. Immunol. 158:5277-5282(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98044205; PubMed=9382922; DOI=10.1007/s002510050327;
RA Hau M.H., Ember J.A., Wang M., Prossnitz E.R., Hugli T.E., Ye R.D.;
RT "Cloning and functional characterization of the mouse C3a anaphylatoxin receptor gene.";
RL Immunogenetics 47:64-72(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98357887; PubMed=9694514; DOI=10.1016/S0161-5890(98)00021-2;
RA Hollmann T.J., Haviland D.L., Kildgaard J., Watts K., Wetzel R.A.;
RT "Cloning, expression, sequence determination, and chromosome localization of the mouse complement C3a anaphylatoxin receptor gene.";
RL Mol. Immunol. 35:137-148(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes."
RN Genome Res. 10:1617-1630(2000).
RP [5]
RC SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Oviduct;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer."
RN Genome Res. 10:1757-1771(2000).
RP [6]
RC SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Oviduct;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK054017; BAB35622.1; --
DR MGD: MGI:1097680; C3arl.
DR GO: GO:0016021; C: integral to membrane; TAS.
DR InterPro: IPR002234; Anaphylx_receptor.
DR InterPro: IPR001644; C3Aantx_receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR01104; ANPHYLATOXNR.
DR PRINTS: PR01060; C3ANPHYLTXNR.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 477 AA; 53591 MW; B21C0952B21D16D6 CRC64;
Query Match 60.8%; Score 1551.5; DB 2; Length 477;
Best Local Similarity 64.1%; Pred. NO. 4e-102;
Matches 309; Conservative 51; Mismatches 109; Indels 13; Gaps 6;
QY 1 MASFAETNSDLSQPNNEPVLISWVLSITFLGLPGHGLVLAAGLQKQRTVNTI 60
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 MGSPDADNTSLDSRPLFPQDIAASMVLGLTCLLGLGLGLVLAAGVAKKTTVTNW 60
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 FLHLLTADLLCLSLPFLSLAHLAGOWPYGRFLKLPISIVLNMFAVFLTAISLDR 120
DB 61 FLHLLTADLLCLSLPFLSLAHLLQCHWPYGLFLKLPISIVLNMFAVFLTAISLDR 120
QY 121 CLWFKPIWQNRHNVGMACTSCGCIWVAFVFCIPVFVYRIFFTDNNRCGYKFLGS 180
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 121 CLIVHKPIWQNRHNVRTAFACGCVWVAFVYVYVYRDLFTMDNRSICRYNFDSSR 180
QY 181 SLIDYPDF---YGDPLENSLENIVOPGEMNDRLDPSSFQTNHDTWTVTFVQPTQRP 237
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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DB 181 SYDYWDVYVKLSLPESNSTDNSTAQLTGHMNDRSAPSSVRARDYFWTVTTALQSQPFLTS 240
QY 238 SADSLPKSGSARLTSONLYSNVFPADVSPKIPSGFFIEDHETSPLDNSDAFLSTHLKLP 297
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 241 PEDSFLSDSA--NQQPHYGG--KPPNVLTAAVPSGFEVDRKNTL--NADAFLSAHTFLF 295
QY 298 PSASSNSFYSESLPQGFQDQVYVNLGQFDDQVPTPLVAITITRLVVGFLPLSPVIMCIACS 357
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 296 PTASSGHLY----PYDQGY--VDQFYDNHVPFPLMAITITRLVVGFLVFPFFIWCYS 350
QY 358 FIYFRMQRGRFAKSKTFRVAVVAVFLVCMVTPYHIFGVLSLLTDPETPLGKTLMSWD 417
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 351 LIVFRMKTNTKSRNKTFRVAVAVTVFICWTPYHLVGVLLITDPSSSLGAVNSWD 410
QY 418 HVCIALASANSNCFNPFYLLGKDFRKAQSQISOGILEAAFSSELTSTHCPNNSVNER 477
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 411 HMSIALASANSNCFNPFYLLGKDFRKAQSQISOGILEAAFSSELTSTHCPNNSVNER 470
QY 478 NS 479
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 471 NN 472
RESULT 5
C3AR_CAVPO STANDARD; PRT; 475 AA.
ID C3AR_CAVPO
AC O88680; Q9WQ99;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).
GN Name=C3AR;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98391014; PubMed=97251598;
RA Lienenklaus S., Ames R.S., Tornetta M.A., Sarau H.M., Foley J.J.,
RA Crass T., Sohns B., Raffetseder U., Grove M., Hoelzer A., Klos A.,
RA Koehl J., Bautsch W.;
RT "Human anaphylatoxin C4a is a potent agonist of the guinea pig but not
RT the human C3a receptor."
RL J. Immunol. 161:2089-2093 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RX STRAIN=Hartley; TISSUE=Spleen;
RX MEDLINE=98414293; PubMed=9743361;
RA Fukuoka Y., Ember J.A., Hugli T.E.;
RT "Molecular cloning of two isoforms of the guinea pig C3a anaphylatoxin
RT receptor: alternative splicing in the large extracellular loop."
RL J. Immunol. 161:2977-2984(1998).
CC -1- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
CC enzyme release and superoxide anion production.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=gpc3ar-L;
CC IsoId=O88680-1; Sequence=Displayed;
CC Name=2; Synonyms=gpc3ar-S;
CC IsoId=O88680-2; Sequence=VSP_010628;
CC -1- TISSUE SPECIFICITY: Expressed in the heart, kidney, lung, liver,
CC peritoneal macrophages and spleen.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC EMBL; AJ006402; CAA07002.1; --
CC EMBL; U86378; AAC36503.1; --
CC InterPro; IPR002234; Anaphylx_receptor.
CC InterPro; IPR001644; C3Aantx_receptor.
CC DR Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PR01104; ANPHYLATOXNR.
CC DR PRINTS; PR01060; C3ANPHYLTXNR.
CC DR PRINTS; PR00237; GPCR_Rhodopsn.
CC DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC DR Alternative splicing; Chemotaxis; G-protein coupled receptor;
CC Glycoprotein; Sulfation; Transmembrane.
CC KW DOMAIN 1 23 Extracellular (Potential).
CC FT TRANSMEM 24 46 1 (Potential).
CC FT DOMAIN 47 57 Cytoplasmic (Potential).
CC FT TRANSMEM 58 80 2 (Potential).
CC FT DOMAIN 81 96 Extracellular (Potential).
CC FT TRANSMEM 97 118 3 (Potential).
CC FT DOMAIN 119 139 Cytoplasmic (Potential).
CC FT TRANSMEM 140 160 4 (Potential).
CC FT DOMAIN 161 331 Extracellular (Potential).
CC FT TRANSMEM 332 351 5 (Potential).
CC FT DOMAIN 352 368 Cytoplasmic (Potential).
CC FT TRANSMEM 369 391 6 (Potential).
CC FT DOMAIN 392 408 Extracellular (Potential).
CC FT TRANSMEM 409 429 7 (Potential).
CC FT DOMAIN 430 475 Cytoplasmic (Potential).
CC FT DISULFID 95 172 By similarity.
CC FT MOD_RES 174 174 Sulfotyrosine (By similarity).
CC FT MOD_RES 183 183 Sulfotyrosine (By similarity).
CC FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 273 273 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 254 288 Missing (in isoform 2).
CC FT /FTID=VSP_010628.
CC CONFLICT 2 2 E -> D (in Ref. 2).
CC CONFLICT 357 357 V -> A (in Ref. 2).
CC SEQUENCE 475 AA; 53570 MW; 0D6PFF5627A3330 CRC64;

Query Match
Best Local Similarity 57.1%; Score 1456.5; DB 1; Length 475;
Matches 288; Conservative 59.1%; 59; Mismatches 115; Indels 25; Gaps 7;

QY 1 MAFSAETNSDLSQPNWPPVLSVILSLTLGLPGNGLVWAGLKMORTVNIW 60
DB 1 MESSAETNSGLHLEPYQPTETLMAILGLTFLVGLPGNGLVWAGLKMRTVNW 60
QY 61 FLHLTLADLLCLSLPESLAHLALQGWPGYGRFLCKLIPSIIVLNMFAVFLTLAISLDR 120
DB 61 FLHLTVADFVCLSLPESMAHLALRGWPGYGEILCKEIPVIVLNMFAVFLTLAISLDR 120
QY 121 CLVVFKPIWQNHNRVGMACISGCIWVAFVWCMIPVYVREIPTTDHNRGCKYKGLSS 180
DB 121 CLMWLKEIWKQNHNRVGTACIICGCIWVAFVLCIPVYVREITLENHTICTVNFSPG 179
QY 181 SLDPYDF-----YGDPLENRSLENIQPPGEMNDRLDPSSQOTDHNPTVPTVFPQ 232
DB 180 SFYLDYAYDRDANGYGT-----DPVQLPGEMEHRSPSSQOTQDGPMSVTTLYSQ 233
QY 233 TFQPSADSLPRGSARLTQNLVSNVFKPADVSPKIPSGFPIEDHETSPLDNSDAFLST 292
DB 234 TSQRPSEDSFMSAKSLSGQGY-----VDVVLPTNLGLPMEENITVILHNA-AFLSS 286
QY 293 HLKLPASNSFVESLPQGFQYNYLNGQFTDDQVPTPLVAITITRLVVGFLPLPSVIM 352
DB 287 DLQV-SNATOKCLSTPEPPQDFND--DLSPFTHEYRTPLRLKVTITFRLVVGFLPLMIIM 343
QY 353 IACYSFTVFMQRGRFAKSKTFRVAVVVAVVAVLCVWTPVHIFGLVSLTDPETPLGKT 412

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Db 344 VACVTLIIIFRMRRVRVVKSWNKALHLAMVVVTVFLICWAPYHVFGLILFINPESRVGAA 403
QY 413 LMSWDHVCIALASANSFNPFLYALIGKDFKKAROSIQIGILEAAFSLELTRSTHCPNN 472
DB 404 LLSWDHVSIALASANSFNPFLYALLGRDLRKVRQSMKGLAFAFSEDISKSTSFIOAK 463
QY 473 VISERN 479
DB 464 AFSEKHS 470

RESULT 6
C3AR RAT
ID C3AR RAT STANDARD; PRT; 473 AA.
AC O55197;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).
GN Name=C3arl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Lung;
RC MEDLINE=98125550; PubMed=9464274; DOI=10.1006/bbrc.1997.8034;
RA Fukuoaka Y., Ember J.A., Hugli T.E.;
RT "Cloning and characterization of rat C3a receptor: differential
RL expression of rat C3a and C5a receptors by LPS stimulation.";
RL Biochem. Biophys. Res. Commun. 242:663-668(1998).
CC -1- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
CC enzyme release and superoxide anion production.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC EMBL; U86378; AAC40071.1; --
CC FIR; JCS835; JCS835.
CC RGD; 620537; C3arl.
CC InterPro; IPR002234; Anaphylx_receptor.
CC InterPro; IPR001644; C3Aantx_receptor.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR01104; ANPHYLATOXNR.
CC PRINTS; PR01060; C3ANPHYLTXNR.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
CC Transmembrane.
CC KW DOMAIN 1 23 Extracellular (Potential).
CC FT TRANSMEM 24 46 1 (Potential).
CC FT DOMAIN 47 57 Cytoplasmic (Potential).
CC FT TRANSMEM 58 80 2 (Potential).
CC FT DOMAIN 81 96 Extracellular (Potential).
CC FT TRANSMEM 97 118 3 (Potential).
CC FT DOMAIN 119 139 Cytoplasmic (Potential).
CC FT TRANSMEM 140 160 4 (Potential).
CC FT DOMAIN 161 331 Extracellular (Potential).
CC FT TRANSMEM 332 349 5 (Potential).
CC FT DOMAIN 350 366 Cytoplasmic (Potential).
CC FT TRANSMEM 367 389 6 (Potential).
CC FT DOMAIN 390 406 Extracellular (Potential).

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FT TRANSMEM 407 427 7 (Potential).
 FT DOMAIN 428 472 Cytoplasmic (Potential).
 FT DISULFID 95 172 By similarity.
 FT MOD RES 174 174 Sulfotyrosine (By similarity).
 FT MOD RES 184 184 Sulfotyrosine (By similarity).
 FT MOD RES 308 308 Sulfotyrosine (By similarity).
 FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 473 AA; 52896 MW; 722F16F6F4B16451 CRC64;

Query Match 55.9%; Score 1426.5; DB 1; Length 473;
 Best Local Similarity 59.4%; Pred. No. 3e-93;
 Matches 290; Conservative 59; Mismatches 118; Indels 21; Gaps 9;

Qy 1 MASPSAETNSTDLSQPNNEPVPVLSMVLSTFLGLPGNGLVWAGLQKQRTVNTIW 60
 Db 1 MESFTADNTDLSRPLFKPDQIASMVLSTLCLGLPGNGLVWAGVWVKRTVNTVW 60

Qy 61 FLHLTLADLCLSLPSPSLAHALOGQWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Db 61 FLHLTLADFLCCLSLPSPSLAHALIRGHWPYGLFLCKLIPSIIVLNMFAVFLTAISLDR 120

Qy 121 CLVVPKPIWQCNHRNVGMACIGCGIWWAFVWCIPVYVREIFTDNNHRCGYKFLGSS 180
 Db 121 CLWVKPIWQCNHRNVGMACIGCGIWWAFVWCIPVYVREIFTDNNHRCGYKFLGSS 180

Qy 181 SLDPDFYDGPLNRSLENIQVPP-----GEMNDRLDPSFQTNHDPVTVTFQQTQF 236
 Db 181 AYDYWDY----WYNHLPPI-NPPDNSTGHVDDRTAPSSVPARDLWATTALQSQTEHT 235

Qy 237 PSADSLPRGSLRSLTQNLVSNVFPKIPSGFPDIEDHETSPLDNSDAFLSTHLKL 296
 Db 236 SPEDPFSQDSA--SQPHYGG--KPTVLIATIPGGFPVDEHKSNTL--NTGAFLSAHTEP 290

Qy 297 FPSASSNFYSELSLPQGFQDYVNLQGFDDQVPTPLVAITITRLVGVFLPLSPVIMIA 356
 Db 291 SLTASSSPLVADFP--DDVFD--QLMVGNAHWTPQVAITISRLVGLVFPFFIMITY 345

Qy 357 SPVIFRMQRGPAKQSKTFRVAVVAVFLVCTWTPYHFGVLSLLTDPETPLGKTLMSW 416
 Db 346 SLVIFRMKTNLTGSRNKTFRVAVVAVVFFVCTWTPYHFGVLSLLTDPETPLGKTLMSW 405

Qy 417 DHVCTALASNCFPPLVALLGKDFRKARQSIQIIEAFAESELSTHCPNSNVNISE 476
 Db 406 DHMSTALASNCFPPLVALLGKDFRKARQSVKGLLEAFAESELSTHCTQDKAPSK 465

Qy 477 RN--STTV 482
 Db 466 RNMSTDV 473

RESULT 7

C5AR_RABBIT
 ID_C5AR_RABBIT STANDARD; PRT; 350 AA.
 AC Q9TUE1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5ar) (Fragment).
 GN Name=C5R1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=99441277; PubMed=10510441;
 RA Bachvarov D.R., Houle S., Bachvarova M., Bouthillier J.,
 RA St Pierre S.A., Fukuoka Y., Ember J.A., Marceau F.;
 RT "Cloning and preliminary pharmacological characterization of the
 RT anaphylatoxin C5a receptor in the rabbit."
 RL Br. J. Pharmacol. 128:321-326 (1999).

-!- FUNCTION: Receptor for the chemotactic and inflammatory peptide anaphylatoxin C5a. This receptor stimulates chemotaxis, granule enzyme release and superoxide anion production (By similarity).
 -!- SUBCELLULAR LOCATION: Integral membrane protein.
 -!- PTM: Sulfation plays a critical role in the association of C5ar with C5a, but no significant role in the ability of the receptor to transduce a signal and mobilize calcium in response to a small peptide agonist (By similarity).
 -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL: AF068680; AAF13030.1;
 InterPro: IPR002234; Anaphylx_receptor.
 InterPro: IPR001274; CSAantx_receptor.
 InterPro: IPR000276; GPCR_Rhodopsn.
 Pfam: PF00001; 7tm.1; 1.
 PRINTS: PR01104; ANPHYLATOKNR.
 PRINTS: PR00426; CSANPHYLTKNR.
 PRINTS: PR00237; GPCRHOOPS.
 PROSITE: PS00237; G-PROTEIN RECEPTOR FL_1; 1.
 PROSITE: PS0262; G-PROTEIN RECEPTOR FL_2; 1.
 Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 Transmembrane.
 NON_TER 1
 DOMAIN 41 36 Extracellular (Potential).
 TRANSMEM 37 59 1 (Potential).
 DOMAIN 60 70 Cytoplasmic (Potential).
 TRANSMEM 71 93 2 (Potential).
 DOMAIN 94 109 Extracellular (Potential).
 TRANSMEM 110 131 3 (Potential).
 DOMAIN 132 152 Cytoplasmic (Potential).
 TRANSMEM 153 173 4 (Potential).
 DOMAIN 174 200 Extracellular (Potential).
 TRANSMEM 201 226 5 (Potential).
 DOMAIN 227 242 Cytoplasmic (Potential).
 TRANSMEM 243 265 6 (Potential).
 DOMAIN 266 282 Extracellular (Potential).
 TRANSMEM 283 303 7 (Potential).
 DOMAIN 304 350 Cytoplasmic (Potential).
 DISULFID 108 187 By similarity.
 MOD_RES 8 8 Sulfotyrosine (By similarity).
 MOD_RES 10 10 Sulfotyrosine (By similarity).
 MOD_RES 13 13 Sulfotyrosine (By similarity).
 SQ SEQUENCE 350 AA; 38585 MW; C69871B3E20897C2 CRC64;

Query Match 22.8%; Score 583; DB 1; Length 350;
 Best Local Similarity 29.1%; Pred. No. 2e-33;
 Matches 132; Conservative 54; Mismatches 112; Indels 156; Gaps 6;

Qy 21 PPIVLSMVLSTFLGLPGNGLVWAGLQKQRTVNTIWFLHLTLADLCLSLPFSLA 80
 Db 34 PTTIVLVYMAVFLVGVGNALVWVTALEAKRTVNAIFLNLAVADLLSCLALPILFV 93

Qy 81 HIALQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDRCLVVPKPIWQCNHRNVGMAC 140
 Db 94 SIIOEGHWPFGRAACSVLPISLLNMYSAILLATISADRFLLNPNPWCQTRNGLA 153

Qy 141 STCGIWWAFVWCIPVYVREIFTDNNHRCGYKFLGSSLSLDYDFYDGPLNRSLENI 200
 Db 154 LACCVAGLALLTIPSLYRKVLQD-----DYP----- 182

Qy 201 VQPPGEMNDRLDPSFQTNHDPVTVTFQQTQFQPSADSLPRGSLRSLTQNLVSNVFPK 260
 Db 183 ----- 182

Qy 261 PADVVPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLFPSASSNFYSELSLPQGFQDY 320

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Db 183 -----PRTTCGV-----|||-----DYCHE 194
Qy 321 GQFTDDDDQVPTPLVAITITRLVWGFLPSVIMIACYSFIVFMORGRPAKSQSKTFRVAV 380
Db 195 GVRAER-----AVATVRLVWGFLPLFTLSVCYTFELLRTW-SRNGTSTKTLKVVV 245
Qy 381 VVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANCENPELYALGK 440
Db 246 AVVVSFFFWLFPYQVGMILALLHPSSATFWATRLDPLCLALAVVNCINPIIYVAGK 305
Qy 441 DFRKAROSIQGILEAAFSSE-----LTRST 466
Db 306 GFGQGLRKSPLSLRLNVLAEBSVIQGSKFSRST 339

RESULT 8
CSAR_PANTR STANDARD; PRT; 340 AA.
AC P79240;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5aR) (Fragment).
GN Name=C5R1; Synonyms=C5AR;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
human primates.";
RL Immunogenetics 44:446-452(1996).

-!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
anaphylatoxin C5a. This receptor stimulates chemotaxis, granule
enzyme release and superoxide anion production.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: Sulfation plays a critical role in the association of C5aR
with C5a, but no significant role in the ability of the receptor
to transduce a signal and mobilize calcium in response to a small
peptide agonist (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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-----
EMBL; X97730; CAA66314.1; .
InterPro; IPR002234; Anphylx receptor.
InterPro; IPR001274; C5Aantx receptor.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01104; ANPHYLATXNR.
PRINTS; PR00426; CSANPHYLTXNR.
PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 53 1 (Potential).
FT DOMAIN 54 64 Cytoplasmic (Potential).
FT TRANSMEM 65 87 2 (Potential).
FT DOMAIN 88 103 Extracellular (Potential).
FT TRANSMEM 104 125 3 (Potential).

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FT DOMAIN 126 146 Cytoplasmic (Potential).
FT TRANSMEM 147 167 4 (Potential).
FT DOMAIN 168 193 Extracellular (Potential).
FT TRANSMEM 194 219 5 (Potential).
FT DOMAIN 220 235 Cytoplasmic (Potential).
FT TRANSMEM 236 258 6 (Potential).
FT DOMAIN 259 275 Extracellular (Potential).
FT TRANSMEM 276 296 7 (Potential).
FT DOMAIN 297 340 Cytoplasmic (Potential).
FT DISULFID 102 181 By similarity.
FT MOD RES 4 4 Sulfotyrosine (By similarity).
FT MOD RES 7 7 Sulfotyrosine (By similarity).
FT NON TER 340
SQ SEQUENCE 340 AA; 38209 MW; B3BD4ADBA909513F CRC64;

Query Match 21.7%; Score 553.5; DB 1; Length 340;
Best Local Similarity 27.2%; Pred. No. 2.4e-31;
Matches 123; Conservative 63; Mismatches 110; Indels 157; Gaps 6;

Qy 22 PVILSMVLSLTFLGLPGNGLVWAGLWAGLMQRTVNTWFLHLTLADLCLCLSLPFLSLAH 81
Db 29 PDILALVIFAVVLVGVIGNALVVMVTAFAKRTIINAIWFLNLAADVFLSCALPILFTS 88
Qy 82 LALQGWPGYGRFLCKLIPSIIVLNMFAVFLLTATSLDRCLVVPKPIWQCNHRNVGMACS 141
Db 89 IVQHHPWPGGAACSLPLSLLNMYASILLATISADRLFLVFKPIWQCNFRGAGLAWI 148
Qy 142 ICGGIWVAVFVWCIPVYVREIFTTDNHNRGKYFGLSSLDYDFYGDPLENRSLENIV 201
Db 149 ACAVANGALALLITIPSLYR----- 168
Qy 202 QPPEMNDRLDPSSFQNDHPWTVPVTPQTFORPSADSLPRGSARLTSLQNLVSNVFKP 261
Db 169 -----VVREYF----- 175
Qy 262 ADVVSPKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPFSASSNSFYSELPOGFQDYNNLG 321
Db 176 ----PPKVLGV----- 183
Qy 322 QFTDDDDQVPTPLVAITITRLVWGFLPSVIMIACYSFIVFMORGRPAKSQSKTFRVAVV 381
Db 184 DYSHDKRRER---AVATVRLVWGFLPLFTLSVCYTFELLRTW-SRNGTSTKTLKVVVA 239
Qy 382 VVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANCENPELYALGKD 441
Db 240 VVASFFFWLFPYQVGMILALLHPSSATFWATRLDPLCLALAVVNCINPIIYVAGQG 299
Qy 442 FRKAROSIQGILEAAFSSE-----LTRST 466
Db 300 FGRLQKSLPSLLRLNVLTEBSVVRKSKFSRST 332

RESULT 9
CSAR_GORGO STANDARD; PRT; 340 AA.
AC P79175;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5aR) (Fragment).
GN Name=C5R1; Synonyms=C5AR;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
human primates.";
RL Immunogenetics 44:446-452(1996).

-!- FUNCTION: Receptor for the chemotactic and inflammatory peptide

```

CC anaphylatoxin C5a. This receptor stimulates chemotaxis, granule
 CC enzyme release and superoxide anion production.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: Sulfation plays a critical role in the association of C5a
 CC with C5a, but no significant role in the ability of the receptor
 CC to transduce a signal and mobilize calcium in response to a small
 CC peptide agonist (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X97733; CAA66317.1; -;
 CC InterPro: IPR002234; Anaphylx_receptor.
 CC InterPro: IPR001274; C5antx_receptor.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR01104; ANPHYLATXNR.
 CC PRINTS: PR00426; CSANPHYLXNR.
 CC PRINTS: PR00237; GPCRHHODPSN.
 CC PROSITE: PS00237; G_PROTEIN_RCEP_F1_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_RCEP_F1_2; 1.
 CC Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 KW Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN <1 30 Extracellular (Potential).
 FT TRANSMEM 31 53 1 (Potential).
 FT DOMAIN 54 64 Cytoplasmic (Potential).
 FT TRANSMEM 65 87 2 (Potential).
 FT DOMAIN 88 103 Extracellular (Potential).
 FT TRANSMEM 104 125 3 (Potential).
 FT DOMAIN 126 146 Cytoplasmic (Potential).
 FT TRANSMEM 147 167 4 (Potential).
 FT DOMAIN 168 193 Extracellular (Potential).
 FT TRANSMEM 194 219 5 (Potential).
 FT DOMAIN 220 235 Cytoplasmic (Potential).
 FT TRANSMEM 236 258 6 (Potential).
 FT DOMAIN 259 275 Extracellular (Potential).
 FT TRANSMEM 276 296 7 (Potential).
 FT DOMAIN 297 >340 Cytoplasmic (Potential).
 FT DISULFID 102 181 By similarity.
 FT MOD_RES 4 4 Sulfotyrosine (By similarity).
 FT MOD_RES 7 7 Sulfotyrosine (By similarity).
 FT NON_TER 340 340
 FT SEQUENCE 340 AA; 38235 MW; 214CFCE78A47B304 CRC64;
 Query Match 21.6%; Score 551.5; DB 1; Length 340;
 Best Local Similarity 27.2%; Pred. No. 3.4e-31;
 Matches 123; Conservative 62; Mismatches 111; Indels 157; Gaps 6;
 QY 22 PVLSMWLSLTFLGLPGNLVWAGLKQWRTWNTWFLHTLADLCCLSLPFLSLAH 81
 DB 29 PDILALVIVAVVFLVGLVGNVWVWTAFAEKRTINAIWFLNLAVALFSLCALPILFTS 88
 QY 82 LALQGWVPGRLCKLPISIVLNNFASVFLITATSLDRCLVVPKIPQCNHNVGMACS 141
 DB 89 IVQHHHPGGACRLISLILUNMYASILLATISADRFLLVFPINQCNFRGAGLAWI 148
 QY 142 ICGCIWVAVVNCIFVVFREIFTTDNNHRCQYKFGLSLSDYDPDGPDLNRSLENIV 201
 DB 149 ACAVAGLALLTIFSLYR----- 168
 QY 202 QPPGEWDRLDPSFSQTNDHPWTVVTPQTFQPSADSLPRGSARLTSQLNLSNVKFP 261
 DB 169 -----VREYF----- 175
 QY 262 ADVVSPKIPSGFPIEDHETSLDSDAFLSLHLKFLPSASSNSFYSELSLPGQFDYINLG 321

Db 176 ----PPKVLGV----- 183
 QY 322 QFTDDQVPTPLVAITITRLVWGLLPSVIMACYSFIVFMQGRFPAKSKTFRVAVV 381
 Db 184 DYSHKRRER---AVAVRLVGLFWPLLTICVTFLLRTWRRATRS-TKTLKVVA 239
 QY 382 VVAVFLVCTVPHIFGVLSLTDPTPLGKTLMSDHWICIALASANSFNPFLYALLGKD 441
 Db 240 VVAFSFFFWLPTQVGTGMMSEFSPSTFLNKLKLSLCVFAYNCCINFIYVAGQG 299
 QY 442 FRKAROSIQGLEAFSE-----LTRST 466
 Db 300 FQGRLRKSLPSLLRLNVLTEESVVRKSFTST 332
 RESULT 10
 CSAR HUMAN
 ID CSAR HUMAN STANDARD; PRT; 350 AA.
 AC P21730;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5aR) (CD88 antigen).
 GN Name=C5R1; Synonyms=C5AR;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91156029; PubMed=1847994; DOI=10.1038/349614a0;
 RA Gerard N.P., Gerard C.;
 RT "The chemotactic receptor for human C5a anaphylatoxin.";
 RL Nature 349:614-617(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91175748; PubMed=2007135;
 RA Boulay F., Mery L., Tardif M., Bouchon L., Vignais P.;
 RT "Expression cloning of a receptor for C5a anaphylatoxin on
 RL differentiated HL-60 cells.";
 RL Biochemistry 30:2993-2999(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SULFATION.

RX MEDLINE=21240629; PubMed=11342590;
 RA Farzan M., Schnitzler C.E., Vasiliou N., Leung D., Kuhn J.,
 RA Gerard C., Gerard N.P., Choe H.,
 RT "Sulfated tyrosines contribute to the formation of the csa docking
 RL site of the human csa anaphylatoxin receptor."
 RL J. Exp. Med. 193:1059-1066(2001).
 CC -|- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 CC anaphylatoxin C5a. This receptor stimulates chemotaxis, granule
 CC enzyme release and superoxide anion production.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- PTM: Sulfation plays a critical role in the association of the
 CC receptor with C5a, but no significant role in the ability of the
 CC receptor to transduce a signal and mobilize calcium in response to
 CC a small peptide agonist.
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD88 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd88.htm".
 CC -----
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 CC -----
 CC EMBL; X58674; CAB37830.1; -;
 CC EMBL; M62505; AAR62831.1; -;
 CC EMBL; X57250; CAA40530.1; -;
 CC EMBL; AY221091; AAO65969.1; -;
 CC EMBL; BC008982; AAO08982.1; -;
 CC PIR; A37963; A37963.
 CC Genbank; HGNC:1338; C5R1.
 CC H-InvDB; HIX0015270; -;
 CC MIM; 113995; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004944; F: C5a anaphylatoxin receptor activity; TAS.
 CC GO; GO:0000187; P: activation of MAPK; TAS.
 CC GO; GO:0006968; P: cellular defense response; TAS.
 CC GO; GO:0006935; P: chemotaxis; TAS.
 CC GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 CC GO; GO:0007202; P: phospholipase C activation; TAS.
 CC GO; GO:0007606; P: sensory perception of chemical stimulus; TAS.
 CC GO; GO:0007165; P: signal transduction; TAS.
 CC InterPro; IPR002234; Anaphylx_receptor.
 CC InterPro; IPR001274; C5Aantx_receptor.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7cm_1; 1.
 CC PRINTS; PR01104; ANPHYLATXNR.
 CC PRINTS; PR00426; CSANPHYLTXNR.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 KW Transmembrane.
 FT DOMAIN 1 37 Extracellular (Potential).
 FT TRANSMEM 38 60 1 (Potential).
 FT DOMAIN 61 71 Cytoplasmic (Potential).
 FT TRANSMEM 72 94 2 (Potential).
 FT DOMAIN 95 110 Extracellular (Potential).
 FT TRANSMEM 111 132 3 (Potential).
 FT DOMAIN 133 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 174 4 (Potential).
 FT DOMAIN 175 200 Extracellular (Potential).
 FT TRANSMEM 201 226 5 (Potential).
 FT DOMAIN 227 242 Cytoplasmic (Potential).
 FT TRANSMEM 243 265 6 (Potential).
 FT DOMAIN 266 282 Extracellular (Potential).
 FT TRANSMEM 283 303 7 (Potential).
 FT DOMAIN 304 350 Cytoplasmic (Potential).
 FT DISULFID 109 188 By similarity.
 FT MOD_RES 11 11 Sulfotyrosine.
 FT MOD_RES 14 14 Sulfotyrosine.

FT CARBOHYD 5 5 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 350 AA; 39320 MW; DD1D0D71D327CDD0 CRC64;
 Query Match 21.6%; Score 551.5; DB 1; Length 350;
 Best Local Similarity 27.4%; Pred. No. 3.5e-31;
 Matches 124; Conservative 60; Mismatches 112; Indels 157; Gaps 6;
 Qy 22 PVILSMVLSITLGLPGNGLVWAGLKMQRVNTWTFHLTLADLLCGLSIPFSLAH 81
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 36 PDILALVIFAVVFLVGLVGNLVVWVFAFAKRTINAIFLNLAVADFLSCIALPILFTS 95
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 82 LALQGMQPGFRFLCKLIPSIIVLNWAFSVLLTAISLDRCLVWFKPIWQCNHNVGMACS 141
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 96 IVQHHPFGGACGACSLPSILLNNYASILLATISADRFLLVFKPIWQCNFRGLAWI 155
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 142 ICGIWWVAFVWCIPVYVYRIFFTDNNHRCGYKFGLSLSDYDFYGDPLENRSLENI 201
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 156 ACAVANGALLATIPSLYR----- 175
 Qy QPQGMNDLDPSSFQNDHPWTVPTVQTFQPSADSLPRGSARLTSQNLVSNVFKP 261
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 176 -----VREYF----- 182
 Qy ADVVSPKIPSGFTIEDHETSPLDNSDAPLSTHLKLPSSASSNSFYSELPQGFQDYVNLG 321
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 183 ----PPKVLGV----- 190
 Qy QFTDDQVPTPLVAITITRLVGHLLPSVIMACYSTIVFMQRGRFAKSOSKTRFVAVV 381
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 191 DYSHDKRER---AVAVRLVGLFELWELLTTCITFILLRTWRRATRS-TKTLKVVA 246
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 382 VVAVFLVCTPYHIFGVLSLTDPTPLGLTMSWDHVCIALASANCENPFLYALLQKD 441
 Qy |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 247 VVASFFFWLPYQVTGIMMSFLEPSSPTFLLNKLDSLCVSFAYINCINPIIIVVAGQG 306
 Qy 442 FRKARQSIQGLEAFSEE-----LTRST 466
 Db |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
 307 FGRLRKLSPLLRNVLTEESVVRSSKSFTRST 339
 RESULT 11
 O88536 PRELIMINARY; PRT; 351 AA.
 ID O88536
 AC O88536;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE N-formylpeptide receptor-like 2 (Lipoxin A4 receptor-like
 DE protein).
 GN Name=Ppr-rs2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98390190; PubMed=972950; DOI=10.1006/geno.1998.5376;
 RA Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
 RT "Differential expansion of the N-formylpeptide receptor gene cluster
 RT in human and mouse."
 RL Genomics 51:270-276(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=B10.A;
 RC MEDLINE=22206880; PubMed=12218158;
 RA Vaughn M.W., Proske R.J., Haviland D.L.;
 RT "Identification, cloning, and functional characterization of a murine
 RT lipoxin A4 receptor homologue gene."
 RL J. Immunol. 169:3363-3369(2002).
 DR EMBL; AF071180; AAC34585.1; -;
 DR EMBL; AY138248; AAN06932.1; -;
 DR MGD; MGI:1278319; Ppr-rs2.
 DR GO; GO:0016021; C: integral to membrane; IEA.

QY 314 FQDYVNLGQTDQVPTPLVAITITRLVGVGLPSVIMVACYSFIVFRMQRGRPAKQS 373
 Db 192 --DVGSGVGVVER-----GVALLRLMGFLGELVILSCYTPFLLRTW-SRKATRST 240
 QY 374 KTRFVAVVAVFVLCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSCEPNPF 433
 Db 241 KTLKVVAVVSVFFVWLPYQVTGMMALFYKHSEFRRVSRDLSCVAVAYINCCINPI 300
 QY 434 LYALLGKDKPRKARQSIQILEAFSEE 461
 Db 301 IYVLAAGQGFHGRFLKSLPARLRQVLAEE 328

RESULT 13

CSAR_MOUSE STANDARD; PRT; 347 AA.
 AC P30993;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5aR).
 GN Name=C5r1; Synonyms=C5ar;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93017861; PubMed=1401897;
 RA Gerard C., Bao L., Orozco O., Pearson M., Kunz D., Gerard N.P.;
 RT "Structural diversity in the extracellular faces of peptidergic G-
 protein-coupled receptors. Molecular cloning of the mouse C5a
 anaphylatoxin receptor";
 RL J. Immunol. 149:2600-2606(1992).
 CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 anaphylatoxin C5a. This receptor stimulates chemotaxis, granule
 enzyme release and superoxide anion production.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: Sulfation plays a critical role in the association of C5ar
 with C5a, but no significant role in the ability of the receptor
 to transduce a signal and mobilize calcium in response to a small
 peptide agonist (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 EMBL; S46665; AAB97774.1; ALT SEQ.
 EMBL; S50577; AAB97774.1; JOINED.
 DR MGD; MGI:88232; C5r1.
 DR InterPro; IPR002234; Anaphylx receptor.
 DR InterPro; IPR001274; CSAantx receptor.
 DR InterPro; IPR000276; GPCR_RhoGpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR01104; ANPHYLATOXNR.
 DR PRINTS; PR00426; CSAANTXNR.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECF_F1_2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 Transmembrane. 1 33 Extracellular (Potential).
 DOMAIN 34 56 1 (Potential).
 FT DOMAIN 57 67 Cytoplasmic (Potential).
 FT TRANSMEM 68 90 2 (Potential).
 FT DOMAIN 91 106 Extracellular (Potential).
 FT TRANSMEM 107 128 3 (Potential).
 FT DOMAIN 129 149 Cytoplasmic (Potential).

FT TRANSMEM 150 170 4 (Potential).
 FT DOMAIN 171 197 Extracellular (Potential).
 FT TRANSMEM 198 223 5 (Potential).
 FT DOMAIN 224 239 Cytoplasmic (Potential).
 FT TRANSMEM 240 262 6 (Potential).
 FT DOMAIN 263 279 Extracellular (Potential).
 FT TRANSMEM 280 300 7 (Potential).
 FT DOMAIN 301 347 Cytoplasmic (Potential).
 FT DISULFID 105 184 By similarity.
 FT MOD RES 9 Sulfotyrosine (By similarity).
 FT MOD RES 12 Sulfotyrosine (By similarity).
 FT CARBOHYD 2 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 347 AA; 38510 MW; 3C614DADDDDF53B CRC64;
 Query Match 21.4%; Score 545.5; DB 1; Length 347;
 Best Local Similarity 26.7%; Pred. No. 9.2e-31;
 Matches 127; Conservative 59; Mismatches 135; Indels 155; Gaps 5;
 QY 12 DLLSQWNEPPVILSMVLSITLTLGLPGNGLVWAGLKMQRVTNTWFLHLTLADLLC 71
 Db 22 DGIHLPRQGDVAALIIYSVFLVGVFGNALVVMVTAFFPDGFSNAIWFNLAVADLLS 81
 QY 72 CLSLPFLSLAHLAQGWPFYGRFLCKLIPSIIVLMNFASVFLITATISLDRCLVVFKEPIWCQ 131
 Db 82 CLAMPVLTFTVHNHNYWVFEDATACIVLPSSLILLNMVYASILLLATISADRFLLVFKPIWCQ 141
 QY 132 NHRVNGMACSICGCIWVAVFVCMIPVYVYREIFTT--DNHNRCCYKFGLSLSLDYDPFYG 189
 Db 142 KVRGTGLAMACGVAVVLAALLLTIPSFVREAYKDFYSEHTVCVGINYGGG----- 192
 QY 190 DPLENRSLENIQVPGEMNDRLDSSFTQNDHPWTVTFVQPQTFQRPASDLSLRGSARL 249
 Db 193 ----- 192
 QY 250 TSONLYSNVFKPADWSPKIPSGFPPIEDHETSLDNLSDAFLSTHLKFLPSASSNSFYSE 309
 Db 193 -----FPKEK----- 197
 QY 310 LPOGFQDYNLGQTDQVPTPLVAITITRLVGVGLPSVIMVACYSFIVFRMQRGRPA 369
 Db 198 -----AVAILRLMVGFLVPLLTLLNICVTFELLRTW-SRKA 231
 QY 370 KSQSKTRFVAVVAVFVLCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANS 429
 Db 232 TRSTKTLKVVAVVAVVLCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANS 291
 QY 430 FNFPLYALLGKDKPRKARQSIQILEAFSEEIT---RSTHCPSNVVISERNSTTV 482
 Db 292 VNPFIYVMAGQGFHGRLLRSLPSIIRNALSSEDSVGRDSKTFTFSTDTSPRKSQAV 347

RESULT 14

CSAR_PONPY STANDARD; PRT; 340 AA.
 AC P79234;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C5a anaphylatoxin chemotactic receptor (C5a-R) (C5aR) (Fragment).
 GN Name=C5r1; Synonyms=C5AR;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
 RA Alvarez V., Coto E., Sehen F., Gouzalet-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
 human primates";
 RL Immunogenetics 44:446-452(1996).
 CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 anaphylatoxin C5a. This receptor stimulates chemotaxis, granule

CC enzyme release and superoxide anion production.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PM: Sulfation plays a critical role in the association of CSAR
 CC with C5a, but no significant role in the ability of the receptor
 CC to transduce a signal and mobilize calcium in response to a small
 CC peptide agonist (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL; X97732; CRA66316.1; -
 DR InterPro; IPR002234; Anphylx receptor.
 DR InterPro; IPR001274; CSAantx receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01104; ANPHYLXTOXNR.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 DR Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 KW Transmembrane.
 FT NON TER 1 1
 FT DOMAIN <1 30 Extracellular (Potential).
 FT TRANSMEM 31 53 1 (Potential).
 FT DOMAIN 54 64 Cytoplasmic (Potential).
 FT TRANSMEM 65 87 2 (Potential).
 FT DOMAIN 88 103 Extracellular (Potential).
 FT TRANSMEM 104 125 3 (Potential).
 FT DOMAIN 126 146 Cytoplasmic (Potential).
 FT TRANSMEM 147 167 4 (Potential).
 FT DOMAIN 168 193 Extracellular (Potential).
 FT TRANSMEM 194 219 5 (Potential).
 FT DOMAIN 220 235 Cytoplasmic (Potential).
 FT TRANSMEM 236 258 6 (Potential).
 FT DOMAIN 259 275 Extracellular (Potential).
 FT TRANSMEM 276 296 7 (Potential).
 FT DOMAIN 297 >340 Cytoplasmic (Potential).
 FT DISULFID 102 181 By similarity.
 FT MOD RES 4 4 Sulfotyrosine (By similarity).
 FT MOD RES 7 7 Sulfotyrosine (By similarity).
 FT NON TER 340 340
 SQ SEQUENCE 340 AA; 38241 MW; 2790316E0C963185 CRC64;
 Query Match 21.3%; Score 544.5; DB 1; Length 340;
 Best Local Similarity 27.4%; Pred. No. 1.1e-30;
 Matches 124; Conservative 61; Mismatches 111; Indels 157; Gaps 7;
 QY 22 PVILSMVLSLTELGLPNGVLVWAGLWKQRTVNTIWLHLTLADLCLSLPFLSLAH 81
 DB PDILALVFAVFLVGLVGNALVWVWVTAFAKRTINAIWFLNLAVADFLSCLALPILFTS 88
 QY 82 LALOCQWPGYRFLCKLIPSIIVLNMFAVFLITAIISLDRCLVWFKPIWCQNRNVGMACS 141
 DB IVQHHWPFPGAACILPSSLILLNMYASILLATISADRFLLVFNPIWCQNRFGNGLAWI 148
 QY 142 ICGIIVWVAVFVICPIVVFVRIEFTTDNHNRCGYKFGLSGLSSLDYDFYGDPLENLSNIV 201
 DB ACAVANGALLLTIPSLFYLR----- 168
 QY 202 QPPGEMNDLPSSQTDNDHWVTPVTPQTFQFPQSADSLPRGSARLTSQNLVSNVFKP 261
 DB -----VVREYVF----- 175
 QY 262 ADVVSPKIPGFPIDHETSPLDNDFAFLSTHLKLFPSASSNSFYSELPGQFDYVNLG 321
 DB -----PPKVLGV---DH-----G 186

QY 322 QFTDDDDQVPTPLVAITITRLVGVFLPSVIMICIACYSIVFMQGRGPAKQSQKTRFVAV 381
 DB 187 HDKRRER-----AVAILRVLVGLVFWPLLTTCYCTELLRTWSRRATRS-TKTLKVVVA 239
 QY 382 VVAVFLVCTPYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSCFNPFYALLGKD 441
 DB 240 VVASFFTFWLPYQVTGMMSPFLPSSPTFLLKLLKSLCISFAVINCINPIIIVVAGOG 299
 QY 442 FRKAKRSIQIGILEAASFEE-----LTRST 466
 DB 300 FQGLRKSPLSLRLNVLTEESVVRKSKSFTRST 332

RESULT 15

CML1 MOUSE
 ID CML1 MOUSE STANDARD; PRT; 371 AA.
 AC P97458;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Chemokine receptor-like 1 (G-protein coupled receptor DEZ).
 GN Name=Cmk1r1; Synonym=Des, Gpcr27;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97289630; PubMed=9144535; DOI=10.1006/bbrc.1997.6455;
 RA Methner A., Herney G., Schinke B., Hermans-Borgmeyer I.;
 RT "A novel G protein-coupled receptor with homology to neurotrophin and
 RT chemottractant receptors expressed during bone development.";
 RL Biochem. Biophys. Res. Commun. 233:336-342(1997).
 CC -1- FUNCTION: Orphan receptor. Could be a chemotactic peptide
 CC receptor. May have a function in bone metabolism.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: Expressed during bone development and in
 CC adult parathyroid glands. Expressed at day E11 in the caudal part
 CC of the tongue and the umbilical cord and the expression in the
 CC tongue was maintained throughout adulthood. Expression increases
 CC in bone and cartilaginous forming zones of embryo up to stage
 CC E14.5 and at E16.5 expression is seen in the lung.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL; U79525; AAB53789.1; -
 DR PIR; JC5498; JC5498.
 DR MGD; MGI:109603; Cmk1r1.
 DR InterPro; IPR002258; DEZorph receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 39 Extracellular (Potential).
 FT TRANSMEM 40 62 1 (Potential).
 FT DOMAIN 63 73 Cytoplasmic (Potential).
 FT TRANSMEM 74 95 2 (Potential).
 FT DOMAIN 96 112 Extracellular (Potential).
 FT TRANSMEM 113 133 3 (Potential).
 FT DOMAIN 134 152 Cytoplasmic (Potential).
 FT TRANSMEM 153 174 4 (Potential).
 FT DOMAIN 175 222 Extracellular (Potential).

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OM protein - protein search, using sw model

Run on: April 13, 2005, 09:47:28 ; Search time 174 Seconds

(without alignment)
1071.371 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 482

Sequence: 1 MASFSAEINSTDLLSQPWE.....TRSTHCPNNVLSRNSITTV 482

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Genesep 16Dec04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	100.0	482	2	Aaw42376 Homo sapi
2	482	100.0	482	5	Aau99102 Human ana
3	482	100.0	482	6	Abu79122 Chemoat
4	482	100.0	482	6	Abp81797 Human com
5	482	100.0	482	7	Adc86209 Human gpc
6	482	100.0	482	7	Adf43378 Chemoat
7	482	100.0	482	8	Adr05360 Human ana
8	384	79.7	415	8	Abm83496 Human dia
9	381	79.0	482	2	Aaw02151 Human G-p
10	381	79.0	482	2	Aaw23367 Novel G-p
11	381	79.0	482	7	Abu62861 Putative
12	381	79.0	482	7	Add46294 Human Pro
13	381	79.0	482	8	Adl22832 Human C3a
14	381	79.0	482	8	Ado29203 Human gpc
15	381	79.0	482	8	Adq19275 Human sof
16	381	79.0	482	8	Ado50920 Complem
17	331	68.7	485	3	Aab58319 Lung canc
18	280	58.1	482	4	Abb56336 Non-endog
19	242	50.2	482	2	Aaw06540 C5a-like
20	30	6.2	477	4	Aay72389 Mouse C3a
21	30	6.2	477	5	Aau75166 Mouse ana
22	30	6.2	477	5	Adl22834 Murine C3
23	30	6.2	477	8	Ado29204 Mouse gpc
24	30	6.2	477	8	Adr05368 Mouse ana
25	29	6.0	473	7	Add46292 Rat Prote

26	20	4.1	20	5	AAU99103	Aau99103 Human ana
27	20	4.1	20	5	AAU99104	Aau99104 Human ana
28	20	4.1	20	6	ABP82198	Abp82198 G protein
29	20	4.1	20	6	ABP82195	Abp82195 G protein
30	20	4.1	20	6	ABP82196	Abp82196 G protein
31	19	3.9	19	5	AAU99106	Aau99106 Human ana
32	19	3.9	19	5	AAU99105	Aau99105 Human ana
33	19	3.9	19	6	ABP82197	Abp82197 G protein
34	10	2.1	10	4	AAG94981	Aag94981 Human com
35	10	2.1	10	4	AAG94975	Aag94975 Human com
36	10	2.1	10	4	AAG94991	Aag94991 Human com
37	10	2.1	10	4	AAG94977	Aag94977 Human com
38	10	2.1	10	4	AAG94979	Aag94979 Human com
39	10	2.1	10	4	AAG94985	Aag94985 Human com
40	10	2.1	10	4	AAG94983	Aag94983 Human com
41	10	2.1	10	4	AAG94989	Aag94989 Human com
42	10	2.1	10	4	AAG94993	Aag94993 Human com
43	10	2.1	10	4	AAG94987	Aag94987 Human com
44	10	2.1	10	8	ADH68236	Adh68236 Human G-p
45	10	2.1	177	4	AAU25587	Aau25587 Human G P
46	10	2.1	309	4	AAAB73099	Aab73099 Rat LTC4
47	10	2.1	309	4	AAAB85095	Aab85095 Rat cysLT
48	10	2.1	309	8	ADO29278	Ado29278 Mouse GPC
49	10	2.1	337	3	AAy81949	Aay81949 Human C5L
50	10	2.1	337	4	AAU25608	Aau25608 Human G P
51	10	2.1	337	4	AAAG64290	Aag64290 Human GTP
52	10	2.1	337	4	ABD11830	Abd11830 Human GPC
53	10	2.1	337	4	AAAM78358	Aam78358 Human pro
54	10	2.1	337	4	AAAM79342	Aam79342 Human pro
55	10	2.1	337	4	AAE06757	Aae06757 Human G-p
56	10	2.1	337	4	AAAB85473	Aab85473 7 traneme
57	10	2.1	337	4	AAU04364	Aau04364 Human G-p
58	10	2.1	337	4	AAU04585	Aau04585 Human G-p
59	10	2.1	337	5	AAE19353	Aae19353 Human G-p
60	10	2.1	337	5	AAE24982	Aae24982 Human C5a
61	10	2.1	337	6	ABP81708	Abp81708 Human G P
62	10	2.1	337	7	ADL96452	Adl96452 Human G P
63	10	2.1	337	8	ADE52370	Ade52370 Human C5L
64	10	2.1	337	8	ADH68219	Adh68219 Human G-p
65	10	2.1	337	8	ADO29440	Ado29440 Human GPC
66	10	2.1	345	4	AAAB73098	Aab73098 Pig LTC4
67	9	1.9	19	2	AAAR37902	Aar37902 Chemoat
68	9	1.9	304	2	AAAR48714	Aar48714 G-protein
69	9	1.9	304	2	AAW02686	Aaw02686 G-protein
70	9	1.9	320	5	AAU080479	Aau080479 Dog brady
71	9	1.9	350	4	ABBB56337	Abb56337 Non-endog
72	9	1.9	350	5	AAU080480	Aau080480 Dog/human
73	9	1.9	350	6	ABU09503	Abu09503 Human C5a
74	9	1.9	350	6	ABP81798	Abp81798 Human com
75	9	1.9	350	7	ABU62862	Abu62862 Human C5a
76	9	1.9	350	7	ABR63913	AbR63913 Human C5a
77	9	1.9	350	7	ADJ68582	Adj68582 Human hea
78	9	1.9	350	8	ADO29205	Ado29205 Human GPC
79	9	1.9	350	8	ADQ19520	Adq19520 Human sof
80	9	1.9	350	8	ADR05362	Adr05362 Human ana
81	9	1.9	350	8	ADR67242	Adr67242 Human bla
82	9	1.9	350	8	ADS15321	AdS15321 Human com
83	9	1.9	350	8	ADO29364	Ado29364 Mouse GPC
84	9	1.9	368	8	ABM83764	Abm83764 Human dia
85	9	1.7	9	3	AAy65999	Aay65999 G-protein
86	8	1.7	10	3	AAy66000	Aay66000 G-protein
87	8	1.7	18	2	AAAR64890	Aar64890 Human C5a
88	8	1.7	63	3	AAy66002	Aay66002 G-protein
89	8	1.7	64	3	AAy66001	Aay66001 G-protein
90	8	1.7	258	4	AAU25589	Aau25589 Human G P
91	8	1.7	333	8	ADR05370	Adr05370 Mouse ana
92	8	1.7	339	8	ADO29717	Ado29717 Mouse gpc
93	8	1.7	343	8	ABO58630	AbO58630 Human gen
94	8	1.7	347	8	ADO29206	Ado29206 Mouse GPC
95	8	1.7	350	8	ADP29740	Adp29740 Human sec
96	8	1.7	355	2	AAAR81461	Aar81461 G-protein
97	8	1.7	355	2	AAW73635	Aaw73635 Human C5a
98	8	1.7	355	3	AAy90643	Aay90643 Human mut

99	8	1.7	355	3	AAY90609	Aay90609 Human G p	172	8	1.7	888	7	ABO69221	Abc69221 Pseudomon
100	8	1.7	355	4	AAU93557	Aam93557 Human pol	173	8	1.7	1138	5	AAU98553	Aau98553 Novel hum
101	8	1.7	355	4	AAU01299	Aau01299 Human G-p	174	8	1.7	1210	5	AU98551	Au98551 Novel hum
102	8	1.7	355	4	AAU01301	Aau01301 Human G-p	175	8	1.7	1211	6	ABR61471	Abf61471 Human sec
103	8	1.7	355	4	AAU01300	Aau01300 Human G-p	176	8	1.7	1277	4	AAAB70236	Aab70236 170KDa su
104	8	1.7	355	5	AAE13306	Aae13306 Human mat	177	8	1.7	1292	2	AAR70681	Aar70681 Entamoeba
105	8	1.7	355	6	ABU09501	Abu09501 Human ana	178	8	1.7	1292	4	AAB70235	Aab70235 170KDa su
106	8	1.7	355	6	ABP81879	Abp81879 Human p	179	8	1.7	19	6	ABU13490	Abu13490 Zona pell
107	8	1.7	355	7	ADC22683	Adc22683 Human G p	180	7	1.5	19	6	ABU13489	Abu13489 Zona pell
108	8	1.7	355	7	ADC22521	Adc22521 Human G p	181	7	1.5	22	2	AAW34031	Aaw34031 Angiotens
109	8	1.7	355	7	ADH13994	Adh13994 Human GPR	182	7	1.5	30	8	ADR44124	Adr44124 Human OC-
110	8	1.7	355	7	ADH14156	Adh14156 Mutated h	183	7	1.5	33	2	AAW40022	Aaw40022 Peptide e
111	8	1.7	355	8	ADL31292	Adl31292 Human pro	184	7	1.5	37	4	AAE01496	Aae01496 Human gen
112	8	1.7	355	8	ADO29363	Ado29363 Human GPC	185	7	1.5	37	4	AAE01451	Aae01451 Human alb
113	8	1.7	358	3	AAE02841	Aae02841 Human G p	186	7	1.5	37	5	ABG63916	Abg63916 Human gen
114	8	1.7	358	3	AAV71307	Aav71307 Human orp	187	7	1.5	37	5	ABG63915	Abg63915 Human alb
115	8	1.7	358	4	AAE65627	Aae65627 Human leu	188	7	1.5	37	8	ADL77180	Adl77180 Albumin f
116	8	1.7	358	4	AAE65630	Aae65630 Rat leuko	189	7	1.5	37	8	ADL77181	Adl77181 Albumin f
117	8	1.7	358	4	AAE64296	Aae64296 Human GTP	190	7	1.5	44	4	AAW91259	Aaw91259 Human imm
118	8	1.7	358	4	AAE02934	Aae02934 Human LTB	191	7	1.5	45	4	ABW17241	Abw17241 Human ner
119	8	1.7	358	4	AAE04568	Aae04568 Human G-p	192	7	1.5	52	3	ABW34482	Abw34482 Human sec
120	8	1.7	358	4	AAE73096	Aae73096 Human leu	193	7	1.5	52	6	ADA98238	Ada98238 Human sec
121	8	1.7	358	6	ABG73112	Abg73112 Human leu	194	7	1.5	52	6	ADA44085	Ada44085 Human sec
122	8	1.7	358	6	ABU92275	Abu92275 Human G p	195	7	1.5	52	7	ADC20410	Adc20410 Human sec
123	8	1.7	358	6	ABG72596	Abg72596 Novel hum	196	7	1.5	52	7	ADF10723	Adf10723 Human sec
124	8	1.7	358	7	ADG98780	Adg98780 Human orp	197	7	1.5	55	4	AAO08097	Aao08097 Human pol
125	8	1.7	358	7	ADK52560	Adk52560 Hematolog	198	7	1.5	57	4	AAO16854	Aao16854 Peptide #
126	8	1.7	358	7	ADJ26943	Adj26943 Human end	199	7	1.5	57	4	ABW35838	Abw35838 Peptide #
127	8	1.7	358	8	ADG86397	Adg86397 Human end	200	7	1.5	57	4	ABW29339	Abw29339 Peptide #
128	8	1.7	358	8	ADP20190	Adp20190 Human G p	201	7	1.5	57	4	ABW30666	Abw30666 Peptide #
129	8	1.7	358	8	ADQ75094	Adq75094 Human G p	202	7	1.5	57	4	AAW69020	Aaw69020 Human bon
130	8	1.7	360	8	ADO29533	Ado29533 Mouse GPC	203	7	1.5	57	4	AAW56644	Aaw56644 Human bra
131	8	1.7	363	4	AAW16016	Aaw16016 Peptide #	204	7	1.5	57	4	ABG50690	Abg50690 Human liv
132	8	1.7	363	4	AAW28517	Aaw28517 Peptide #	205	7	1.5	57	4	AAW04563	Aaw04563 Peptide #
133	8	1.7	363	4	AAW68196	Aaw68196 Human bon	206	7	1.5	57	5	ABG38617	Abg38617 Human pep
134	8	1.7	363	4	AAW55822	Aaw55822 Human bra	207	7	1.5	61	4	AAW21853	Aaw21853 Peptide #
135	8	1.7	382	8	ADO29405	Ado29405 Mouse GPC	208	7	1.5	61	4	ABW44222	Abw44222 Peptide #
136	8	1.7	389	2	AAAY54756	Aay54756 Human fis	209	7	1.5	61	4	AAW38177	Aaw38177 Peptide #
137	8	1.7	389	3	AAAY94477	Aay94477 Human HG0	210	7	1.5	61	4	AAW77959	Aaw77959 Human bon
138	8	1.7	389	4	AAU25609	Aau25609 Human G p	211	7	1.5	61	4	ABW65254	Abw65254 Human bra
139	8	1.7	389	4	AAE02933	Aae02933 Human LTB	212	7	1.5	61	4	ABG59595	Abg59595 Human liv
140	8	1.7	389	5	AAU09008	Aau09008 Human leu	213	7	1.5	69	5	ABP01046	Abp01046 Human ORF
141	8	1.7	389	5	AAE14391	Aae14391 Human leu	214	7	1.5	71	4	ABW17405	Abw17405 Peptide #
142	8	1.7	389	5	AAE51857	Aae51857 Human leu	215	7	1.5	71	4	ABW36428	Abw36428 Peptide #
143	8	1.7	389	6	ABP81978	Abp81978 Human leu	216	7	1.5	71	4	AAW29927	Aaw29927 Peptide #
144	8	1.7	389	6	ADN05969	Adn05969 Antipsori	217	7	1.5	71	4	ABW31221	Abw31221 Peptide #
145	8	1.7	389	8	ADO29532	Ado29532 Human GPC	218	7	1.5	71	4	ABW21780	Abw21780 Protein #
146	8	1.7	395	2	AAW44703	Aaw44703 Human Th2	219	7	1.5	71	4	AAW69591	Aaw69591 Human bon
147	8	1.7	395	5	ABP65225	Abp65225 Hypoxia-r	220	7	1.5	71	4	AAW57186	Aaw57186 Human bra
148	8	1.7	395	6	ABR55449	AbR55449 Amino aci	221	7	1.5	71	4	ABG51265	Abg51265 Human liv
149	8	1.7	395	6	ABP81999	Abp81999 Human G p	222	7	1.5	71	4	AAW05090	Aaw05090 Peptide #
150	8	1.7	395	6	ABR61470	AbR61470 Human sec	223	7	1.5	71	5	ABG39212	Abg39212 Human pep
151	8	1.7	395	8	ADO29404	Ado29404 Human GPC	224	7	1.5	72	3	ABW16774	Abw16774 Bacteriop
152	8	1.7	408	2	AAW77867	Aaw77867 S. clavul	225	7	1.5	73	8	ADG19671	Adg19671 G-protein
153	8	1.7	408	6	AAE14864	Aae14864 S. clavul	226	7	1.5	74	3	AAW64792	Aaw64792 Human 5'
154	8	1.7	409	4	AAE07915	Aae07915 S. clavul	227	7	1.5	74	3	AAW02212	Aaw02212 Human sec
155	8	1.7	409	6	ABU62223	Abu62223 Clavulani	228	7	1.5	74	3	AAW05176	Aaw05176 Arabidops
156	8	1.7	409	7	ADD26441	Add26441 Streptomy	229	7	1.5	75	4	AAW82115	Aaw82115 Human hae
157	8	1.7	409	7	ADG47786	Adg47786 Streptomy	230	7	1.5	76	4	AAE09572	Aae09572 Cytotoxic
158	8	1.7	429	7	ABO81630	AbO81630 Pseudomon	231	7	1.5	93	2	AAW50807	Aaw50807 G-protein
159	8	1.7	466	2	ABW59669	Abw59669 Bovine al	232	7	1.5	93	2	AAW02999	Aaw02999 G-protein
160	8	1.7	466	5	ADI40991	Adi40991 Bovine al	233	7	1.5	94	2	AAW22506	Aaw22506 Sugar bee
161	8	1.7	467	5	ABW78211	AbW78211 Amino aci	234	7	1.5	94	5	AAW96181	Aaw96181 Human sec
162	8	1.7	472	5	ABW78210	AbW78210 Amino aci	235	7	1.5	94	5	ABG64803	Abg64803 Human alb
163	8	1.7	486	5	ABP52435	Abp52435 Human G p	236	7	1.5	94	8	ADL78070	Adl78070 Albumin f
164	8	1.7	518	5	ABW92812	Abw92812 Herbicida	237	7	1.5	103	5	ABP01442	Abp01442 Human ORF
165	8	1.7	587	4	AAU34198	Aau34198 Staphyloc	238	7	1.5	105	3	ABW62918	Abw62918 Human g35
166	8	1.7	603	4	AAU37074	Aau37074 Staphyloc	239	7	1.5	111	2	AAW72669	Aaw72669 Cladospor
167	8	1.7	662	5	AAU98554	Aau98554 Novel hum	240	7	1.5	116	4	AAU18097	Aau18097 Novel hum
168	8	1.7	714	6	ABG73643	Abg73643 Human G-p	241	7	1.5	116	4	AAU18646	Aau18646 Renal and
169	8	1.7	733	5	AAU98552	Aau98552 Novel hum	242	7	1.5	116	4	AAU21583	Aau21583 Novel hum
170	8	1.7	735	7	ADE34400	Ade34400 Human G-p	243	7	1.5	116	4	AAW99963	Aaw99963 Human exp
171	8	1.7	801	4	ABG21468	Abg21468 Novel hum	244	7	1.5	116	4	ABB10174	Abb10174 Human CDN

245	7	1.5	116	4	AAU87123	Aau87123 Novel	cen	318	7	1.5	226	7	ADC26149	Adc26149 Human	PRO
246	7	1.5	116	4	AAU18292	Aau18292 Human	end	319	7	1.5	226	7	ADE04976	Ade04976 Human	PRO
247	7	1.5	116	4	ADG15148	Adg15148 Human	7 t	320	7	1.5	226	7	ADE11282	Ade11282 Human	PRO
248	7	1.5	116	5	ABJ05724	Abj05724 Novel	hum	321	7	1.5	226	7	ADD88213	Add88213 Human	PRO
249	7	1.5	116	5	ABP66761	Abp66761 Human	pol	322	7	1.5	226	7	ADD95508	Add95508 Human	sec
250	7	1.5	116	6	ABU97261	Abu97261 Human	neo	323	7	1.5	226	7	ADE06438	Ade06438 Human	PRO
251	7	1.5	116	7	ADC46224	Adc46224 Human	pol	324	7	1.5	226	7	ADE38213	Ade38213 Human	PRO
252	7	1.5	116	8	ADI54438	Adi54438 Novel	hum	325	7	1.5	226	7	ADD88329	Add88329 Human	PRO
253	7	1.5	121	3	AB62916	Ab62916 Human	g35	326	7	1.5	226	7	ADD90910	Add90910 Human	sec
254	7	1.5	124	5	ABB89377	Abb89377 Human	pol	327	7	1.5	226	7	ADF99465	Adf99465 Human	sec
255	7	1.5	129	5	ABB90003	Abb90003 Human	pol	328	7	1.5	226	7	ADG06558	Adg06558 Human	PRO
256	7	1.5	131	4	AAU17657	Aau17657 Peptide	#	329	7	1.5	226	7	ADG05509	Adg05509 Human	PRO
257	7	1.5	131	4	ABB36674	Abb36674 Peptide	#	330	7	1.5	226	7	ADG82510	Adg82510 Human	PRO
258	7	1.5	131	4	AAU30175	Aau30175 Peptide	#	331	7	1.5	226	7	AD162708	Ad162708 Human	apo
259	7	1.5	131	4	ABB31464	Abb31464 Peptide	#	332	7	1.5	226	8	ADE51763	Ade51763 Human	sec
260	7	1.5	131	4	ABB22010	Abb22010 Protein	#	333	7	1.5	226	8	ADE51879	Ade51879 Human	sec
261	7	1.5	131	4	AAU69834	Aau69834 Human	bon	334	7	1.5	226	8	ADE37737	Ade37737 Human	sec
262	7	1.5	131	4	AAU57437	Aau57437 Human	bra	335	7	1.5	226	8	ADE37621	Ade37621 Human	sec
263	7	1.5	131	4	AAU51527	Aau51527 Human	liv	336	7	1.5	226	8	ADD95392	Add95392 Human	sec
264	7	1.5	131	4	AAU05317	Aau05317 Peptide	#	337	7	1.5	226	8	ADG38092	Adg38092 Human	PRO
265	7	1.5	131	5	ABG39463	Abg39463 Human	pep	338	7	1.5	226	8	ADE76181	Ade76181 Human	PRO
266	7	1.5	132	3	AAU62917	Aau62917 Human	g35	339	7	1.5	226	8	ADE39504	Ade39504 Human	PRO
267	7	1.5	137	5	ABU51177	Abu51177 Helicobac		340	7	1.5	226	8	ADE04308	Ade04308 Human	PRO
268	7	1.5	139	5	AAE14762	Aae14762 Human	CCR	341	7	1.5	226	8	ADG39905	Adg39905 Human	PRO
269	7	1.5	143	4	AAU001146	Aau001146 Human	pol	342	7	1.5	226	8	ADE19770	Ade19770 Human	PRO
270	7	1.5	147	4	AAU14830	Aau14830 Novel	hum	343	7	1.5	226	8	ADE77348	Ade77348 Human	sec
271	7	1.5	163	4	ABG13137	Abg13137 Novel	hum	344	7	1.5	226	8	ADE65456	Ade65456 Human	PRO
272	7	1.5	167	4	ABG21389	Abg21389 Novel	hum	345	7	1.5	226	8	ADE76065	Ade76065 Human	PRO
273	7	1.5	169	3	AAU19447	Aau19447 Arabidops		346	7	1.5	226	8	ADE37976	Ade37976 Human	PRO
274	7	1.5	170	7	ADN95937	Adn95937 Human	BEC	347	7	1.5	226	8	ADE64586	Ade64586 Human	PRO
275	7	1.5	170	8	ADP55304	Adp55304 Human	PRO	348	7	1.5	226	8	ADE38921	Ade38921 Human	PRO
276	7	1.5	178	5	AAE14761	Aae14761 Human	CCR	349	7	1.5	226	8	ADE51995	Ade51995 Human	sec
277	7	1.5	178	5	AAE14760	Aae14760 Human	CCR	350	7	1.5	226	8	ADD91026	Add91026 Human	sec
278	7	1.5	178	5	AAE14754	Aae14754 Human	CCR	351	7	1.5	226	8	ADE38805	Ade38805 Human	PRO
279	7	1.5	178	5	ABU97608	Abu97608 Novel	hum	352	7	1.5	226	8	ADE06321	Ade06321 Human	PRO
280	7	1.5	178	7	ADD49059	Add49059 Human	NOV	353	7	1.5	226	8	ADG06321	Adg06321 Human	PRO
281	7	1.5	178	8	ADI30553	Adi30553 Novel	hum	354	7	1.5	226	8	ADD90181	Add90181 Human	sec
282	7	1.5	180	5	ABP64208	Abp64208 Human	ORF	355	7	1.5	226	8	ADG38689	Adg38689 Human	PRO
283	7	1.5	190	4	AAU93518	Aau93518 Human	pol	356	7	1.5	226	8	ADE39620	Ade39620 Human	PRO
284	7	1.5	190	8	ADL31212	Adl31212 Human	pro	357	7	1.5	226	8	ADD89225	Add89225 Human	PRO
285	7	1.5	200	2	AAU25961	Aau25961 ORF 5	pro	358	7	1.5	226	8	ADG88992	Adg88992 Human	PRO
286	7	1.5	200	7	ADU04678	Adu04678 Human	APP	359	7	1.5	226	8	ADE19886	Ade19886 Human	PRO
287	7	1.5	201	4	AAU881430	Aau881430 Human	APP	360	7	1.5	226	8	ADE77464	Ade77464 Human	sec
288	7	1.5	201	5	ABU66809	Abu66809 Human	NGP	361	7	1.5	226	8	ADE65340	Ade65340 Human	PRO
289	7	1.5	205	4	AAU99922	Aau99922 Human	pol	362	7	1.5	226	8	ADE39388	Ade39388 Human	PRO
290	7	1.5	205	7	ADU94886	Adu94886 Human	gen	363	7	1.5	226	8	ADE38573	Ade38573 Human	sec
291	7	1.5	207	7	ADC97738	Adc97738 Rhizobito		364	7	1.5	226	8	ADG11126	Adg11126 Human	sec
292	7	1.5	209	7	ADD78236	Add78236 Human	GPD	365	7	1.5	226	8	ADG11010	Adg11010 Human	sec
293	7	1.5	211	4	AAU25590	Aau25590 Human	G P	366	7	1.5	226	8	ADH31538	Adh31538 Human	PRO
294	7	1.5	211	8	ADU42085	Adu42085 Bacteri	al	367	7	1.5	226	8	ADH38786	Adh38786 Human	sec
295	7	1.5	217	4	ABG16226	Abg16226 Novel	hum	368	7	1.5	226	8	ADH23724	Adh23724 Human	sec
296	7	1.5	217	8	ADM87785	Adm87785 Human	EST	369	7	1.5	226	8	ADH27054	Adh27054 Human	sec
297	7	1.5	218	4	AAU64442	Aau64442 Human	sec	370	7	1.5	226	8	ADH38322	Adh38322 Novel	hum
298	7	1.5	220	7	ABO66908	Ab066908 Klebsiell		371	7	1.5	226	8	ADH26938	Adh26938 Human	sec
299	7	1.5	220	4	AAU60516	Aau60516 Propionib		372	7	1.5	226	8	ADH26938	Adh26938 Human	sec
300	7	1.5	225	6	ABU57035	Abu57035 Propionib		373	7	1.5	226	8	ADH38206	Adh38206 Novel	hum
301	7	1.5	226	5	ABP69284	Abp69284 Human	pol	374	7	1.5	226	8	ADH38902	Adh38902 Human	sec
302	7	1.5	226	5	ABG34085	Abg34085 Human	pro	375	7	1.5	226	8	ADH23840	Adh23840 Human	sec
303	7	1.5	226	6	ADA01380	Ada01380 Human	PRO	376	7	1.5	226	8	ADH40215	Adh40215 Human	PRO
304	7	1.5	226	6	ADA43809	Ada43809 Human	sec	377	7	1.5	226	8	ADH40100	Adh40100 Human	PRO
305	7	1.5	226	6	ADA43577	Ada43577 Human	sec	378	7	1.5	226	8	ADH31422	Adh31422 Human	PRO
306	7	1.5	226	6	ADA01252	Ada01252 Human	PRO	379	7	1.5	226	8	ADH29300	Adh29300 Human	sec
307	7	1.5	226	6	ADA01136	Ada01136 Human	sec	380	7	1.5	226	8	ADH49515	Adh49515 Novel	hum
308	7	1.5	226	7	ADA43693	Ada43693 Human	sec	381	7	1.5	226	8	ADH51979	Adh51979 Novel	hum
309	7	1.5	226	7	ADA06955	Ada06955 Human	PRO	382	7	1.5	226	8	ADH49834	Adh49834 Novel	hum
310	7	1.5	226	7	ADA08443	Ada08443 Novel	hum	383	7	1.5	226	8	ADH52435	Adh52435 Novel	hum
311	7	1.5	226	7	ADU99736	Adu99736 Human	PRO	384	7	1.5	226	8	ADH52551	Adh52551 Novel	hum
312	7	1.5	226	7	ADH87019	Adh87019 Human	PRO	385	7	1.5	226	8	ADH58548	Adh58548 Novel	hum
313	7	1.5	226	7	ADU66174	Adu66174 Human	sec	386	7	1.5	226	8	ADH51863	Adh51863 Novel	hum
314	7	1.5	226	7	ADU99852	Adu99852 Human	PRO	387	7	1.5	226	8	ADH58424	Adh58424 Novel	hum
315	7	1.5	226	7	ADU99507	Adu99507 Novel	hum	388	7	1.5	226	8	ADH113621	Adh113621 Novel	hum
316	7	1.5	226	7	ADU66058	Adu66058 Human	sec	389	7	1.5	226	8	ADK00877	Adk00877 Human	PRO
317	7	1.5	226	7	ADC23456	Adc23456 Human	tra	390	7	1.5	226	8	ADL08618	Adl08618 Human	sec

391	7	1.5	226	8	ADM96335	Adm96335 Human FLJ	464	7	1.5	330	8	ADM33339	Adm33339 Human GPR
392	7	1.5	227	4	AB63809	Ab63809 Human pro	465	7	1.5	330	8	ABO60434	Ab60434 Human gen
393	7	1.5	227	6	AE35124	Ae35124 Woody pla	466	7	1.5	330	8	ADN89164	Adn89164 Human G-p
394	7	1.5	235	4	AG11554	Ag11554 Novel hum	467	7	1.5	330	8	ADO29403	Ado29403 Mouse GPC
395	7	1.5	253	6	ADA48420	Ada48420 Rice prot	468	7	1.5	330	8	ADO29402	Ado29402 Human GPC
396	7	1.5	253	8	ADR98894	Adr98894 Lung spec	469	7	1.5	330	8	ADS17072	Adsl17072 Human 123
397	7	1.5	260	7	ADC26233	Adc26233 Human NOV	470	7	1.5	332	7	ADI21649	Adi21649 Novel hum
398	7	1.5	261	2	AAV37756	Aav37756 Amino aci	471	7	1.5	332	7	ADI21648	Adi21648 Novel hum
399	7	1.5	262	4	AB58782	Ab58782 Drosophil	472	7	1.5	333	7	ADI21176	Adi21176 Novel hum
400	7	1.5	262	4	ABG23628	Abg23628 Novel hum	473	7	1.5	340	6	ABJ37911	Abj37911 NOVX prot
401	7	1.5	266	6	ADA54948	Ada54948 Human pro	474	7	1.5	341	6	ABU63310	Abu63310 Mouse P u
402	7	1.5	266	7	ADJ70696	Adj70696 Human hea	475	7	1.5	342	8	ADG19668	Adg19668 Mature hu
403	7	1.5	270	2	AAR66551	Aar66551 Cynomolg	476	7	1.5	343	2	AAR96145	Aar96145 G protein
404	7	1.5	270	2	AAW81819	Aaw81819 M. cynomo	477	7	1.5	343	2	AAR97222	Aar97222 Human G-p
405	7	1.5	270	2	AAW42482	Aaw42482 Cynomolg	478	7	1.5	343	4	AAR88477	Aar88477 Human mem
406	7	1.5	270	3	AAV52986	Aav52986 Cynomolg	479	7	1.5	343	5	ABB08348	Abb08348 RTA-like
407	7	1.5	270	3	AAV82217	Aav82217 Monkey zo	480	7	1.5	343	6	ABP71355	Abp71355 Human IGP
408	7	1.5	270	3	AAV52691	Aav52691 Cynomolg	481	7	1.5	343	6	ABP81197	Abp81197 Human G p
409	7	1.5	270	3	AAV52182	Aav52182 Monkey zo	482	7	1.5	343	6	ABG73784	Abg73784 Rat RTA o
410	7	1.5	271	6	ADA34342	Ada34342 Acinetoba	483	7	1.5	343	6	ABG73783	Abg73783 Human G p
411	7	1.5	276	6	ABR44284	Ab44284 Human BAG	484	7	1.5	343	6	ABJ37912	Abj37912 NOVX prot
412	7	1.5	276	8	ADR94603	Adr94603 Novel S.	485	7	1.5	343	6	ADB12836	Adb12836 Human G p
413	7	1.5	277	7	ADM05771	Adm05771 Human pro	486	7	1.5	343	6	ADB12843	Adb12843 Rat orpha
414	7	1.5	278	3	AAG18015	Aag18015 Arabidops	487	7	1.5	343	8	ADC89679	Adc89679 Human mas
415	7	1.5	279	7	ADH86594	Adh86594 Enterococ	488	7	1.5	343	8	ADO29550	Ado29550 Human GPC
416	7	1.5	284	4	ABB69768	Abb69768 Drosophil	489	7	1.5	343	8	ADO29551	Ado29551 Mouse GPC
417	7	1.5	285	5	AAW51648	Aaw51648 Rat GPCR	490	7	1.5	345	2	AAR76499	Aar76499 Human thy
418	7	1.5	289	5	AAW51647	Aaw51647 Human GPC	491	7	1.5	345	2	AAR93188	Aar93188 Thymopoie
419	7	1.5	289	8	ADO29554	Ado29554 Human GPC	492	7	1.5	345	2	AAR94357	Aar94357 Human thy
420	7	1.5	289	8	ADM20974	Adm20974 Bacterial	493	7	1.5	345	2	AAV41297	Aav41297 Human thy
421	7	1.5	298	2	AAAR48755	Aar48755 Human tho	494	7	1.5	345	3	AAV70506	Aav70506 Human BAG
422	7	1.5	298	2	AAW02727	Aaw02727 Human tho	495	7	1.5	345	6	AAE37660	Aae37660 Bcl2 rela
423	7	1.5	299	6	ABU48038	Abu48038 Protein e	496	7	1.5	345	7	ABW01304	Abw01304 Human Bcl
424	7	1.5	299	6	ABU44893	Abu44893 Protein e	497	7	1.5	345	8	ADH97140	Adh97140 E. faecal
425	7	1.5	299	7	ADM05522	Adm05522 Human pro	498	7	1.5	345	8	ADL69732	Adl69732 Human Bcl
426	7	1.5	304	7	ADM06190	Adm06190 Human pro	499	7	1.5	345	8	ADO51114	Ado51114 Human BCL
427	7	1.5	306	5	ABB48543	Abb48543 Listeria	500	7	1.5	345	8	ABM81028	Abm81028 Tumour-as
428	7	1.5	306	6	ABP57009	Abp57009 Buchnera	501	7	1.5	347	5	ABG33036	Abg33036 Human opi
429	7	1.5	316	8	ADR89630	Adr89630 Human-uri	502	7	1.5	352	7	ADC87349	Adc87349 Human GPC
430	7	1.5	320	5	AAU96167	Aau96167 Human sec	503	7	1.5	355	4	AAU01302	Aau01302 Human G-p
431	7	1.5	320	5	ABG64831	Abg64831 Human alb	504	7	1.5	356	3	ADA35054	Ada35054 Acinetoba
432	7	1.5	320	8	ADL78098	Adl78098 Albumin f	505	7	1.5	356	3	AAV90683	Aav90683 Human mut
433	7	1.5	323	4	AAU25612	Aau25612 Human G P	506	7	1.5	356	3	AAV90678	Aav90678 Human G p
434	7	1.5	323	5	AAU76411	Aau76411 Novel hum	507	7	1.5	356	6	ABP81198	Abp81198 Human G p
435	7	1.5	323	5	ABB06257	Abb06257 Human G p	508	7	1.5	356	7	ADC22765	Adc22765 Human G p
436	7	1.5	323	6	ABP71354	Abp71354 Human IGP	509	7	1.5	356	7	ADC22789	Adc22789 Human G p
437	7	1.5	325	2	AAAR48730	Aar48730 G-protein	510	7	1.5	356	7	ADC24766	Adc24766 Human 186
438	7	1.5	325	2	AAW02702	Aaw02702 G-protein	511	7	1.5	356	7	ADH14238	Adh14238 Human GPR
439	7	1.5	326	3	AAAG52550	Aag52550 Arabidops	512	7	1.5	356	7	ADH14262	Adh14262 Mutated h
440	7	1.5	326	3	AAAG29016	Aag29016 Arabidops	513	7	1.5	356	8	ADG19666	Adg19666 Human G p
441	7	1.5	327	5	AAE14729	Aae14729 Human G-p	514	7	1.5	356	8	ADG19681	Adg19681 G-protein
442	7	1.5	327	6	ABP96693	Abp96693 Human G p	515	7	1.5	356	8	ADO05704	Ado05704 Human G p
443	7	1.5	330	2	AAW59906	Aaw59906 Human HTA	516	7	1.5	356	8	ADO29696	Ado29696 Human GPC
444	7	1.5	330	2	AAW75245	Aaw75245 Fragment	517	7	1.5	356	8	ADO29696	Ado29696 Human GPC
445	7	1.5	330	2	AAW05384	Aaw05384 Mouse GCR	518	7	1.5	359	2	AAAR44531	Aaar44531 Human ang
446	7	1.5	330	2	AAV05384	Aav05384 Human GCR	519	7	1.5	359	3	AAAB02848	Aaab02848 Human G p
447	7	1.5	330	3	AAV90681	Aav90681 Human G p	520	7	1.5	359	3	AAAB02844	Aaab02844 Human G p
448	7	1.5	330	3	AAV90686	Aav90686 Human mut	521	7	1.5	359	3	AAAB02849	Aaab02849 Human G p
449	7	1.5	330	3	AAV94269	Aav94269 Mouse 7-t	522	7	1.5	359	5	AAO20951	Aao20951 Protein o
450	7	1.5	330	5	AAE27011	Aae27011 Human gen	523	7	1.5	359	5	AAU78656	Aau78656 Human Ang
451	7	1.5	330	5	AAE27149	Aae27149 Human gen	524	7	1.5	359	5	AAU78655	Aau78655 Human Ang
452	7	1.5	330	6	ABP81990	Abp81990 Human G p	525	7	1.5	359	5	AAU78654	Aau78654 Rat angio
453	7	1.5	330	6	ABU65022	Abu65022 Human sec	526	7	1.5	359	5	ABB79863	Abb79863 Rat angio
454	7	1.5	330	6	ABR82313	Ab82313 Human G-p	527	7	1.5	359	6	ABU09502	Abu09502 Human C5a
455	7	1.5	330	7	ADC22795	Adc22795 Human G p	528	7	1.5	359	6	ABP81921	Abp81921 Human ang
456	7	1.5	330	7	ADC22777	Adc22777 Human G p	529	7	1.5	359	7	ADE58154	Ade58154 Human Pro
457	7	1.5	330	7	ADF05018	Adf05018 GPCR GPR4	530	7	1.5	359	7	ADE58152	Ade58152 Rat Prote
458	7	1.5	330	7	ADH14268	Adh14268 Mutated h	531	7	1.5	359	7	ADD47291	Add47291 Human Pro
459	7	1.5	330	7	ADH14250	Adh14250 Human GPR	532	7	1.5	359	7	ADD47289	Add47289 Rat Prote
460	7	1.5	330	7	ADH14250	Adh14250 Human GPR	533	7	1.5	359	8	ADG86461	Adg86461 Human AT1
461	7	1.5	330	8	ADG89831	Adg89831 Human sec	534	7	1.5	359	8	ADG86451	Adg86451 Human AT1
462	7	1.5	330	8	ADM33349	Adm33349 Mouse GPR	535	7	1.5	359	8	ADG86455	Adg86455 Human AT1
463	7	1.5	330	8	ADM33347	Adm33347 Rat GPR43	536	7	1.5	359	8	ADG86427	Adg86427 Human ang

537	7	1.5	359	8	ADH50089	Adh50089 Rat type	610	7	1.5	391	4	ABB56335	Abb56335 Non-endog
538	7	1.5	359	8	ADO28767	Ado28767 Rat angio	611	7	1.5	391	5	ABG77009	Abg77009 Human bra
539	7	1.5	359	8	ADO29184	Ado29184 Mouse GPC	612	7	1.5	391	5	ABG77010	Abg77010 Human bra
540	7	1.5	359	8	ADO29183	Ado29183 Human GPC	613	7	1.5	391	5	ABG77024	Abg77024 Human bra
541	7	1.5	359	8	ADP20244	Adp20244 Angiotens	614	7	1.5	391	5	ABG77008	Abg77008 Human bra
542	7	1.5	359	8	ADP20220	Adp20220 Human ang	615	7	1.5	391	5	ABG76986	Abg76986 Human bra
543	7	1.5	359	8	ADP20254	Adp20254 Angiotens	616	7	1.5	391	5	ABG77027	Abg77027 Human bra
544	7	1.5	359	8	ADP20248	Adp20248 Angiotens	617	7	1.5	391	6	ABP81783	Abp81783 Human bra
545	7	1.5	360	3	AA002851	Aa002851 Human G p	618	7	1.5	391	8	ADH50090	Adh50090 Human bra
546	7	1.5	360	8	ADG86467	Adg86467 Human AT1	619	7	1.5	391	8	ADJ75571	Adj75571 Marker ge
547	7	1.5	360	8	ADP20260	Adp20260 Angiotens	620	7	1.5	391	8	ADO29197	Ado29197 Human GPC
548	7	1.5	361	5	AD116985	Adi16985 Rat NOVX	621	7	1.5	391	8	ADO39351	Ado39351 Human myo
549	7	1.5	361	7	ADH62990	Adh62990 Rat orpha	622	7	1.5	391	8	ADQ39352	Adq39352 Human myo
550	7	1.5	361	8	ADF91782	Adf91782 Rat orpha	623	7	1.5	391	8	ADL70541	Adl70541 Human G-p
551	7	1.5	361	8	ADO29599	Ado29599 Mouse GPC	624	7	1.5	394	8	ADA55451	Ada55451 Human pro
552	7	1.5	361	8	ADR89629	Adr89629 Rat G-pro	625	7	1.5	395	6	AAE34476	Aae34476 Human AGT
553	7	1.5	362	5	AAU10964	Aau10964 Xyllella f	626	7	1.5	395	6	ADJ70703	Adj70703 Human hea
554	7	1.5	364	5	AAE25675	Aae25675 Human BK-	627	7	1.5	395	7	ADJ70703	Adj70703 Human hea
555	7	1.5	365	2	AAW23606	Aaw23606 Human P2Y	628	7	1.5	395	8	ADS10801	Ads10801 Human the
556	7	1.5	365	4	AAE04391	Aae04391 Human P2Y	629	7	1.5	396	2	AAW62598	Aaw62598 Human 7-t
557	7	1.5	365	6	ABP81923	Abp81923 Human pyr	630	7	1.5	396	4	AGG77798	Agg77798 Human EX3
558	7	1.5	365	7	ADE40463	Ade40463 Human pyr	631	7	1.5	396	5	AGG80225	Agg80225 Human MAR
559	7	1.5	365	8	ADO29598	Ado29598 Human GPC	632	7	1.5	396	5	ABP95618	Abp95618 Human GPC
560	7	1.5	365	8	ADP49193	Adp49193 Human P2Y	633	7	1.5	396	6	ABJ19755	Abj19755 Human MP2
561	7	1.5	366	8	ABM83600	Abm83600 Human dia	634	7	1.5	396	6	ABP81705	Abp81705 Human G p
562	7	1.5	367	2	AAW69999	Aaw69999 Rodent ch	635	7	1.5	396	6	ABB82500	Abb82500 Human TGR
563	7	1.5	367	2	ADN40064	Adn40064 Mouse CXC	636	7	1.5	396	6	ABB82509	Abb82509 Mouse TGR
564	7	1.5	367	8	ADO29459	Ado29459 Mouse GPC	637	7	1.5	396	6	ABRG2422	Abrg2422 Human hp1
565	7	1.5	373	5	AAE20604	Aae20604 Mus muscu	638	7	1.5	396	8	ADO29448	Ado29448 Human GPC
566	7	1.5	373	8	ADO29597	Ado29597 Mouse GPC	639	7	1.5	396	8	ADO29449	Ado29449 Mouse GPC
567	7	1.5	374	7	ADE62764	Ade62764 Rat Prote	640	7	1.5	396	8	ADR67005	Adr67005 Mouse can
568	7	1.5	374	8	ADR89633	Adr89633 Rat P20 p	641	7	1.5	397	4	AAU03851	Aau03851 G protein
569	7	1.5	375	2	AAE01144	Aae01144 Human P20	642	7	1.5	400	8	ADH52878	Adh52878 Bovine ap
570	7	1.5	377	4	AAE01144	Aae01144 Human pur	643	7	1.5	403	4	AAU00205	Aau00205 Human nov
571	7	1.5	377	4	AAE01143	Aae01143 Human pur	644	7	1.5	404	4	AAW99936	Aaw99936 Human exp
572	7	1.5	377	4	AAE04392	Aae04392 Human P2-	645	7	1.5	404	6	ABP57058	Abp57058 Human GPC
573	7	1.5	377	4	AAE48502	Aae48502 Mouse APJ	646	7	1.5	405	6	ABJ39100	Abj39100 Molecule
574	7	1.5	377	4	AAE48502	Aae48502 Mouse APJ	647	7	1.5	410	3	ABG52548	Abg52548 Arabidops
575	7	1.5	377	6	ABP81866	Abp81866 Human pur	648	7	1.5	410	3	ABG29014	Abg29014 Arabidops
576	7	1.5	377	6	ADE62766	Ade62766 Human Pro	649	7	1.5	411	6	ABU17303	Abu17303 Protein e
577	7	1.5	377	8	ADO29188	Ado29188 Mouse GPC	650	7	1.5	411	6	ADA36165	Ada36165 Acinetoba
578	7	1.5	377	8	ADO29596	Ado29596 Human GPC	651	7	1.5	413	5	ABB54954	Abb54954 Lactococc
579	7	1.5	377	8	ADP49189	Adp49189 Human P2Y	652	7	1.5	413	8	ADS29431	Ads29431 Bacterial
580	7	1.5	378	6	ABR41624	AbR41624 Human DIT	653	7	1.5	414	4	ABG01012	Abg01012 Novel hum
581	7	1.5	378	6	ABU11820	Abu11820 Human MDD	654	7	1.5	414	4	ABO80414	AbO80414 Pseudomon
582	7	1.5	378	8	ADN14011	Adn14011 Human pro	655	7	1.5	417	7	ADM03826	Adm03826 Human pro
583	7	1.5	380	2	AAW53750	Aaw53750 Seven tra	656	7	1.5	419	5	ABP29664	Abp29664 Streptoco
584	7	1.5	380	2	AAW48731	Aaw48731 Human R20	657	7	1.5	425	5	ADC12734	Adc12734 Human GPC
585	7	1.5	380	2	AAW4952	Aaw4952 G protein	658	7	1.5	427	6	ABR52845	AbR52845 Protein s
586	7	1.5	380	3	AAW87466	Aaw87466 Human APJ	659	7	1.5	427	6	AAU03852	Aau03852 G protein
587	7	1.5	380	3	AAW88442	Aaw88442 G-protein	660	7	1.5	433	4	AAU03852	Aau03852 G protein
588	7	1.5	380	3	AAW90626	Aaw90626 Human G p	661	7	1.5	437	5	ABBS3780	Abbs3780 Lactococc
589	7	1.5	380	3	AAW90660	Aaw90660 Human mut	662	7	1.5	445	5	ADJ33829	Adj33829 Protein o
590	7	1.5	380	3	AAW21695	Aaw21695 Human 7TM	663	7	1.5	448	6	ABG73645	Abg73645 Human G-p
591	7	1.5	380	4	AAW93647	Aaw93647 Human pol	664	7	1.5	449	3	ABG53314	Abg53314 Arabidops
592	7	1.5	380	4	AAW52725	Aaw52725 Human APJ	665	7	1.5	453	3	ABG53313	Abg53313 Arabidops
593	7	1.5	380	5	AAU91237	Aau91237 Human 7 t	666	7	1.5	453	3	ABO76308	AbO76308 Pseudomon
594	7	1.5	380	5	AAU11309	Aau11309 Human ang	667	7	1.5	454	2	AAW76498	Aaw76498 Human thy
595	7	1.5	380	5	AAU11310	Aau11310 Human ang	668	7	1.5	454	2	AAW93187	Aaw93187 Thymopoie
596	7	1.5	380	6	ABP81874	Abp81874 Human ape	669	7	1.5	454	2	AAW94356	Aaw94356 Human thy
597	7	1.5	380	6	ABG74898	Abg74898 Human APJ	670	7	1.5	454	2	AAW41296	Aaw41296 Human thy
598	7	1.5	380	7	ADC22581	Adc22581 Human G p	671	7	1.5	454	8	ADP84517	Adp84517 Human bre
599	7	1.5	380	7	ADC22717	Adc22717 Human G p	672	7	1.5	455	8	ADP84517	Adp84517 Human bre
600	7	1.5	380	7	ADH14190	Adh14190 Mutated h	673	7	1.5	456	4	ABG28643	Abg28643 Novel hum
601	7	1.5	380	7	ADH14054	Adh14054 Human APJ	674	7	1.5	463	4	ABO80179	AbO80179 Pseudomon
602	7	1.5	380	7	ADK14731	Adk14731 Bovine ap	675	7	1.5	464	2	AAW03632	Aaw03632 Hypoxia-r
603	7	1.5	380	8	ADL34474	Adl34474 Human pro	676	7	1.5	464	6	ABU63751	Abu63751 Rat prote
604	7	1.5	380	8	ADO29187	Ado29187 Human GPC	677	7	1.5	464	6	ABU63751	Abu63751 Rat prote
605	7	1.5	380	8	ADS73996	Ads73996 Human APJ	678	7	1.5	464	7	ADC63795	Adc63795 Hypoxia-r
606	7	1.5	382	3	AAW29015	Aaw29015 Arabidops	679	7	1.5	475	6	ABW01150	Abw01150 Hypoxia-r
607	7	1.5	382	3	AAW52549	Aaw52549 Arabidops	680	7	1.5	481	8	AAU029509	Aau029509 Mouse GPC
608	7	1.5	384	5	ABP25675	Abp25675 Streptoco	681	7	1.5	499	4	AAU03820	Aau03820 G protein
609	7	1.5	387	8	ADO29284	Ado29284 Mouse GPC	682	7	1.5	504	2	AAW54682	Aaw54682 Mouse bra

683 Aae20596 Mus muscu 7 1.5 504 5 AAE20596
684 Adb65313 Human pro 7 1.5 504 8 ADB65313
685 ADO29011 Mouse nov 7 1.5 507 8 ADO29011
686 AAU00203 Human nov 7 1.5 512 4 AAU00203
687 Aab95487 Human pro 7 1.5 512 4 AAB95487
688 Abp81698 Human G p 7 1.5 512 6 ABP81698
689 Adn40010 Cancer/an 7 1.5 512 7 ADN40010
690 ADO29010 Human nov 7 1.5 512 8 ADO29010
691 ADR46685 Cancer-as 7 1.5 512 8 ADR46685
692 Aaw98850 H. pylori 7 1.5 514 2 AAW98850
693 ABO63523 Klebsiell 7 1.5 516 2 ABO63523
694 ABU42471 Mycobacte 7 1.5 526 6 ABU42471
695 ABM71801 Staphyloc 7 1.5 527 6 ABM71801
696 Aaw79067 Sorghum b 7 1.5 530 2 AAW79067
697 ADJ48457 Maize oil 7 1.5 531 2 ADJ48457
698 AAG31551 Arabidops 7 1.5 531 3 AAG31551
699 AAG31550 Arabidops 7 1.5 536 3 AAG31550
700 Abg26118 Novel hum 7 1.5 537 4 ABG26118
701 AAU74538 Human p2Y 7 1.5 537 5 AAU74538
702 ADI16981 Xenopus p 7 1.5 537 5 ADI16981
703 ADR89632 Mycobacte 7 1.5 537 8 ADR89632
704 Aau00202 Human nov 7 1.5 538 7 Aau00202
705 ADB74322 Thermococ 7 1.5 541 4 ADB74322
706 Aae23658 Human sec 7 1.5 541 5 AAE23658
707 Abb97263 Novel hum 7 1.5 541 5 ABB97263
708 ABJ38830 Human G-p 7 1.5 541 6 ABJ38830
709 ADI40983 Human GPC 7 1.5 541 8 ADI40983
710 Adl13202 Human ste 7 1.5 541 8 ADL13202
711 Adn47612 Thermococ 7 1.5 552 8 ADN47612
712 Aag53312 Arabidops 7 1.5 554 3 AAG53312
713 Abb92295 Herbicida 7 1.5 554 5 ABB92295
714 Aag31549 Arabidops 7 1.5 555 3 AAG31549
715 Adf70484 Orphan re 7 1.5 561 7 ADF70484
716 Aar55207 Human zon 7 1.5 566 2 AAR55207
717 Aaw81816 Human ZPB 7 1.5 566 2 AAW81816
718 Aay42479 Human zon 7 1.5 566 2 AAY42479
719 Aay52983 Human zon 7 1.5 566 3 AAY52983
720 Aay82214 Human zon 7 1.5 566 3 AAY82214
721 Aay52688 Human ooc 7 1.5 566 3 AAY52688
722 Aay52179 Human ooc 7 1.5 566 3 AAY52179
723 Adf75101 A_gossyp 7 1.5 574 7 ADF75101
724 Adf70414 Orphan re 7 1.5 581 7 ADF70414
725 Adf70496 Orphan re 7 1.5 594 7 ADF70496
726 Abm68790 Phototrab 7 1.5 599 6 ABM68790
727 ABR53284 Protein s 7 1.5 599 6 ABR53284
728 Adk63582 Disease t 7 1.5 599 7 ADK63582
729 Aaw98112 T-cell me 7 1.5 614 2 AAW98112
730 Aaw98113 T-cell me 7 1.5 614 2 AAW98113
731 ABR43098 Human T-c 7 1.5 614 6 ABR43098
732 Abm81282 Tumour-as 7 1.5 614 8 ABM81282
733 Adf06009 Bacterial 7 1.5 621 7 ADF06009
734 Abm68585 Phototrab 7 1.5 625 6 ABM68585
735 ADF70501 Orphan re 7 1.5 634 7 ADF70501
736 ADF70501 Orphan re 7 1.5 634 7 ADF70501
737 ADF70501 Orphan re 7 1.5 634 7 ADF70501
738 ABO79460 Pseudomon 7 1.5 646 7 ABO79460
739 AAB96088 Putative 7 1.5 655 4 AAB96088
740 ABUS4612 Human NOV 7 1.5 661 6 ABUS4612
741 Abg25473 Novel hum 7 1.5 665 4 ABG25473
742 ADB65678 Human pro 7 1.5 678 7 ADB65678
743 ADS23787 Bacterial 7 1.5 685 8 ADS23787
744 ABB54123 Lactococ 7 1.5 696 5 ABB54123
745 ABU45498 Protein e 7 1.5 709 6 ABU45498
746 ABUS4613 Human NOV 7 1.5 723 6 ABUS4613
747 AAY59724 Human nov 7 1.5 725 2 AAY59724
748 ABO71361 Pseudomon 7 1.5 731 4 ABO71361
749 ABB66761 Drosophil 7 1.5 774 4 ABB66761
750 ABB58616 Drosophil 7 1.5 774 4 ABB58616
751 AAG39671 Arabidops 7 1.5 775 3 AAG39671
752 AAG28659 Arabidops 7 1.5 775 3 AAG28659
753 ABB93478 Herbicida 7 1.5 781 5 ABB93478
754 Adh22516 Human tra 7 1.5 787 8 ADH22516
755 Abm84820 Human dia 7 1.5 787 8 ABM84820

756 7 1.5 788 4 AAB88505
757 7 1.5 788 5 AAU91436
758 7 1.5 788 5 ABO23510
759 7 1.5 822 2 AAW41943
760 7 1.5 822 5 ABB81811
761 7 1.5 822 5 ADR44119
762 7 1.5 830 8 ADI28834
763 7 1.5 830 8 ADP12465
764 7 1.5 830 8 ABM81281
765 7 1.5 840 7 ABO70815
766 7 1.5 877 4 AAB93668
767 7 1.5 878 4 ABG25491
768 7 1.5 898 4 ABUS3123
769 7 1.5 898 5 AAU76957
770 7 1.5 898 5 AUC31082
771 7 1.5 898 7 ADI15915
772 7 1.5 905 5 AAU76967
773 7 1.5 909 6 ABR53535
774 7 1.5 909 7 ADK64420
775 7 1.5 946 4 ABB72016
776 7 1.5 958 4 AAG70685
777 7 1.5 958 8 ADN18793
778 7 1.5 963 8 ADO39174
779 7 1.5 969 8 ADQ66627
780 7 1.5 1023 6 ABP97078
781 7 1.5 1059 8 ADQ08670
782 7 1.5 1083 4 AAU00714
783 7 1.5 1084 4 AAU00718
784 7 1.5 1084 4 AAU00209
785 7 1.5 1111 4 AAU00197
786 7 1.5 1112 4 AAU00201
787 7 1.5 1112 4 AAU00193
788 7 1.5 1165 7 ADC59261
789 7 1.5 1165 7 ADC49331
790 7 1.5 1165 7 ADC40460
791 7 1.5 1165 7 ADF75907
792 7 1.5 1175 7 ADC40464
793 7 1.5 1178 6 ABU44244
794 7 1.5 1181 3 AAY82707
795 7 1.5 1182 3 AAB42517
796 7 1.5 1192 4 AAU00719
797 7 1.5 1192 4 AAU00712
798 7 1.5 1193 4 AAU00207
799 7 1.5 1193 4 AAU00716
800 7 1.5 1193 7 ADC40452
801 7 1.5 1203 7 ADC40456
802 7 1.5 1216 8 ADQ67740
803 7 1.5 1220 3 AAY82708
804 7 1.5 1220 4 AAU00195
805 7 1.5 1220 4 AAE04770
806 7 1.5 1220 6 AAO30439
807 7 1.5 1220 7 ADC40462
808 7 1.5 1220 7 ADE54916
809 7 1.5 1220 7 ADE54912
810 7 1.5 1220 7 ADF09578
811 7 1.5 1220 8 ABM80571
812 7 1.5 1221 4 AAU00199
813 7 1.5 1221 4 AAU00191
814 7 1.5 1221 4 AAU00210
815 7 1.5 1221 7 ADC59257
816 7 1.5 1221 7 ADC49327
817 7 1.5 1221 7 ADC40448
818 7 1.5 1221 7 ADF75903
819 7 1.5 1222 4 AAU00206
820 7 1.5 1222 4 AAU00715
821 7 1.5 1230 7 ADC40466
822 7 1.5 1232 4 AAB32866
823 7 1.5 1248 7 ADC40454
824 7 1.5 1249 4 AAU00194
825 7 1.5 1249 7 ADE54910
826 7 1.5 1249 7 ADE54914
827 7 1.5 1250 4 AAU00198
828 7 1.5 1250 4 AAU00190

Aab88505 Haemophil
Aau91436 Haemophil
Abo23510 Haemophil
Aaw41943 Human OC-
Abb81811 Human OC-
Adr44119 Human 116
Adi28834 Human mod
Adp12465 Protein e
Abm81281 Tumour-as
Abo70815 Pseudomon
Aab93668 Human pro
Abg25491 Novel hum
Abu53123 Intracell
Aau76957 Novel hum
Auc31082 Human nov
Adi15915 Human PP
Aau76967 Novel hum
Abr53535 Protein s
Adk64420 Disease t
Abb72016 Drosophil
Aag70685 S cerevis
Adn18793 Bacterial
Ado39174 Human sol
Adq66627 Novel hum
Abp97078 Human G p
Adq08670 Ciona int
Aau00714 Human nov
Aau00718 Human nov
Aau00209 Human nov
Aau00197 Human nov
Aau00201 Human nov
Aau00193 Human nov
Adc59261 Mouse G p
Adc49331 Mouse G p
Adc40460 Mouse G-p
Adf75907 Murine AP
Abu44244 Protein e
Aay82707 Human apo
Aab42517 Human ORF
Aau00719 Human nov
Aau00712 Human nov
Aau00207 Human nov
Aau00716 Human nov
Adc40452 Mouse G-p
Adc40456 Mouse G-p
Adq67740 Novel hum
Aay82708 Human apo
Aau00195 Human nov
Aae04770 Human ves
Aao30439 Human Sec
Adc40462 Mouse G-p
Ade54916 Human Pro
Ade54912 Human Pro
Adf09578 Human pum
Abm80571 Tumour-as
Aau00199 Human nov
Aau00191 Human nov
Aau00210 Human nov
Ade59257 Human G p
Adc49327 Human G p
Adc40448 Human G-p
Adf75903 Human APG
Aau00206 Human nov
Aau00715 Human nov
Adc40466 Mouse G-p
Aab32866 Novel hum
Adc40454 Mouse G-p
Aau00194 Human nov
Ade54910 Rat Prote
Ade54914 Rat Prote
Aau00198 Human nov
Aau00190 Human nov

829	7	1.5	1250	7	ADC59259	Adc59259 Human G p	902	6	1.2	10	6	ABR10711	Abr10711 Human can
830	7	1.5	1250	7	ADC49329	Adc49329 Human G p	903	6	1.2	10	6	ABR1319	Abr1319 Human can
831	7	1.5	1250	7	ADF75905	Adf75905 Human APG	904	6	1.2	10	6	ABR10548	Abr10548 Human can
832	7	1.5	1258	7	ADC40458	Adc40458 Mouse G-p	905	6	1.2	10	6	ABR10913	Abr10913 Human can
833	7	1.5	1311	2	AW52197	Aaw52197 Precis co	906	6	1.2	10	6	ABR10517	Abr10517 Human can
834	7	1.5	1311	2	AAW72971	Aaw72971 Precis co	907	6	1.2	10	6	ABR11104	Abr11104 Human can
835	7	1.5	1311	4	AB67156	Ab67156 Butterfly	908	6	1.2	10	6	ABR11308	Abr11308 Human can
836	7	1.5	1311	5	AG79573	Ag79573 Butterfly	909	6	1.2	10	6	ABR10555	Abr10555 Human can
837	7	1.5	1311	7	ABU62149	Abu62149 Buckeye b	910	6	1.2	10	6	ABR11313	Abr11313 Human can
838	7	1.5	1311	7	ADE94209	Ad94209 Peacock p	911	6	1.2	10	6	ABR11675	Abr11675 Human can
839	7	1.5	1311	7	ADH62716	Adh62716 Butterfly	912	6	1.2	10	6	ABR11726	Abr11726 Human can
840	7	1.5	1311	8	ABE48974	Ab48974 Butterfly	913	6	1.2	10	6	ABR10879	Abr10879 Human can
841	7	1.5	1342	4	AB664632	Ab664632 Drosophil	914	6	1.2	10	6	ABR11684	Abr11684 Human can
842	7	1.5	1459	7	ADF70497	Adf70497 Orphan re	915	6	1.2	10	6	ABR11514	Abr11514 Human can
843	7	1.5	1535	5	AAU87934	Aau87934 Human pro	916	6	1.2	10	6	ABR10918	Abr10918 Human can
844	7	1.5	1544	7	AAE37934	Aae37934 Human CGD	917	6	1.2	10	6	ABR10961	Abr10961 Human can
845	7	1.5	1551	6	ABO07162	Ab007162 Human p53	918	6	1.2	10	6	ABR11106	Abr11106 Human can
846	7	1.5	1564	8	ADO43997	Ado43997 Amino aci	919	6	1.2	10	8	ADL77529	Adl77529 Albumin f
847	7	1.5	1597	6	ARR53450	Arr53450 Protein s	920	6	1.2	10	8	ADN69928	Adn69928 Human 273
848	7	1.5	1597	7	ADK64624	Adk64624 Disease t	921	6	1.2	10	8	ADN69577	Adn69577 Human 273
849	7	1.5	1609	7	AAE37935	Aae37935 Human CGD	922	6	1.2	10	8	ADN66507	Adn66507 Human 273
850	7	1.5	1617	6	ABB99403	Abb99403 Amino aci	923	6	1.2	10	8	ADN70016	Adn70016 Human 273
851	7	1.5	1627	6	ADA35317	Ada35317 Acinetoba	924	6	1.2	11	5	AAU96283	Aau96283 Class I G
852	7	1.5	1630	6	ABU28412	Abu28412 Protein e	925	6	1.2	11	5	AAU96296	Aau96296 Class I G
853	7	1.5	1630	8	ADO34026	Ado34026 Human MBC	926	6	1.2	11	6	AAE34270	Aae34270 Human thy
854	7	1.5	1665	8	ABM84470	Abm84470 Human dia	927	6	1.2	11	6	AAE34258	Aae34258 Human oxy
855	7	1.5	1678	8	ADQ21326	Adq21326 Human sof	928	6	1.2	11	8	ADH50066	Adh50066 Active G
856	7	1.5	1694	2	AAW40109	Aaw40109 Human alp	929	6	1.2	11	8	ADH50054	Adh50054 Active G
857	7	1.5	1853	3	AAV53668	Aav53668 Protein 6	930	6	1.2	11	8	ADM99620	Adm99620 Murine in
858	7	1.5	2387	3	AAV53665	Aav53665 Mechanica	931	6	1.2	11	8	ADN06299	Adn06299 Human imm
859	7	1.5	2597	3	AAV53664	Aav53664 Mechanica	932	6	1.2	11	8	ADO40036	Ado40036 Human imm
860	7	1.5	2597	5	ABG31316	Abg31316 Rat prote	933	6	1.2	12	2	AAW27588	Aaw27588 Anti-TNF-
861	7	1.5	2597	5	AB47933	Ab47933 Rat OCP	934	6	1.2	12	5	AAO11132	Aao11132 Ovary cel
862	7	1.5	2597	5	ABG32890	Abg32890 Rat osteo	935	6	1.2	12	6	AAO16481	Aao16481 Human ant
863	7	1.5	2597	5	ABG32889	Abg32889 Rat osteo	936	6	1.2	12	7	ADG85052	Adg85052 Phage dis
864	7	1.5	2597	8	ADL02233	Adl02233 Rat OCP p	937	6	1.2	12	7	ADJ57642	Adj57642 TNFalpha
865	7	1.5	2597	8	ADL02254	Adl02254 Rat OCP p	938	6	1.2	12	8	ADJ58773	Adj58773 Human VH1
866	7	1.5	2597	8	ADL02222	Adl02222 Rat OCP p	939	6	1.2	12	8	ADO01467	Ado01467 Human mut
867	7	1.5	2597	8	ADL02230	Adl02230 Rat OCP p	940	6	1.2	13	4	AAW97591	Aaw97591 Human pep
868	7	1.5	2787	3	AAV81807	Aav81807 Human mah	941	6	1.2	15	4	ABR51502	Abr51502 Pen a 1 I
869	7	1.5	3227	8	ADQ91710	Adq91710 Polyketid	942	6	1.2	15	4	ABR51503	Abr51503 Pen a 1 I
870	6	1.2	7	6	AAO19800	Aao19800 Mutant hu	943	6	1.2	15	4	ABR52291	Abr52291 IGR-react
871	6	1.2	8	2	AAW73537	Aaw73537 Human TSH	944	6	1.2	15	4	ABR51359	Abr51359 Shrimp pe
872	6	1.2	9	4	ABR51554	Abr51554 Pen a 1 r	945	6	1.2	15	4	ABR51360	Abr51360 Shrimp pe
873	6	1.2	9	4	AAU00794	Aau00794 HIV-1 Tat	946	6	1.2	15	6	ABR32874	Abr32874 Human can
874	6	1.2	9	5	AAO15789	Aao15789 Human imm	947	6	1.2	15	6	ABR33031	Abr33031 Human can
875	6	1.2	9	5	ABP54735	Abp54735 HIV-1 tat	948	6	1.2	15	6	ABR32807	Abr32807 Human can
876	6	1.2	9	6	ABM6302	Abm6302 Propionib	949	6	1.2	15	6	ABR32927	Abr32927 Human can
877	6	1.2	9	6	ABP75263	Abp75263 Chlamydia	950	6	1.2	15	6	ABR32881	Abr32881 Human can
878	6	1.2	9	6	ABR10578	Abr10578 Human can	951	6	1.2	15	6	ABR33033	Abr33033 Human can
879	6	1.2	9	6	ABR10463	Abr10463 Human can	952	6	1.2	15	6	ABR32795	Abr32795 Human can
880	6	1.2	9	6	ABR11043	Abr11043 Human can	953	6	1.2	15	6	ABR33032	Abr33032 Human can
881	6	1.2	9	6	ABR10437	Abr10437 Human can	954	6	1.2	15	6	ABR32757	Abr32757 Human can
882	6	1.2	9	6	ABR11011	Abr11011 Human can	955	6	1.2	15	6	ABR32890	Abr32890 Human can
883	6	1.2	9	6	ABR11420	Abr11420 Human can	956	6	1.2	15	6	ABR33081	Abr33081 Human can
884	6	1.2	9	6	ABR10608	Abr10608 Human can	957	6	1.2	15	8	ADN70567	Adn70567 Human 273
885	6	1.2	9	6	ABR10840	Abr10840 Human can	958	6	1.2	15	8	ADN71356	Adn71356 Human 273
886	6	1.2	9	6	ABR11415	Abr11415 Human can	959	6	1.2	15	8	ADN71740	Adn71740 Human 273
887	6	1.2	9	6	ABR11579	Abr11579 Human can	960	6	1.2	15	8	ADN71499	Adn71499 Human 273
888	6	1.2	9	6	ABR10806	Abr10806 Human can	961	6	1.2	15	8	ADN71122	Adn71122 Human 273
889	6	1.2	9	6	ABR10825	Abr10825 Human can	962	6	1.2	15	8	ADN70810	Adn70810 Human 273
890	6	1.2	9	6	ABR11220	Abr11220 Human can	963	6	1.2	15	8	ADN71686	Adn71686 Human 273
891	6	1.2	9	6	ABR11457	Abr11457 Human can	964	6	1.2	15	8	ADN70617	Adn70617 Human 273
892	6	1.2	9	8	ADN66323	Adn66323 Human 273	965	6	1.2	15	8	ADN71291	Adn71291 Human 273
893	6	1.2	9	8	ADN68383	Adn68383 Human 273	966	6	1.2	15	8	ADN71091	Adn71091 Human 273
894	6	1.2	9	8	ADN68027	Adn68027 Human 273	967	6	1.2	15	8	ADN71433	Adn71433 Human 273
895	6	1.2	9	8	ADN67934	Adn67934 Human 273	968	6	1.2	15	8	ADN70750	Adn70750 Human 273
896	6	1.2	9	8	ADN67150	Adn67150 Human 273	969	6	1.2	15	8	ADN71576	Adn71576 Human 273
897	6	1.2	9	8	ADN68623	Adn68623 Human 273	970	6	1.2	15	8	ADN71434	Adn71434 Human 273
898	6	1.2	10	4	AAW73418	Aaw73418 Human gen	971	6	1.2	16	2	AAW28481	Aaw28481 Sequence
899	6	1.2	10	4	AAW86959	Aaw86959 Saccharom	972	6	1.2	16	2	AAW97058	Aaw97058 Rat AQP2
900	6	1.2	10	4	AAW43301	Aaw43301 Mycoplasma	973	6	1.2	17	2	AAW28482	Aaw28482 Sequence
901	6	1.2	10	5	ABG64264	Abg64264 Human alb	974	6	1.2	18	2	AAW06905	Aaw06905 Human ela

KW G protein-coupled receptor; GPCR; anaphylatoxin C3a receptor; AR;
KW Alzheimer's disease; Parkinson's disease; cell signalling; proliferation;
KW differentiation; leukocyte migration; gene transcription; vision; smell;
KW neurotransmission; hormonal response; ulcerative colitis; diabetes;
KW myocardial infarction; hypertension; asthma; bronchitis; pneumonia;
KW Crohn's disease; rheumatoid arthritis; Hodgkin's disease; glioblastoma;
KW neurodegenerative disorder.
XX Homo sapiens.
XX WO200244737-A2.
XX 06-JUN-2002.
XX 29-NOV-2001; 2001WO-US045220.
XX 29-NOV-2000; 2000US-0250251P.
XX 30-NOV-2000; 2000US-0250452P.
XX 17-OCT-2001; 2001US-0330036P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Brown JP, Burmer GC, Roush CL, Morningstar DA;
XX WPI; 2002-508526/54.
XX N-PSDB; ABK86860.
XX Isolated and purified composition useful for manufacture of medicament
XX for inhibiting, preventing or treating Alzheimer's or Parkinson's
XX disease, comprises G protein-coupled receptor anaphylatoxin C3a receptor.
XX Disclosure; Fig 1; 112pp; English.
XX The invention discloses an isolated and purified composition including
XX the G protein-coupled receptor (GPCR) anaphylatoxin C3a receptor (AR) and
XX a pharmaceutically acceptable carrier for use in the manufacture of a
XX medicament for inhibiting, preventing or treating Alzheimer's disease or
XX Parkinson's disease. G protein-coupled receptors are involved in cell
XX signalling and play key roles in cell proliferation, differentiation,
XX leukocyte migration, gene transcription, vision, smell, neurotransmission
XX and hormonal response. Compositions relating to the anaphylatoxin C3a
XX receptor can also be used against ulcerative colitis, diabetes,
XX myocardial infarction, hypertension, asthma, bronchitis, pneumonia,
XX Crohn's disease, rheumatoid arthritis, Hodgkin's lymphoma, glioblastomas
XX and other neurodegenerative disorders. The compositions include
XX antibodies, agonists, antagonists, probes, antisense and gene therapies.
XX The anaphylatoxin C3a receptor sequence can be used to manufacture
XX medicaments able to reduce symptoms associated with Alzheimer's or
XX Parkinson's disease in a human patient, by combining a pharmaceutically
XX effective amount of an AR agonist or antagonist, a pharmaceutically
XX acceptable carrier, adjuvant, excipient, buffer and diluent, and for
XX detecting an increased possibility of Alzheimer's or Parkinson's disease.
XX The sequence presented is the human anaphylotoxin C3a receptor
XX Sequence 482 AA;
XX Query Match 100.0%; Score 482; DB 5; Length 482;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 MASFAETNSTDLSPQNEPPVILSMVLSITLFLGLPGNGLVWAGLKMQRVTWITW 60
XX 1 MASFAETNSTDLSPQNEPPVILSMVLSITLFLGLPGNGLVWAGLKMQRVTWITW 60
XX 61 FLHLTLADLCLSPSLAHALOGQWPGYGRFLCKLPSIIIVNMFASVFLTLAISDR 120
XX 61 FLHLTLADLCLSPSLAHALOGQWPGYGRFLCKLPSIIIVNMFASVFLTLAISDR 120
XX 121 CLVWFKPIWQNRHNVGMACISCGICWVAVFWCIPVYVYRIFFTDHNRCYGFGLSS 180
XX 121 CLVWFKPIWQNRHNVGMACISCGICWVAVFWCIPVYVYRIFFTDHNRCYGFGLSS 180
XX 181 SLDDYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVTVFQOTFORPSAD 240

Db 181 SLDDYDFYGDPLENRSLENIQPPGEMNDRLDPSFQTNHDPWTVTVFQOTFORPSAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
Qy 301 SSNSFYSELPGQFQDYNNLQFTDDDDQVTPPLVAITITRLVVGFLLSVMIACYSIV 360
Db 301 SSNSFYSELPGQFQDYNNLQFTDDDDQVTPPLVAITITRLVVGFLLSVMIACYSIV 360
Qy 361 FMQGRGFAKQSKTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMQGRGFAKQSKTFRVAVVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFCNPFYLLGKDFRKKARQSIQGIILAAFPSELTSTHCPNNVIERNST 480
Db 421 IALASANSFCNPFYLLGKDFRKKARQSIQGIILAAFPSELTSTHCPNNVIERNST 480
Qy 481 TV 482
Db 481 TV 482
XX RESULT 3
XX ABU79122
XX ID ABU79122 standard; protein; 482 AA.
XX AC ABU79122;
XX XX
XX DT 18-JUN-2003 (first entry)
XX XX
XX DE Chemoattractant protein.
XX KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW tumoricidal immunocyte; antitumour.
XX OS Unidentified.
XX XX
XX PN US2002177551-A1.
XX XX
XX PD 28-NOV-2002.
XX XX
XX PF 30-MAY-2001; 2001US-00870759.
XX XX
XX PR 31-MAY-2000; 2000US-0208128P.
XX XX
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX XX
XX DR WPI; 2003-361759/34.
XX DR N-PSDB; ACA64730.
XX XX
XX PT A mammalian cell receptor, useful in the treatment of cancer by binding
XX to tumor associated lipids where the binding induces anergy or apoptosis
XX in T cells and antigen presenting cells.
XX XX
XX PS Example 2; Page; 167pp; English.
XX XX
XX CC The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (MI) a tumoricidal immunocyte population in vivo in a mammal
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or

deleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal immunocyte population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipids to contact T cells ex vivo, and administering the tumouricidal immunocyte population, and administering a superantigen-lipid raft to contact T cells ex vivo, and (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated), and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"

Sequence 482 AA;

Query Match 100.0%; Score 482; DB 6; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MASFSATNSTDLLSQWNEPPVILSMVILSLTLLGLPGNGLVWAGLQKQRTVNTI 60
1 MASFSATNSTDLLSQWNEPPVILSMVILSLTLLGLPGNGLVWAGLQKQRTVNTI 60
61 FLHITLADLLCCLSLPFLSLAHLAQGGWPYGRFLCKLIPSIIVLNMFAVFLITAI 120
61 FLHITLADLLCCLSLPFLSLAHLAQGGWPYGRFLCKLIPSIIVLNMFAVFLITAI 120
121 CLVVFKPIWQNHVGNVCHACISCCIVVAFVWVCIPVFVREIPTTNDHNRGKFG 180
121 CLVVFKPIWQNHVGNVCHACISCCIVVAFVWVCIPVFVREIPTTNDHNRGKFG 180
181 SLDPDFYGPDPLENRSLNIVOPGEMNDRLDSSFOITNDHPWTVFQPTQFQPSAD 240
181 SLDPDFYGPDPLENRSLNIVOPGEMNDRLDSSFOITNDHPWTVFQPTQFQPSAD 240
241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPDIEDHETSPLDSDAFLSTHLK 300
241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPDIEDHETSPLDSDAFLSTHLK 300
301 SSNSFYSESLPQGGQDYNNIGQFTDDQVTPPLVAITITRLVWGLFPLPSVIMT 360
301 SSNSFYSESLPQGGQDYNNIGQFTDDQVTPPLVAITITRLVWGLFPLPSVIMT 360
361 FRMQRGFAKSSQSKTFRAVVVAVFLVVCVTPVHIFGVLISLLTDPETPLKTLMS 420
361 FRMQRGFAKSSQSKTFRAVVVAVFLVVCVTPVHIFGVLISLLTDPETPLKTLMS 420

Qy 421 IALASANSFNPFYALLGKDFRKARQSIQGLEAFAFSEELTRSTPCSPNNVISERNST 480
Db |||||
Qy 481 TV 482
Db ||
481 TV 482

RESULT 4
ABP81797
ID ABP81797 standard; protein; 482 AA.
XX
AC ABP81797;
DT 04-MAR-2003 (first entry)
DE Human complement component 3a receptor 1 protein SEQ ID NO:78.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regenerative-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42643.
XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,

CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX Sequence 482 AA;

Query Match 100.0%; Score 482; DB 6; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLSPQWNEPVLMSVILSLTFLGLPGNGLVWAGLKKQRTVNTIW 60
 Db 1 MASPSAETNSTDLSPQWNEPVLMSVILSLTFLGLPGNGLVWAGLKKQRTVNTIW 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Qy 121 CLVVFKEPIWCONHNRVGMACSIQCGIWWVAFVVCIPVYREIFTTNNHRCGYKFLSS 180
 Db 121 CLVVFKEPIWCONHNRVGMACSIQCGIWWVAFVVCIPVYREIFTTNNHRCGYKFLSS 180
 Qy 181 SLDPYDFYGDPLENRSLENIQVPPGEMNDRLDPSFQNDHPWTVPTVFQQTQRPASD 240
 Db 181 SLDPYDFYGDPLENRSLENIQVPPGEMNDRLDPSFQNDHPWTVPTVFQQTQRPASD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGFPEDHETSPLDNSDAFLSTHLKLPSPA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGFPEDHETSPLDNSDAFLSTHLKLPSPA 300
 Qy 301 SSNSFYSELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYFIV 360
 Db 301 SSNSFYSELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYFIV 360
 Qy 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALIGKDFRKKAROSIQGILEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSFNPFLYALIGKDFRKKAROSIQGILEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 5
 ADC86209 standard; protein; 482 AA.

XX AC ADC86209;

XX 01-JAN-2004 (first entry)

XX Human GPCR protein SEQ ID NO:662.

XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 KW gene therapy.

XX OS Homo sapiens.

XX PN EP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002EP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX
 PA
 FA
 PI
 PI
 XX
 DR
 DR
 XX
 PT
 PT
 XX
 PS
 XX
 CC
 CC
 CC
 CC
 CC
 CC
 XX
 SQ

Query Match 100.0%; Score 482; DB 7; Length 482;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLSPQWNEPVLMSVILSLTFLGLPGNGLVWAGLKKQRTVNTIW 60
 Db 1 MASPSAETNSTDLSPQWNEPVLMSVILSLTFLGLPGNGLVWAGLKKQRTVNTIW 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Qy 121 CLVVFKEPIWCONHNRVGMACSIQCGIWWVAFVVCIPVYREIFTTNNHRCGYKFLSS 180
 Db 121 CLVVFKEPIWCONHNRVGMACSIQCGIWWVAFVVCIPVYREIFTTNNHRCGYKFLSS 180
 Qy 181 SLDPYDFYGDPLENRSLENIQVPPGEMNDRLDPSFQNDHPWTVPTVFQQTQRPASD 240
 Db 181 SLDPYDFYGDPLENRSLENIQVPPGEMNDRLDPSFQNDHPWTVPTVFQQTQRPASD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGFPEDHETSPLDNSDAFLSTHLKLPSPA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSPIKPSGFPEDHETSPLDNSDAFLSTHLKLPSPA 300
 Qy 301 SSNSFYSELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYFIV 360
 Db 301 SSNSFYSELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMACYFIV 360
 Qy 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FMQGRGFAKQSQTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALIGKDFRKKAROSIQGILEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSFNPFLYALIGKDFRKKAROSIQGILEAAAFSEBLTRSTHCPSPNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 6
 ADF43378 standard; protein; 482 AA.

XX AC ADF43378;

XX DT 12-FEB-2004 (first entry)

assaying the ability of the test compound to modulate the expression of a anaphylatoxin receptor nucleic acid or the activity of a anaphylatoxin receptor polypeptide, thus identifying a compound capable of modulating anaphylatoxin receptor mediated metabolic activity, where the anaphylatoxin receptor comprises C3aR or C5aR) and modulating (M5) an anaphylatoxin receptor mediated metabolic activity (involving contacting a cell or a tissue expressing the anaphylatoxin receptor with a anaphylatoxin receptor modulator, thus modulating the anaphylatoxin receptor mediated metabolic activity, where the anaphylatoxin receptor is C3aR or C5aR). (M1) is useful for identifying a nucleic acid molecule or polypeptide associated with a metabolic disorder. (M2) is useful for identifying subject having metabolic disorder, for detecting mRNA and genomic DNA in the sample. (M3) is useful for identifying a compound capable of treating a metabolic disorder such as obesity, diabetes (especially non-insulin dependent), or insulin resistance. The metabolic disorders treated by the compound include endocrine abnormalities, triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon syndrome, Prader-Labhart-Willi syndrome and disorders of lipid metabolism. The present sequence represents human C3aR.

Sequence 482 AA;
Query Match 100.0%; Score 482; DB 8; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASFSATNSTDLSSQPNNEPVLISVILSTFLGLPGNGLVWAGLKMQRVTNTI 60
Db 1 MASFSATNSTDLSSQPNNEPVLISVILSTFLGLPGNGLVWAGLKMQRVTNTI 60
Qy 61 FLHTLADLLCCLSLPFLSLAHALQGGQMPYGRFLCKLPSIIVLNMFASVFLTAISLDR 120
Db 61 FLHTLADLLCCLSLPFLSLAHALQGGQMPYGRFLCKLPSIIVLNMFASVFLTAISLDR 120
Qy 121 CLVVFKEPIWQCNHNVGACISGCIWVAVFVCIPIVFPVYREIFTTNDNRCGYKFGLS 180
Db 121 CLVVFKEPIWQCNHNVGACISGCIWVAVFVCIPIVFPVYREIFTTNDNRCGYKFGLS 180
Qy 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPWTVPTVFQPTQRPSPAD 240
Db 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPWTVPTVFQPTQRPSPAD 240
Qy 241 SLRGSARLTSONLSNVKPKADVVSPKIPSGFPEDHETSPDLSNDAFLSTHLKLPESA 300
Db 241 SLRGSARLTSONLSNVKPKADVVSPKIPSGFPEDHETSPDLSNDAFLSTHLKLPESA 300
Qy 301 SSNSFYSELPQGFQDYNNLQGFDDQVPTPLVAITITRLVVGFLPSVIMIACTSYIV 360
Db 301 SSNSFYSELPQGFQDYNNLQGFDDQVPTPLVAITITRLVVGFLPSVIMIACTSYIV 360
Qy 361 FRMQRGRPAKSQKTRFVAVVAVFVLCVTPYHIFGVLSLLTDPTPLGKTLMSWDHVC 420
Db 361 FRMQRGRPAKSQKTRFVAVVAVFVLCVTPYHIFGVLSLLTDPTPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFLYALGKDFRKKAROSIOGILEAFSEELTRSTHCPSSNNVLSERNST 480
Db 421 IALASANSFNPFLYALGKDFRKKAROSIOGILEAFSEELTRSTHCPSSNNVLSERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 8
ID ABM83496
XX ABM83496 standard; protein; 415 AA.
AC ABM83496;
XX

18-NOV-2004 (first entry)
Human diagnostic and therapeutic pprotein SEQ ID NO:3745.

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
FN WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Aitua CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panzer IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LT;
PI Legace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX WPI: 2004-329368/30.
DR N-PSDB; ACN42148.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
in diagnosing a condition, disease or disorder associated with human
molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
in gene mapping.
XX Claim 27; Page: 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The dithp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a dithp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly
from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 415 AA;
Query Match 79.7%; Score 384; DB 8; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASFSATNSTDLSSQPNNEPVLISVILSTFLGLPGNGLVWAGLKMQRVTNTI 60
Db 1 MASFSATNSTDLSSQPNNEPVLISVILSTFLGLPGNGLVWAGLKMQRVTNTI 60
Qy 61 FLHTLADLLCCLSLPFLSLAHALQGGQMPYGRFLCKLPSIIVLNMFASVFLTAISLDR 120
Db 61 FLHTLADLLCCLSLPFLSLAHALQGGQMPYGRFLCKLPSIIVLNMFASVFLTAISLDR 120
Qy 121 CLVVFKEPIWQCNHNVGACISGCIWVAVFVCIPIVFPVYREIFTTNDNRCGYKFGLS 180
Db 121 CLVVFKEPIWQCNHNVGACISGCIWVAVFVCIPIVFPVYREIFTTNDNRCGYKFGLS 180
Qy 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPWTVPTVFQPTQRPSPAD 240
Db 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSFQNDHPWTVPTVFQPTQRPSPAD 240

241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
 241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
 301 SSNSFYSESELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIAICYSFIV 360
 301 SSNSFYSESELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIAICYSFIV 360
 361 FMQGRFAKSQSKTFRVAVVVVA 384
 361 FMQGRFAKSQSKTFRVAVVVVA 384

RESULT 9
 AAW02151
 ID AAW02151 standard; protein; 482 AA.
 XX
 AC
 XX
 XX
 DT 08-DEC-1996 (first entry)
 XX
 DE Human G-protein coupled receptor.
 XX
 KW G-coupled receptor; asthma; transplant rejection; immunodeficiency;
 KW severe infection; membrane protein.
 XX
 OS Homo sapiens.
 XX
 FN WO9625432-A1.
 XX
 PD 22-AUG-1996.
 XX
 PF 17-FEB-1995; 95WO-US001992.
 XX
 PR 17-FEB-1995; 95WO-US001992.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y, Rosen CA;
 XX
 DR WPI; 1996-393343/39.
 DR N-PSDB; AAT36375.
 XX
 PT DNA encoding G-protein coupled receptor - and antagonists and agonists,
 PT useful to treat asthma and transplant rejection, and immunodeficiency and
 PT severe infections, respectively.
 XX
 PS Claim 1; Page 45-48; 63pp; English.
 XX
 CC This sequence of a human G-protein coupled receptor may be expressed in a
 CC host cell using a vector, for production of the recombinant protein. An
 CC antagonist of this G-protein coupled receptor (GPCR) can be used to
 CC inhibit GPCR, to treat conditions relating to over-expression of the
 CC receptor, e.g. asthma, SLE, transplant rejection and abnormal cell
 CC growth. The agonist of GPCR can be used to stimulate GPCR, to treat
 CC conditions relating to under-expression of the receptor, e.g.
 CC immunodeficiency and severe infections, and for the prophylaxis of
 CC bacteril and viral infections, and C5a immunoregulatory effect
 CC stimulation
 XX
 SQ Sequence 482 AA;

Query Match 79.0%; Score 381; DB 2; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASPSAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60
 DB 1 MASPSAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMQRVTNTI 60
 QY 61 FLHLTLADLLCCLSLPSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120
 DB 61 FLHLTLADLLCCLSLPSLAHLALOGQWPYGRFLCKLIPSIIVLNMFASVFLTLAISLDR 120

QY 121 CLVVFKDIWCONHNHNVGMACSIQCIWVAVFVVCIPVFTVREIFTTNDHNRCGKFGGLSS 180
 DB 121 CLVVFKDIWCONHNHNVGMACSIQCIWVAVFVVCIPVFTVREIFTTNDHNRCGKFGGLSS 180
 QY 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFOTNDHPMTVPTVFQQTFFORPSAD 240
 DB 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFOTNDHPMTVPTVFQQTFFORPSAD 240
 QY 241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
 DB 241 SLPRGSARLTSONLYSNVFKPADVSPKIPSGFFIEDHETSPLDNSDAFLSTHLKLPESA 300
 QY 301 SSNSFYSESELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIAICYSFIV 360
 DB 301 SSNSFYSESELPGQFDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIAICYSFIV 360
 QY 361 FMQGRFAKSQSKTFRVAVVVVAFLVVCWTPVHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 DB 361 FMQGRFAKSQSKTFRVAVVVVAFLVVCWTPVHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSNPFYLLGKDFRKARQSIQGLEAAAFSEBELTRSTHCPSNNVISERNST 480
 DB 421 IALASANSNPFYLLGKDFRKARQSIQGLEAAAFSEBELTRSTHCPSNNVISERNST 480
 QY 481 TV 482
 DB 481 TV 482

RESULT 10
 AAW23367
 ID AAW23367 standard; protein; 482 AA.
 XX
 AC AAW23367;
 XX
 DT 30-MAR-1998 (first entry)
 XX
 DE Novel G-protein coupled receptor with an enlarged extracellular domain.
 XX
 KW G-protein coupled receptor; enlarged extracellular loop;
 KW inflammatory disease; asthma; chronic obstructive pulmonary disease;
 KW cystic fibrosis; multiple sclerosis; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9
 FT Domain /note= "predicted N-glycosylation site"
 FT Domain /note= "putative transmembrane domain"
 FT Domain 163..327
 FT Modified-site /note= "enlarged extracellular loop"
 FT Domain 194
 FT Domain /note= "predicted N-glycosylation site"
 FT Domain 333..439
 FT Domain /note= "putative transmembrane domain"
 XX
 FN WO9728188-A1.
 XX
 PD 07-AUG-1997.
 XX
 PF 30-JAN-1997; 97WO-US001736.
 XX
 PR 30-JAN-1996; 96US-0010808P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Ye RD;
 XX
 DR WPI; 1997-402552/37.
 DR N-PSDB; AAT64946.
 XX

PT G-protein-coupled receptor with enlarged extracellular domain - between
 PT fourth and fifth transmembrane domains, also nucleic acid and antibodies
 PT useful for treating inflammation and neurological disease.

PS Claim 4; Fig 1; 54pp; English.

XX The present sequence represents a novel G-protein coupled receptor that
 CC has an enlarged extracellular loop between the fourth and fifth
 CC transmembrane domains. Antibodies generated against the present protein
 CC revealed expression in a variety of tissues, including heart, lung and
 CC placenta. Diseases or conditions mediated by the G-protein coupled
 CC receptor can be treated by administering reagents such as the present
 CC sequence, antisense nucleic acid or antibodies generated against the
 CC receptor. Reagents may comprise a molecule binding to the receptor but
 CC not transmitting a signal across the cell membrane or reducing
 CC effectiveness of binding of the natural ligand. The reagent may also
 CC alter the interaction of the receptor with the G-protein with which it
 CC naturally reacts e.g. by altering phosphorylation sites in intracellular
 CC domains of the receptor. Inflammatory diseases or conditions mediated by
 CC the novel receptor which can be treated include e.g. asthma, chronic
 CC obstructive pulmonary disease, cystic fibrosis, multiple sclerosis. The
 CC antibody can also be used to diagnose these diseases e.g. in brain tissue
 CC from patients with suspected neurological disease, especially
 CC Alzheimer's, in skin samples especially from patients with a suspected
 CC inflammatory disease or in haematopoietic cells. The nucleic acids are
 CC also useful in screening for compounds modulating gene expression by
 CC standard assays

XX Sequence 482 AA;

Query Match 79.0%; Score 381; DB 2; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPVLMSVLSLTLGLPGNGLVWAGLKMQRVTW 60
 DB 1 MASFAETNSTDLLSQPNNEPVLMSVLSLTLGLPGNGLVWAGLKMQRVTW 60
 QY 61 FLHLLADLCLSLPFLSLAHALQGWYGRFLCKLIPSIIVLNMFSVFLTLAISDR 120
 DB 61 FLHLLADLCLSLPFLSLAHALQGWYGRFLCKLIPSIIVLNMFSVFLTLAISDR 120
 QY 121 CLVFKPTWCQHRNVGACSTCGCIWVAFVWCIPVFVYREIFTDNHNRCYKFGLS 180
 DB 121 CLVFKPTWCQHRNVGACSTCGCIWVAFVWCIPVFVYREIFTDNHNRCYKFGLS 180
 QY 181 SLDPDFDGDPLENRSLENIQPCGMDRLDPSSFQNDHPTVPTVFPOTFORPSAD 240
 DB 181 SLDPDFDGDPLENRSLENIQPCGMDRLDPSSFQNDHPTVPTVFPOTFORPSAD 240
 QY 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPIEDHETSPDLSNDAFLSTHLKLPESA 300
 DB 241 SLPRGSARLTQNLVSNVFKPADVVSFKIPSGFPIEDHETSPDLSNDAFLSTHLKLPESA 300
 QY 301 SSNSYSELPGFODYNLGOFTDDQVPTPLVAITITRLVVGFLPSVIMACYSTIV 360
 DB 301 SSNSYSELPGFODYNLGOFTDDQVPTPLVAITITRLVVGFLPSVIMACYSTIV 360
 QY 361 FMQGRGAKSQKTRFVAVVAVVAVLVCWTPIYHFGVLSLTDPTPLGKTLMSDWHVC 420
 DB 361 FMQGRGAKSQKTRFVAVVAVVAVLVCWTPIYHFGVLSLTDPTPLGKTLMSDWHVC 420
 QY 421 IALANSFCNPFVALLGKDPKFKARQSIQGLEAAAFSEELTRTHCPNNVIERNST 480
 DB 421 IALANSFCNPFVALLGKDPKFKARQSIQGLEAAAFSEELTRTHCPNNVIERNST 480
 QY 481 TV 482
 DB 481 TV 482

RESULT 11
 ABU62861

ID ABU62861 standard; protein; 482 AA.
 XX AC ABU62861;
 XX DT 11-SEP-2003 (first entry)
 XX DE Putative mature human G protein coupled receptor.
 XX KW G protein coupled receptor; GPCR; human; infection;
 KW immunodeficiency disease; asthma; bronchial allergy;
 KW chronic inflammation; systemic lupus erythematosus; gout;
 KW transplant rejection; hypertension; abnormal cell growth;
 KW neurological disease; receptor.
 XX OS Homo sapiens.
 XX PN US2003022310-A1.
 XX PD 30-JAN-2003.
 XX PF 30-SEP-2002; 2002US-00259521.
 XX PR 17-FEB-1995; 95WO-US001992.
 PR 05-JUN-1995; 95US-00462314.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Li Y, Rosen CA;
 XX WI WPI; 2003-531445/50.
 DR N-PSDB; ACD26620.
 XX New G-protein coupled receptor polypeptides and polynucleotide, useful
 PT for screening receptor agonists and/or antagonists and/or receptor
 PT ligands, in chromosome identification, and in for producing antibodies.
 XX Claim 1; Fig 1A-D; 26pp; English.

CC The invention describes an isolated polynucleotide (I) comprising a
 CC sequence which: (a) encodes a polypeptide having a sequence of 482 amino
 CC acids (II) given in the specification; (b) encodes a mature polypeptide
 CC encoded or expressed by the DNA contained in ATCC deposit number 75982;
 CC (c) is capable of hybridising to and which is at least 70% identical to
 CC (a) or (b); or (d) a fragment of (a), (b) or (c). The G-protein coupled
 CC receptors (GPCR) are useful for screening receptor agonists and/or
 CC antagonists and/or receptor ligands. GPCR agonists are useful for
 CC stimulating GPCR for the treatment of conditions related to the under-
 CC expression of GPCR, e.g. bacterial or viral infection, immunodeficiency
 CC diseases and severe infections, GPCR antagonists are useful for
 CC inhibiting the action of GPCR for treating conditions associated with
 CC over-expression of the GPCR, e.g. asthma, bronchial allergy, chronic
 CC inflammation, systemic lupus erythematosus, gout, transplant rejection,
 CC hypertension, abnormal cell growth, and neurological diseases. The GPCR
 CC genes are also useful in diagnostic assays for detecting diseases or
 CC susceptibility to diseases related to the presence of mutations in the
 CC GPCR genes. These may also be used in chromosome identification. This is
 CC polypeptides are useful as immunogens for producing antibodies. This is
 CC the amino acid sequence of a putative mature human G protein coupled
 CC receptor

SQ Sequence 482 AA;

Query Match 79.0%; Score 381; DB 7; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPVLMSVLSLTLGLPGNGLVWAGLKMQRVTW 60
 DB 1 MASFAETNSTDLLSQPNNEPVLMSVLSLTLGLPGNGLVWAGLKMQRVTW 60
 QY 61 FLHLLADLCLSLPFLSLAHALQGWYGRFLCKLIPSIIVLNMFSVFLTLAISDR 120
 DB 61 FLHLLADLCLSLPFLSLAHALQGWYGRFLCKLIPSIIVLNMFSVFLTLAISDR 120

QY 121 CLVFKPIWQNRHNVGMACISGCIWVAVFVVCIPVVFYREIFTTDHNRCGYKFLSS 180
 Db 121 CLVFKPIWQNRHNVGMACISGCIWVAVFVVCIPVVFYREIFTTDHNRCGYKFLSS 180
 QY 181 SLDPDFYGDPLENRSLENIWPPGEMNDRLDPSSFQTDNDHPWTVPTVFQPTQRPSPAD 240
 Db 181 SLDPDFYGDPLENRSLENIWPPGEMNDRLDPSSFQTDNDHPWTVPTVFQPTQRPSPAD 240
 QY 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPPIEDHETSPLDNSDAFLSTHLKLPSPA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPPIEDHETSPLDNSDAFLSTHLKLPSPA 300
 QY 301 SSNSFYSESELPOGFQDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
 Db 301 SSNSFYSESELPOGFQDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
 QY 361 FRMQRGRFAKSQSKTRFVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTRFVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSCEPFLYALGKDFRKKAROSIQGILEAAFSBELTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSCEPFLYALGKDFRKKAROSIQGILEAAFSBELTRSTHCPSPNNVISERNST 480
 QY 481 TV 482
 Db 481 TV 482

RESULT 12
 ADD46294
 ID ADD46294 standard; protein; 482 AA.

AC ADD46294;

DT 29-JAN-2004 (first entry)

XX Human Protein Q16581, SEQ ID NO 11969.

XX Human; pain; neuronal tissue; gene therapy;
 XX spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPT; 2003-268312/26.

XX GENBANK; Q16581.

XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 XX or human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 482 AA;

Query Match 79.0%; Score 381; DB 7; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASPSAETNSTDLISQPNWPPVILSNVILSLTLLPGNLVWVAGLKMQRVTNTW 60
 Db 1 MASPSAETNSTDLISQPNWPPVILSNVILSLTLLPGNLVWVAGLKMQRVTNTW 60
 QY 61 FLHLLTADLLCCLSLPPSLAHLAQGWQPYGRFLCKLIPSIIVLNMFASFVLLTAISLDR 120
 Db 61 FLHLLTADLLCCLSLPPSLAHLAQGWQPYGRFLCKLIPSIIVLNMFASFVLLTAISLDR 120
 QY 121 CLVVFKPIWQNRHNVGMACISGCIWVAVFVVCIPVVFYREIFTTDHNRCGYKFLSS 180
 Db 121 CLVVFKPIWQNRHNVGMACISGCIWVAVFVVCIPVVFYREIFTTDHNRCGYKFLSS 180
 QY 181 SLDPDFYGDPLENRSLENIWPPGEMNDRLDPSSFQTDNDHPWTVPTVFQPTQRPSPAD 240
 Db 181 SLDPDFYGDPLENRSLENIWPPGEMNDRLDPSSFQTDNDHPWTVPTVFQPTQRPSPAD 240
 QY 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPPIEDHETSPLDNSDAFLSTHLKLPSPA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSPIPSGFPPIEDHETSPLDNSDAFLSTHLKLPSPA 300
 QY 301 SSNSFYSESELPOGFQDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
 Db 301 SSNSFYSESELPOGFQDYNNLQFTDDQVPTPLVAITITRLVVGFLPLSPVIMIACTYFIV 360
 QY 361 FRMQRGRFAKSQSKTRFVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTRFVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 QY 421 IALASANSCEPFLYALGKDFRKKAROSIQGILEAAFSBELTRSTHCPSPNNVISERNST 480
 Db 421 IALASANSCEPFLYALGKDFRKKAROSIQGILEAAFSBELTRSTHCPSPNNVISERNST 480
 QY 481 TV 482
 Db 481 TV 482

RESULT 13
 ADL22832
 ID ADL22832 standard; protein; 482 AA.
 XX
 AC ADL22832;
 XX

CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.

XX Sequence 482 AA;
 Query Match 79.0%; Score 381; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASFSAEINSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVWAGLKMQRVTNTI 60
 DB 1 MASFSAEINSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVWAGLKMQRVTNTI 60
 QY 61 FLHTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
 DB 61 FLHTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
 QY 121 CLVVFKEPIWQNHNRNMGVACISGCIWVAFVWCIPVFVYREIFTTNDHNRGKFGGLSS 180
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 QY 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTDNDHPVTVPVFPQTFQRPSPAD 240
 DB 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTDNDHPVTVPVFPQTFQRPSPAD 240
 QY 241 SLPRGSA RLTSQNLVSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPSPA 300
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 QY 301 SSNSFYSESLPQGFQDYNNLQGTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 DB 301 SSNSFYSESLPQGFQDYNNLQGTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 QY 361 FMQRGRFAKQSQTFRVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 DB 361 FMQRGRFAKQSQTFRVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420
 QY 421 IALASANSFNFLYALLGKDFRKKARQSIQGLEAAAFSEBELTRSTHCPNNSVIERNST 480
 DB 421 IALASANSFNFLYALLGKDFRKKARQSIQGLEAAAFSEBELTRSTHCPNNSVIERNST 480
 QY 481 TV 482
 DB 481 TV 482

RESULT 15
 ADQ19275
 ID ADQ19275 standard; protein; 482 AA.
 XX
 AC ADQ19275;
 XX
 DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2094.
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW Homo sapiens.
 OS WO2004048938-A2.
 PN 10-JUN-2004.
 PD 26-NOV-2003; 2003WO-US038193.
 PF 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 XX Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 DR Early detection of soft tissue sarcoma comprises determining expression
 XX of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX Example 2; SEQ ID NO 2094; 210pp; English.
 PS The invention relates to a novel method for detecting soft tissue sarcoma
 XX which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytotatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.

XX Sequence 482 AA;
 Query Match 79.0%; Score 381; DB 8; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASFSAEINSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVWAGLKMQRVTNTI 60
 DB 1 MASFSAEINSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVWAGLKMQRVTNTI 60
 QY 61 FLHTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
 DB 61 FLHTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
 QY 121 CLVVFKEPIWQNHNRNMGVACISGCIWVAFVWCIPVFVYREIFTTNDHNRGKFGGLSS 180
 DB 121 CLVVFKEPIWQNHNRNMGVACISGCIWVAFVWCIPVFVYREIFTTNDHNRGKFGGLSS 180
 QY 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTDNDHPVTVPVFPQTFQRPSPAD 240
 DB 181 SLDPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTDNDHPVTVPVFPQTFQRPSPAD 240
 QY 241 SLPRGSA RLTSQNLVSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPSPA 300
 DB 241 SLPRGSA RLTSQNLVSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPSPA 300
 QY 301 SSNSFYSESLPQGFQDYNNLQGTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 DB 301 SSNSFYSESLPQGFQDYNNLQGTDDDDQVPTPLVAITITRLVVGFLPLPSVIMIACYSFIV 360
 QY 361 FMQRGRFAKQSQTFRVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAV 420

Db	361	FRMQGRFAKSQKTRVAVVAVFLVCWTPYHIFGVLSLLTDETPLGKILMSWDHVC	420
Qy	421	IALASANSFNPFLYALLGKDFRKKARQSIQGILEAAPSEELTRSTHCPSNNVISERNST	480
Db	421	IALASANSFNPFLYALLGKDFRKKARQSIQGILEAAPSEELTRSTHCPSNNVISERNST	480
Qy	481	TV 482	
Db	481	TV 482	

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Job time : 209 secs

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OM protein - protein search, using sw model

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(without alignments)
836.764 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 482

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

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- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	381	79.0	482	2	US-08-876-874-2
2	381	79.0	482	4	US-09-117-440-2
3	280	58.1	482	4	US-09-826-509-465
4	10	2.1	337	4	US-09-693-242-2
5	10	2.1	337	4	US-09-786-442B-2
6	9	1.9	304	1	US-08-118-270-35
7	9	1.9	304	5	PCT-US93-08528-35
8	9	1.9	320	4	US-09-576-160B-4
9	9	1.9	350	2	US-08-458-970A-9
10	9	1.9	350	4	US-09-576-160B-5
11	9	1.9	350	4	US-09-826-509-467
12	8	1.7	9	4	US-09-674-973A-316
13	8	1.7	10	4	US-09-674-973A-317
14	8	1.7	16	1	US-08-079-051-2
15	8	1.7	16	5	PCT-US94-06994-2
16	8	1.7	63	4	US-09-674-973A-319
17	8	1.7	64	4	US-09-674-973A-318
18	8	1.7	115	3	US-08-513-974B-351
19	8	1.7	355	2	US-08-458-970A-2
20	8	1.7	355	4	US-09-170-496D-2
21	8	1.7	355	4	US-09-170-496D-164
22	8	1.7	358	4	US-09-400-622-2
23	8	1.7	392	4	US-09-949-016-8826
24	8	1.7	395	3	US-08-981-825-6
25	8	1.7	395	3	US-09-480-784-6
26	8	1.7	409	3	US-09-385-028-12
27	8	1.7	409	4	US-09-726-614-12

28	8	1.7	409	4	US-09-385-040-12	Sequence 12, Appl
29	8	1.7	429	4	US-09-252-991A-30376	Sequence 30376, A
30	8	1.7	466	2	US-08-406-855A-23	Sequence 23, Appl
31	8	1.7	466	3	US-09-206-899-23	Sequence 23, Appl
32	8	1.7	466	4	US-09-688-415-11	Sequence 11, Appl
33	8	1.7	888	4	US-09-252-991A-17967	Sequence 17967, A
34	8	1.7	1277	3	US-08-937-236-6	Sequence 6, Appl
35	8	1.7	1292	3	US-08-569-214-5	Sequence 5, Appl
36	8	1.7	1292	3	US-08-937-236-5	Sequence 5, Appl
37	8	1.7	1292	3	US-08-937-236-5	Sequence 5, Appl
38	7	1.5	19	4	US-09-441-502B-86	Sequence 86, Appl
39	7	1.5	19	4	US-09-441-502B-87	Sequence 87, Appl
40	7	1.5	30	4	US-09-618-304B-7	Sequence 7, Appl
41	7	1.5	32	4	US-09-270-767-62136	Sequence 7, Appl
42	7	1.5	61	4	US-09-248-796A-25577	Sequence 25577, A
43	7	1.5	74	4	US-09-513-999C-6293	Sequence 6293, Ap
44	7	1.5	74	4	US-09-471-276-953	Sequence 953, Ap
45	7	1.5	76	4	US-09-504-132-22	Sequence 22, Appl
46	7	1.5	88	3	US-08-513-974B-340	Sequence 340, Appl
47	7	1.5	93	1	US-08-118-270-348	Sequence 348, App
48	7	1.5	93	5	PCT-US93-08528-348	Sequence 348, App
49	7	1.5	94	3	US-09-091-590A-5	Sequence 5, Appl
50	7	1.5	105	4	US-09-539-333D-43	Sequence 43, Appl
51	7	1.5	121	4	US-09-539-333D-41	Sequence 41, Appl
52	7	1.5	127	4	US-09-270-767-46543	Sequence 46543, A
53	7	1.5	132	4	US-09-539-333D-42	Sequence 42, Appl
54	7	1.5	134	4	US-09-270-767-37944	Sequence 37944, A
55	7	1.5	134	4	US-09-270-767-53161	Sequence 53161, A
56	7	1.5	165	4	US-09-270-767-36842	Sequence 36842, A
57	7	1.5	165	4	US-09-270-767-52059	Sequence 52059, A
58	7	1.5	184	4	US-09-248-796A-27001	Sequence 27001, A
59	7	1.5	199	3	US-08-478-316-34	Sequence 34, Appl
60	7	1.5	199	3	US-09-019-793A-34	Sequence 34, Appl
61	7	1.5	200	4	US-09-601-326-34	Sequence 34, Appl
62	7	1.5	220	4	US-09-489-039A-13425	Sequence 13425, A
63	7	1.5	270	2	US-08-484-993B-47	Sequence 47, Appl
64	7	1.5	270	2	US-08-484-158B-47	Sequence 47, Appl
65	7	1.5	270	2	US-08-484-596A-47	Sequence 47, Appl
66	7	1.5	270	2	US-08-480-150A-47	Sequence 47, Appl
67	7	1.5	270	3	US-08-458-731-47	Sequence 47, Appl
68	7	1.5	270	3	US-08-149-223A-47	Sequence 47, Appl
69	7	1.5	271	4	US-09-328-352-5629	Sequence 5629, Ap
70	7	1.5	276	4	US-09-107-433-3238	Sequence 3238, Ap
71	7	1.5	279	4	US-09-134-000C-4479	Sequence 4479, Ap
72	7	1.5	282	4	US-09-902-540-15311	Sequence 15311, A
73	7	1.5	286	4	US-09-248-796A-22818	Sequence 22818, A
74	7	1.5	298	1	US-08-118-270-76	Sequence 76, Appl
75	7	1.5	298	5	PCT-US93-08528-76	Sequence 76, Appl
76	7	1.5	325	1	US-08-118-270-51	Sequence 51, Appl
77	7	1.5	325	5	PCT-US93-08528-51	Sequence 51, Appl
78	7	1.5	330	2	US-08-788-750-2	Sequence 2, Appl
79	7	1.5	330	3	US-09-187-710-2	Sequence 2, Appl
80	7	1.5	330	4	US-09-152-060-104	Sequence 104, App
81	7	1.5	330	4	US-09-170-496D-258	Sequence 258, App
82	7	1.5	330	4	US-09-170-496D-276	Sequence 276, App
83	7	1.5	345	1	US-08-171-382-6	Sequence 6, Appl
84	7	1.5	345	1	US-08-309-420-6	Sequence 6, Appl
85	7	1.5	345	1	US-08-309-419-6	Sequence 6, Appl
86	7	1.5	345	3	US-09-294-531B-31	Sequence 31, Appl
87	7	1.5	345	4	US-09-394-142B-2	Sequence 2, Appl
88	7	1.5	345	5	PCT-US95-11856-6	Sequence 6, Appl
89	7	1.5	345	5	PCT-US95-11878-6	Sequence 6, Appl
90	7	1.5	347	4	US-08-405-271A-24	Sequence 24, Appl
91	7	1.5	355	4	US-09-328-352-6341	Sequence 6341, Ap
92	7	1.5	355	4	US-09-170-496D-246	Sequence 246, App
93	7	1.5	356	4	US-09-170-496D-270	Sequence 270, App
94	7	1.5	358	2	US-08-458-970A-11	Sequence 11, Appl
95	7	1.5	359	1	US-08-041-219A-6	Sequence 6, Appl
96	7	1.5	359	1	US-08-148-209A-4	Sequence 4, Appl
97	7	1.5	359	1	US-08-417-122-6	Sequence 6, Appl
98	7	1.5	359	4	US-09-867-915-3	Sequence 3, Appl
99	7	1.5	364	4	US-08-148-708-2	Sequence 2, Appl
100	7	1.5	365	4	US-09-745-842-16	Sequence 16, Appl

247	6	1.2	68	4	US-09-270-767-49808	Sequence 49808, A	320	6	1.2	140	4	US-09-489-039A-8311	Sequence 8311, Ap
248	6	1.2	68	4	US-09-248-796A-24269	Sequence 24269, A	321	6	1.2	141	3	US-09-228-986-91	Sequence 91, Appl
249	6	1.2	68	4	US-09-248-796A-26148	Sequence 26148, A	322	6	1.2	141	4	US-09-252-991A-21953	Sequence 21953, A
250	6	1.2	68	4	US-09-248-796A-26936	Sequence 26936, A	323	6	1.2	141	4	US-09-252-991A-23895	Sequence 23895, A
251	6	1.2	70	4	US-09-248-796A-21827	Sequence 21827, A	324	6	1.2	141	4	US-10-101-464A-91	Sequence 91, Appl
252	6	1.2	74	4	US-09-107-433-5017	Sequence 5017, Ap	325	6	1.2	142	3	US-09-441-346A-2	Sequence 2, Appl
253	6	1.2	75	4	US-09-107-532A-4321	Sequence 4321, Ap	326	6	1.2	142	3	US-09-789-453A-2	Sequence 2, Appl
254	6	1.2	76	3	US-09-134-001C-4377	Sequence 4377, Ap	327	6	1.2	142	4	US-09-489-847-346	Sequence 346, App
255	6	1.2	77	4	US-09-252-991A-29583	Sequence 29583, A	328	6	1.2	143	4	US-09-270-767-37046	Sequence 37046, A
256	6	1.2	77	4	US-09-489-039A-9450	Sequence 9450, Ap	329	6	1.2	143	4	US-09-270-767-52263	Sequence 52263, A
257	6	1.2	78	4	US-09-270-767-59336	Sequence 59336, A	330	6	1.2	144	4	US-09-540-236-2838	Sequence 2838, Ap
258	6	1.2	78	4	US-09-248-796A-27274	Sequence 27274, A	331	6	1.2	146	4	US-09-530-880-6	Sequence 6, Appl
259	6	1.2	79	3	US-09-134-001C-3226	Sequence 3226, Ap	332	6	1.2	146	4	US-09-530-880-6	Sequence 6, Appl
260	6	1.2	79	4	US-09-252-991A-28893	Sequence 28893, A	333	6	1.2	146	4	US-09-710-279-576	Sequence 576, App
261	6	1.2	79	4	US-10-101-464A-696	Sequence 696, App	334	6	1.2	147	1	US-08-305-520-6	Sequence 12338, A
262	6	1.2	80	4	US-09-248-796A-25128	Sequence 25128, A	335	6	1.2	147	2	US-08-486-663A-6	Sequence 6, Appl
263	6	1.2	81	4	US-09-489-847-237	Sequence 237, App	336	6	1.2	147	3	US-08-767-942A-6	Sequence 6, Appl
264	6	1.2	81	4	US-09-248-796A-25945	Sequence 25945, A	337	6	1.2	147	4	US-09-328-352-7278	Sequence 7278, Ap
265	6	1.2	81	4	US-09-749-637A-315	Sequence 315, App	338	6	1.2	148	3	US-09-358-580-2	Sequence 2, Appl
266	6	1.2	82	4	US-09-248-796A-26381	Sequence 26381, A	339	6	1.2	148	3	US-09-358-580-4	Sequence 4, Appl
267	6	1.2	83	4	US-09-270-767-34021	Sequence 34021, A	340	6	1.2	148	3	US-09-358-580-6	Sequence 6, Appl
268	6	1.2	83	4	US-09-270-767-49238	Sequence 49238, A	341	6	1.2	148	4	US-09-732-210-135	Sequence 135, App
269	6	1.2	84	4	US-09-716-129-121	Sequence 121, App	342	6	1.2	148	4	US-09-732-210-1683	Sequence 1683, Ap
270	6	1.2	86	4	US-09-513-999C-6033	Sequence 6033, Ap	343	6	1.2	148	4	US-09-134-000C-4507	Sequence 4507, Ap
271	6	1.2	89	4	US-09-513-999C-4301	Sequence 4301, Ap	344	6	1.2	150	4	US-09-430-470-6	Sequence 6, Appl
272	6	1.2	89	4	US-09-902-540-10147	Sequence 10147, A	345	6	1.2	151	4	US-09-430-470-10	Sequence 10, Appl
273	6	1.2	95	4	US-09-270-767-58498	Sequence 58498, A	346	6	1.2	152	4	US-09-430-470-8	Sequence 8, Appl
274	6	1.2	96	4	US-09-248-796A-27733	Sequence 27733, A	347	6	1.2	152	4	US-09-270-767-35128	Sequence 35128, A
275	6	1.2	96	4	US-09-370-838-77	Sequence 77, Appl	348	6	1.2	152	4	US-09-270-767-50345	Sequence 50345, A
276	6	1.2	96	4	US-09-854-133-77	Sequence 77, Appl	349	6	1.2	153	4	US-09-430-470-4	Sequence 4, Appl
277	6	1.2	97	4	US-09-270-767-35957	Sequence 35957, A	350	6	1.2	156	4	US-09-252-991A-17833	Sequence 17833, A
278	6	1.2	97	4	US-09-270-767-51174	Sequence 51174, A	351	6	1.2	156	4	US-09-252-991A-20805	Sequence 20805, A
279	6	1.2	98	4	US-09-248-796A-27672	Sequence 27672, A	352	6	1.2	156	4	US-09-328-352-7343	Sequence 7343, Ap
280	6	1.2	98	4	US-09-248-796A-25502	Sequence 25502, A	353	6	1.2	156	4	US-09-270-767-36461	Sequence 36461, A
281	6	1.2	100	4	US-09-248-796A-14115	Sequence 14115, A	354	6	1.2	156	4	US-09-270-767-43938	Sequence 43938, A
282	6	1.2	102	4	US-09-107-532A-6505	Sequence 6505, Ap	355	6	1.2	156	4	US-09-270-767-51678	Sequence 51678, A
283	6	1.2	105	4	US-10-101-464A-523	Sequence 523, App	356	6	1.2	156	4	US-09-902-540-15493	Sequence 15493, A
284	6	1.2	108	4	US-09-593-360B-109	Sequence 360, App	357	6	1.2	162	3	US-09-575-574-4	Sequence 4, Appl
285	6	1.2	109	4	US-09-270-767-35213	Sequence 35213, A	358	6	1.2	162	4	US-09-198-452A-948	Sequence 948, App
286	6	1.2	109	4	US-09-270-767-39319	Sequence 39319, A	359	6	1.2	162	4	US-09-902-540-13324	Sequence 13324, A
287	6	1.2	109	4	US-09-270-767-50430	Sequence 50430, A	360	6	1.2	164	4	US-09-489-039A-8018	Sequence 8018, Ap
288	6	1.2	109	4	US-09-270-767-54536	Sequence 54536, A	361	6	1.2	164	4	US-09-248-796A-27813	Sequence 27813, A
289	6	1.2	110	4	US-09-543-681A-6190	Sequence 6190, Ap	362	6	1.2	165	3	US-08-799-149C-5	Sequence 5, Appl
290	6	1.2	110	4	US-09-134-000C-4255	Sequence 4255, Ap	363	6	1.2	165	4	US-09-421-630-5	Sequence 5, Appl
291	6	1.2	114	4	US-09-727-739B-43	Sequence 43, Appl	364	6	1.2	165	4	US-09-902-540-14064	Sequence 14064, A
292	6	1.2	114	4	US-10-146-710-1	Sequence 1, Appl	365	6	1.2	165	4	US-09-252-991A-23862	Sequence 23862, A
293	6	1.2	115	4	US-09-248-796A-15885	Sequence 15885, A	366	6	1.2	167	4	US-09-270-767-32760	Sequence 32760, A
294	6	1.2	116	4	US-09-583-110-4891	Sequence 4891, Ap	367	6	1.2	167	4	US-09-252-991A-21901	Sequence 21901, A
295	6	1.2	117	4	US-09-270-767-37550	Sequence 37550, A	368	6	1.2	168	4	US-09-252-991A-31042	Sequence 31042, A
296	6	1.2	117	4	US-09-270-767-39798	Sequence 39798, A	369	6	1.2	169	4	US-09-252-991A-32254	Sequence 32254, A
297	6	1.2	117	4	US-09-270-767-52767	Sequence 52767, A	370	6	1.2	169	4	US-09-902-540-15752	Sequence 15752, A
298	6	1.2	117	4	US-09-270-767-55015	Sequence 55015, A	371	6	1.2	171	4	US-09-543-681A-8312	Sequence 8312, Ap
299	6	1.2	119	4	US-09-902-540-13033	Sequence 13033, A	372	6	1.2	172	4	US-09-270-767-37775	Sequence 37775, A
300	6	1.2	121	4	US-09-902-540-16008	Sequence 16008, A	373	6	1.2	172	4	US-09-270-767-52992	Sequence 52992, A
301	6	1.2	123	4	US-09-489-039A-11581	Sequence 11581, A	374	6	1.2	172	4	US-09-248-796A-22984	Sequence 22984, A
302	6	1.2	123	4	US-09-270-767-39169	Sequence 39169, A	375	6	1.2	173	4	US-09-513-775B-4	Sequence 4, Appl
303	6	1.2	123	4	US-09-248-796A-23309	Sequence 23309, A	376	6	1.2	173	4	US-09-270-767-57280	Sequence 57280, A
304	6	1.2	123	4	US-09-248-796A-23309	Sequence 23309, A	377	6	1.2	173	4	US-09-853-450-40	Sequence 40, Appl
305	6	1.2	124	4	US-09-621-976-4006	Sequence 4006, Ap	378	6	1.2	174	3	US-09-097-889-24	Sequence 24, Appl
306	6	1.2	124	4	US-09-107-433-3333	Sequence 3333, Ap	379	6	1.2	174	4	US-09-098-079-24	Sequence 24, Appl
307	6	1.2	125	4	US-09-902-540-16382	Sequence 16382, A	380	6	1.2	175	1	US-08-220-151-13	Sequence 13, Appl
308	6	1.2	126	3	US-08-513-974B-350	Sequence 350, App	381	6	1.2	175	1	US-08-413-118-13	Sequence 13, Appl
309	6	1.2	126	4	US-09-107-532A-7133	Sequence 7133, Ap	382	6	1.2	175	3	US-08-473-446-13	Sequence 13, Appl
310	6	1.2	129	4	US-09-134-000C-3900	Sequence 3900, Ap	383	6	1.2	175	4	US-09-248-796A-16583	Sequence 16583, A
311	6	1.2	134	4	US-09-489-847-195	Sequence 195, App	384	6	1.2	177	4	US-09-270-767-45660	Sequence 45660, A
312	6	1.2	136	4	US-09-690-454-131	Sequence 131, App	385	6	1.2	177	4	US-09-513-999C-5090	Sequence 5090, Ap
313	6	1.2	136	4	US-09-270-767-31883	Sequence 31883, A	386	6	1.2	177	4	US-09-893-737-174	Sequence 174, App
314	6	1.2	136	4	US-09-270-767-47100	Sequence 47100, A	387	6	1.2	178	4	US-09-489-039A-11561	Sequence 11561, A
315	6	1.2	137	4	US-09-107-532A-3757	Sequence 3757, Ap	388	6	1.2	178	4	US-09-902-540-15556	Sequence 15556, A
316	6	1.2	138	4	US-09-252-991A-29229	Sequence 29229, A	389	6	1.2	180	4	US-09-902-540-10368	Sequence 10368, A
317	6	1.2	139	4	US-08-818-581B-11	Sequence 11, Appl	390	6	1.2	181	3	US-09-066-046-25	Sequence 25, Appl
318	6	1.2	139	4	US-09-489-039A-11161	Sequence 11161, A	391	6	1.2	181	4	US-09-902-540-15851	Sequence 15851, A
319	6	1.2	140	4	US-09-328-352-5805	Sequence 5805, Ap	392	6	1.2	182	4	US-09-248-796A-27645	Sequence 27645, A

393	6	1.2	184	4	US-09-270-767-46275	Sequence 46275, A	466	6	1.2	231	4	US-09-134-000C-3889	Sequence 3889, Ap
394	6	1.2	185	4	US-09-270-767-35694	Sequence 35694, A	467	6	1.2	234	4	US-09-248-796A-16563	Sequence 16563, A
395	6	1.2	186	4	US-09-270-767-50911	Sequence 50911, A	468	6	1.2	235	4	US-09-252-991A-32987	Sequence 32987, A
396	6	1.2	187	4	US-09-540-236-2132	Sequence 2132, Ap	469	6	1.2	239	4	US-09-107-532A-3697	Sequence 3697, Ap
397	6	1.2	188	4	US-09-438-185A-883	Sequence 883, App	470	6	1.2	240	4	US-09-949-016-10616	Sequence 10616, A
398	6	1.2	189	3	US-08-779-764A-29	Sequence 29, Appl	471	6	1.2	241	4	US-09-134-000C-5897	Sequence 5897, Ap
399	6	1.2	189	3	US-08-779-764A-30	Sequence 30, Appl	472	6	1.2	241	4	US-09-270-767-61433	Sequence 61433, A
400	6	1.2	189	4	US-09-563-456-29	Sequence 29, Appl	473	6	1.2	242	4	US-08-818-581B-9	Sequence 9, Appl
401	6	1.2	189	4	US-09-252-991A-18880	Sequence 18880, A	474	6	1.2	242	4	US-09-489-039A-8068	Sequence 8068, Ap
402	6	1.2	190	4	US-09-248-796A-20819	Sequence 20819, A	475	6	1.2	243	4	US-09-949-016-6548	Sequence 6548, Ap
403	6	1.2	191	4	US-09-248-796A-20678	Sequence 20678, A	476	6	1.2	244	4	US-09-543-681A-7039	Sequence 7039, Ap
404	6	1.2	192	4	US-09-853-450-50	Sequence 50, Appl	477	6	1.2	244	4	US-09-270-767-32360	Sequence 32360, A
405	6	1.2	192	4	US-09-032-372-13	Sequence 13, Appl	478	6	1.2	244	4	US-09-270-767-47577	Sequence 47577, A
406	6	1.2	194	3	US-09-078-317-12	Sequence 12, Appl	479	6	1.2	245	2	US-08-321-670-3	Sequence 3, Appl
407	6	1.2	194	3	US-09-454-818-12	Sequence 12, Appl	480	6	1.2	245	2	US-08-321-670-4	Sequence 4, Appl
408	6	1.2	196	4	US-09-252-991A-26130	Sequence 26130, A	481	6	1.2	245	2	US-08-512-955-5	Sequence 5, Appl
409	6	1.2	196	4	US-09-270-767-34969	Sequence 34969, A	482	6	1.2	245	3	US-09-215-252-4	Sequence 4, Appl
410	6	1.2	196	4	US-09-270-767-50186	Sequence 50186, A	483	6	1.2	245	4	US-08-818-581B-13	Sequence 13, Appl
411	6	1.2	196	4	US-09-538-092-455	Sequence 455, App	484	6	1.2	245	4	US-09-970-989A-4	Sequence 4, Appl
412	6	1.2	197	4	US-09-252-991A-27889	Sequence 27889, A	485	6	1.2	245	4	US-09-543-681A-8212	Sequence 8212, Ap
413	6	1.2	197	4	US-09-270-767-48492	Sequence 48492, A	486	6	1.2	249	4	US-09-107-532A-7142	Sequence 7142, Ap
414	6	1.2	197	4	US-09-248-796A-15582	Sequence 15582, A	487	6	1.2	250	4	US-09-902-540-11565	Sequence 11565, A
415	6	1.2	197	4	US-09-036-987A-23	Sequence 23, Appl	488	6	1.2	251	4	US-09-252-991A-22652	Sequence 22652, A
416	6	1.2	198	3	US-09-370-700-23	Sequence 23, Appl	489	6	1.2	253	3	US-09-215-252-9	Sequence 9, Appl
417	6	1.2	198	3	US-09-603-207-23	Sequence 23, Appl	490	6	1.2	253	4	US-09-970-989A-9	Sequence 9, Appl
418	6	1.2	198	4	US-09-107-532A-4514	Sequence 4514, Ap	491	6	1.2	256	4	US-09-252-991A-21475	Sequence 21475, A
419	6	1.2	199	4	US-09-270-767-33647	Sequence 33647, A	492	6	1.2	257	4	US-09-252-991A-18172	Sequence 18172, A
420	6	1.2	202	4	US-09-270-767-48864	Sequence 48864, A	493	6	1.2	257	4	US-09-902-540-10293	Sequence 10293, A
421	6	1.2	202	4	US-09-270-767-48864	Sequence 48864, A	494	6	1.2	258	4	US-09-270-767-32758	Sequence 32758, A
422	6	1.2	202	4	US-09-248-796A-18665	Sequence 18665, A	495	6	1.2	258	4	US-09-949-016-8586	Sequence 8586, Ap
423	6	1.2	203	4	US-09-252-991A-24219	Sequence 24219, A	496	6	1.2	259	3	US-09-261-599B-3	Sequence 3, Appl
424	6	1.2	203	4	US-09-583-110-3736	Sequence 3736, Ap	497	6	1.2	259	4	US-09-456-455A-3	Sequence 3, Appl
425	6	1.2	204	4	US-09-489-039A-12422	Sequence 12422, A	498	6	1.2	261	1	US-08-446-822-15	Sequence 15, Appl
426	6	1.2	205	4	US-09-540-236-2541	Sequence 2541, Ap	499	6	1.2	261	3	US-09-328-314-15	Sequence 15, Appl
427	6	1.2	206	4	US-09-252-991A-31591	Sequence 31591, A	500	6	1.2	261	4	US-09-252-991A-23563	Sequence 23563, A
428	6	1.2	206	4	US-09-902-540-15287	Sequence 15287, A	501	6	1.2	261	4	US-09-252-991A-29007	Sequence 29007, A
429	6	1.2	207	4	US-08-451-947-2	Sequence 15472, A	502	6	1.2	261	5	PCT-US93-12586-15	Sequence 15, Appl
430	6	1.2	210	1	US-08-424-826A-2	Sequence 2, Appl	503	6	1.2	262	4	US-09-328-352-5699	Sequence 5699, Ap
431	6	1.2	210	2	US-08-928-694-2	Sequence 2, Appl	504	6	1.2	262	4	US-09-792-024-79	Sequence 79, Appl
432	6	1.2	210	3	US-08-928-694-2	Sequence 2, Appl	505	6	1.2	263	4	US-09-902-540-14991	Sequence 14991, A
433	6	1.2	210	3	US-08-952-127-20	Sequence 20, Appl	506	6	1.2	267	4	US-09-902-540-15693	Sequence 15693, A
434	6	1.2	210	4	US-08-450-842-2	Sequence 2, Appl	507	6	1.2	267	4	US-09-134-001C-4788	Sequence 4788, Ap
435	6	1.2	210	4	US-08-252-991A-26579	Sequence 26579, A	508	6	1.2	269	3	US-09-602-787A-58	Sequence 58, Appl
436	6	1.2	210	4	US-08-451-390-2	Sequence 2, Appl	509	6	1.2	271	1	US-08-447-554-4	Sequence 4, Appl
437	6	1.2	210	5	PCT-US91-06950-2	Sequence 2, Appl	510	6	1.2	271	1	US-09-448-160-4	Sequence 4, Appl
438	6	1.2	213	4	US-08-553-336A-7	Sequence 7, Appl	511	6	1.2	271	4	US-09-252-991A-23450	Sequence 23450, A
439	6	1.2	214	1	US-09-107-433-3882	Sequence 3882, Ap	512	6	1.2	271	4	US-09-502-540-13493	Sequence 13493, A
440	6	1.2	215	1	US-07-796-106-23	Sequence 23, Appl	513	6	1.2	273	4	US-09-252-991A-22457	Sequence 22457, A
441	6	1.2	215	1	US-08-107-684B-10	Sequence 10, Appl	514	6	1.2	274	4	US-09-489-039A-7343	Sequence 7343, Ap
442	6	1.2	215	3	US-08-247-373B-40	Sequence 40, Appl	515	6	1.2	277	4	US-09-252-991A-31819	Sequence 31819, A
443	6	1.2	215	4	US-09-710-279-1846	Sequence 1846, Ap	516	6	1.2	279	3	US-09-134-001C-4900	Sequence 4900, Ap
444	6	1.2	216	4	US-09-902-540-12244	Sequence 12244, A	517	6	1.2	281	4	US-09-248-796A-19496	Sequence 19496, A
445	6	1.2	216	4	US-09-270-767-40753	Sequence 40753, A	518	6	1.2	282	1	US-08-118-270-52	Sequence 52, Appl
446	6	1.2	216	4	US-09-270-767-59699	Sequence 59699, A	519	6	1.2	282	5	PCT-US93-08528-52	Sequence 52, Appl
447	6	1.2	218	4	US-09-252-991A-29074	Sequence 29074, A	520	6	1.2	283	4	US-09-902-540-12505	Sequence 12505, A
448	6	1.2	220	4	US-09-188-452A-211	Sequence 211, App	521	6	1.2	286	4	US-09-424-378A-7	Sequence 7, Appl
449	6	1.2	220	4	US-09-710-279-1822	Sequence 1822, Ap	522	6	1.2	289	3	US-09-077-674-10	Sequence 10, Appl
450	6	1.2	220	4	US-09-438-185A-194	Sequence 194, App	523	6	1.2	289	4	US-09-252-991A-31549	Sequence 31549, A
451	6	1.2	221	1	US-08-315-695-16	Sequence 16, Appl	524	6	1.2	290	4	US-09-252-991A-26340	Sequence 26340, A
452	6	1.2	221	4	US-09-595-344-2	Sequence 2, Appl	525	6	1.2	291	4	US-09-902-540-15846	Sequence 15846, A
453	6	1.2	222	3	US-09-134-001C-3521	Sequence 3521, Ap	526	6	1.2	291	4	US-08-147-592A-12	Sequence 12, Appl
454	6	1.2	222	4	US-09-897-772-2	Sequence 2, Appl	527	6	1.2	295	3	US-08-292-694A-12	Sequence 12, Appl
455	6	1.2	225	4	US-09-489-039A-13977	Sequence 13977, A	528	6	1.2	295	4	US-09-248-796A-16714	Sequence 16714, A
456	6	1.2	225	4	US-09-917-254-72	Sequence 72, Appl	529	6	1.2	296	4	US-09-252-991A-25983	Sequence 25983, A
457	6	1.2	227	4	US-09-489-039A-7672	Sequence 7672, Ap	530	6	1.2	296	4	US-09-134-000C-6272	Sequence 6272, Ap
458	6	1.2	228	3	US-09-199-637A-205	Sequence 205, App	531	6	1.2	297	4	US-09-868-552-46	Sequence 46, Appl
459	6	1.2	229	3	US-09-199-637A-204	Sequence 204, App	532	6	1.2	298	4	US-09-152-060-76	Sequence 76, Appl
460	6	1.2	229	4	US-09-543-681A-7899	Sequence 7899, Ap	533	6	1.2	298	4	US-09-489-039A-9717	Sequence 9717, Ap
461	6	1.2	229	4	US-09-902-540-14578	Sequence 14578, A	534	6	1.2	301	1	US-08-440-861-2	Sequence 2, Appl
462	6	1.2	230	2	US-08-808-580-34	Sequence 34, Appl	535	6	1.2	301	1	US-08-433-854-2	Sequence 2, Appl
463	6	1.2	230	4	US-09-252-991A-26110	Sequence 26110, A	536	6	1.2	301	1	US-08-174-745A-2	Sequence 2, Appl
464	6	1.2	231	4	US-09-252-991A-27366	Sequence 27366, A	537	6	1.2	301	2	US-08-195-947-2	Sequence 2, Appl
465	6	1.2	231	4	US-09-328-352-6647	Sequence 6647, Ap	538	6	1.2	301	2		

539	6	1.2	301	2	US-08-433-885-2	Sequence 2, Appli	612	6	1.2	317	5	PCT-US93-08528-6	Sequence 6, Appli
540	6	1.2	301	2	US-08-433-908B-2	Sequence 2, Appli	613	6	1.2	318	3	US-09-199-637A-203	Sequence 203, App
541	6	1.2	301	3	US-08-410-614-2	Sequence 2, Appli	614	6	1.2	319	3	US-08-413-118-119	Sequence 119, App
542	6	1.2	301	4	US-09-252-991A-25370	Sequence 25370, A	615	6	1.2	319	3	US-08-473-446-119	Sequence 119, App
543	6	1.2	302	4	US-10-029-180-58	Sequence 58, Appl	616	6	1.2	320	4	US-09-252-991A-26510	Sequence 26510, A
544	6	1.2	303	4	US-09-248-796A-20412	Sequence 20412, A	617	6	1.2	323	4	US-09-252-991A-30172	Sequence 30172, A
545	6	1.2	306	4	US-09-252-991A-32161	Sequence 32161, A	618	6	1.2	323	4	US-08-484-933B-22	Sequence 22, Appl
546	6	1.2	306	4	US-09-107-532A-5995	Sequence 5995, Ap	619	6	1.2	324	2	US-08-484-158B-22	Sequence 22, Appl
547	6	1.2	307	2	US-08-484-905-68	Sequence 68, Appl	620	6	1.2	324	2	US-08-484-596A-22	Sequence 22, Appl
548	6	1.2	307	3	US-08-481-985B-68	Sequence 68, Appl	621	6	1.2	324	2	US-08-480-150A-22	Sequence 22, Appl
549	6	1.2	307	3	US-08-370-476-68	Sequence 68, Appl	622	6	1.2	324	3	US-08-458-731A-22	Sequence 22, Appl
550	6	1.2	308	2	US-08-484-905-71	Sequence 71, Appl	623	6	1.2	324	3	US-08-149-223A-22	Sequence 22, Appl
551	6	1.2	308	2	US-08-484-905-72	Sequence 72, Appl	624	6	1.2	325	4	US-08-387-805-16	Sequence 16, Appl
552	6	1.2	308	2	US-08-481-905B-78	Sequence 78, Appl	625	6	1.2	325	4	US-09-248-796A-20030	Sequence 20030, A
553	6	1.2	308	3	US-08-481-985B-71	Sequence 71, Appl	626	6	1.2	325	4	US-09-248-796A-20531	Sequence 20531, A
554	6	1.2	308	3	US-08-481-985B-72	Sequence 72, Appl	627	6	1.2	325	6	5320941-2	Patent No. 5320941
555	6	1.2	308	3	US-08-481-985B-78	Sequence 78, Appl	628	6	1.2	325	6	5320941-2	Patent No. 5320941
556	6	1.2	308	3	US-08-370-476-71	Sequence 71, Appl	629	6	1.2	327	1	US-08-118-270-55	Sequence 55, Appl
557	6	1.2	308	3	US-08-370-476-72	Sequence 72, Appl	630	6	1.2	327	1	US-08-080-386-2	Sequence 2, Appli
558	6	1.2	308	3	US-08-370-476-78	Sequence 78, Appl	631	6	1.2	327	2	US-08-390-000A-2	Sequence 2, Appli
559	6	1.2	310	2	US-08-484-905-66	Sequence 66, Appl	632	6	1.2	327	4	US-09-583-492-10	Sequence 10, Appl
560	6	1.2	310	2	US-08-484-905-74	Sequence 74, Appl	633	6	1.2	327	5	PCT-US93-08528-55	Sequence 55, Appl
561	6	1.2	310	3	US-08-481-985B-66	Sequence 66, Appl	634	6	1.2	328	1	US-08-148-215A-2	Sequence 2, Appli
562	6	1.2	310	3	US-08-481-985B-74	Sequence 74, Appl	635	6	1.2	328	1	US-08-423-691-2	Sequence 2, Appli
563	6	1.2	310	3	US-08-370-476-66	Sequence 66, Appl	636	6	1.2	328	1	US-08-080-386-4	Sequence 4, Appli
564	6	1.2	310	3	US-08-370-476-74	Sequence 74, Appl	637	6	1.2	328	2	US-08-390-000A-4	Sequence 2, Appli
565	6	1.2	310	3	US-08-328-352-4174	Sequence 4174, Ap	638	6	1.2	328	3	US-08-867-260-2	Sequence 2, Appli
566	6	1.2	311	2	US-08-484-905-70	Sequence 70, Appl	639	6	1.2	328	3	US-09-501-192-9	Sequence 9, Appli
567	6	1.2	311	2	US-08-484-905-73	Sequence 73, Appl	640	6	1.2	328	4	US-09-252-991A-19311	Sequence 19311, A
568	6	1.2	311	3	US-08-481-985B-70	Sequence 70, Appl	641	6	1.2	328	4	US-09-170-496D-12	Sequence 12, Appl
569	6	1.2	311	3	US-08-481-985B-73	Sequence 73, Appl	642	6	1.2	328	4	US-09-170-496D-170	Sequence 170, App
570	6	1.2	311	3	US-08-370-476-70	Sequence 70, Appl	643	6	1.2	329	3	US-08-334-601-10	Sequence 10, Appl
571	6	1.2	311	3	US-08-370-476-73	Sequence 73, Appl	644	6	1.2	329	4	US-08-336-910A-5	Sequence 5, Appli
572	6	1.2	312	4	US-09-254-465A-9	Sequence 9, Appli	645	6	1.2	330	1	US-08-118-270-19	Sequence 19, Appl
573	6	1.2	312	4	US-09-252-991A-22205	Sequence 22205, A	646	6	1.2	330	1	US-08-118-270-20	Sequence 20, Appl
574	6	1.2	312	4	US-09-907-794A-64	Sequence 64, Appl	647	6	1.2	330	1	US-08-118-270-21	Sequence 21, Appl
575	6	1.2	312	4	US-09-905-125A-64	Sequence 64, Appl	648	6	1.2	330	2	US-08-454-549-5	Sequence 5, Appli
576	6	1.2	312	4	US-09-902-775A-64	Sequence 64, Appl	649	6	1.2	330	3	US-08-454-552-5	Sequence 5, Appli
577	6	1.2	312	4	US-09-906-700-64	Sequence 64, Appl	650	6	1.2	330	5	PCT-US93-08528-19	Sequence 19, Appl
578	6	1.2	312	4	US-09-903-603A-64	Sequence 64, Appl	651	6	1.2	330	5	PCT-US93-08528-20	Sequence 20, Appl
579	6	1.2	312	4	US-09-904-920A-64	Sequence 64, Appl	652	6	1.2	330	5	PCT-US93-08528-21	Sequence 21, Appl
580	6	1.2	312	4	US-09-905-064-64	Sequence 64, Appl	653	6	1.2	331	4	US-09-252-991A-19236	Sequence 19236, A
581	6	1.2	312	4	US-09-905-381A-64	Sequence 64, Appl	654	6	1.2	331	4	US-09-252-991A-23301	Sequence 23301, A
582	6	1.2	312	4	US-09-906-618-64	Sequence 64, Appl	655	6	1.2	332	1	US-08-118-270-53	Sequence 53, Appl
583	6	1.2	312	4	US-09-953-499-9	Sequence 9, Appli	656	6	1.2	332	4	US-09-585-858-50	Sequence 50, Appl
584	6	1.2	312	4	US-09-252-991A-30534	Sequence 30534, A	657	6	1.2	332	4	US-10-270-878-50	Sequence 50, Appl
585	6	1.2	315	4	US-09-902-540-14527	Sequence 14527, A	658	6	1.2	332	5	PCT-US93-08528-53	Sequence 53, Appl
586	6	1.2	316	1	US-08-118-270-44	Sequence 44, Appl	659	6	1.2	333	3	US-09-221-456-2	Sequence 2, Appli
587	6	1.2	316	1	US-08-118-270-46	Sequence 46, Appl	660	6	1.2	333	3	US-09-588-740-2	Sequence 2, Appli
588	6	1.2	316	2	US-08-846-762-9	Sequence 9, Appli	661	6	1.2	333	4	US-09-170-496D-16	Sequence 16, Appl
589	6	1.2	316	4	US-09-252-991A-22191	Sequence 22191, A	662	6	1.2	333	4	US-09-170-496D-172	Sequence 172, App
590	6	1.2	316	4	US-09-270-767-43840	Sequence 43840, A	663	6	1.2	333	4	US-09-520-781-2	Sequence 2, Appli
591	6	1.2	316	5	PCT-US93-08528-44	Sequence 44, Appl	664	6	1.2	334	1	US-08-118-270-32	Sequence 22, Appl
592	6	1.2	316	5	PCT-US93-08528-46	Sequence 46, Appl	665	6	1.2	334	1	US-09-270-767-59047	Sequence 59047, A
593	6	1.2	317	1	US-07-866-979-6	Sequence 6, Appli	666	6	1.2	334	5	PCT-US93-08528-22	Sequence 22, Appl
594	6	1.2	317	1	US-08-671-525B-2	Sequence 2, Appli	667	6	1.2	335	4	US-09-252-991A-22013	Sequence 22013, A
595	6	1.2	317	1	US-08-672-109B-2	Sequence 2, Appli	668	6	1.2	335	4	US-09-252-991A-24494	Sequence 24494, A
596	6	1.2	317	1	US-08-842-045-2	Sequence 2, Appli	669	6	1.2	336	1	US-08-118-270-54	Sequence 54, Appl
597	6	1.2	317	2	US-08-465-906B-6	Sequence 6, Appli	670	6	1.2	336	5	PCT-US93-08528-54	Sequence 54, Appl
598	6	1.2	317	2	US-08-842-238-2	Sequence 2, Appli	671	6	1.2	339	4	US-09-252-991A-28751	Sequence 28751, A
599	6	1.2	317	2	US-08-780-789A-4	Sequence 4, Appli	672	6	1.2	340	4	US-09-252-991A-25032	Sequence 25032, A
600	6	1.2	317	3	US-08-706-281A-6	Sequence 6, Appli	673	6	1.2	340	4	US-09-252-991A-18101	Sequence 18101, A
601	6	1.2	317	3	US-08-629-335B-2	Sequence 2, Appli	674	6	1.2	341	4	US-09-743-871B-6	Sequence 6, Appli
602	6	1.2	317	3	US-09-201-746-6	Sequence 6, Appli	675	6	1.2	342	4	US-09-743-871B-1	Sequence 1, Appli
603	6	1.2	317	3	US-09-097-231-6	Sequence 6, Appli	676	6	1.2	343	4	US-09-743-871B-5	Sequence 5, Appli
604	6	1.2	317	3	US-08-870-511-4	Sequence 4, Appli	677	6	1.2	346	2	US-08-185-828A-15	Sequence 15, Appl
605	6	1.2	317	3	US-08-387-805-2	Sequence 2, Appli	678	6	1.2	346	4	US-09-328-352-4982	Sequence 4982, Ap
606	6	1.2	317	4	US-09-353-099-6	Sequence 6, Appli	679	6	1.2	346	4	US-09-248-796A-24285	Sequence 24285, A
607	6	1.2	317	4	US-09-868-552-43	Sequence 43, Appl	680	6	1.2	347	3	US-09-071-709-2	Sequence 2, Appli
608	6	1.2	317	4	US-09-868-552-44	Sequence 44, Appl	681	6	1.2	348	4	US-09-107-532A-6950	Sequence 6950, Ap
609	6	1.2	317	4	US-09-270-767-40937	Sequence 40937, A	682	6	1.2	349	4	US-09-270-767-42023	Sequence 42023, A
610	6	1.2	317	4	US-09-270-767-40937	Sequence 40937, A	683	6	1.2	349	4	US-08-484-905-65	Sequence 65, Appl
611	6	1.2	317	4	US-09-270-767-40937	Sequence 40937, A	684	6	1.2	350	2		

685	6	1.2	350	2	US-08-484-905-67	Sequence 67, Appl	758	1	1.2	367	1	US-08-149-093A-4	Sequence 4, Appl
686	6	1.2	350	3	US-08-481-985B-65	Sequence 65, Appl	759	6	1.2	367	1	US-08-147-949A-2	Sequence 2, Appl
687	6	1.2	350	3	US-08-481-985B-67	Sequence 67, Appl	760	6	1.2	367	2	US-08-911-245-4	Sequence 4, Appl
688	6	1.2	350	3	US-08-370-476-65	Sequence 65, Appl	761	6	1.2	367	2	US-08-553-058C-4	Sequence 4, Appl
689	6	1.2	350	3	US-08-370-476-67	Sequence 67, Appl	762	6	1.2	367	2	US-08-514-451A-4	Sequence 4, Appl
690	6	1.2	350	4	US-09-252-991A-29676	Sequence 29676, A	763	6	1.2	367	2	US-08-454-549-2	Sequence 2, Appl
691	6	1.2	351	4	US-09-248-796A-16176	Sequence 16176, A	764	6	1.2	367	3	US-08-454-552-2	Sequence 2, Appl
692	6	1.2	351	4	US-09-944-807-2	Sequence 2, Appl	765	6	1.2	367	3	US-08-170-331-4	Sequence 2, Appl
693	6	1.2	351	4	US-09-826-509-501	Sequence 501, App	766	6	1.2	367	3	US-08-676-351-2	Sequence 2, Appl
694	6	1.2	353	4	US-09-576-160B-6	Sequence 606, App	767	6	1.2	367	3	US-08-147-592A-6	Sequence 6, Appl
695	6	1.2	353	4	US-09-483-039A-8006	Sequence 8006, App	768	6	1.2	367	3	US-08-889-108-17	Sequence 17, Appl
696	6	1.2	353	4	US-09-710-279-634	Sequence 634, App	769	6	1.2	367	3	US-09-510-473-4	Sequence 4, Appl
697	6	1.2	354	3	US-08-724-984A-2	Sequence 2, Appl	770	6	1.2	367	3	US-08-292-694A-6	Sequence 6, Appl
698	6	1.2	355	4	US-09-134-000C-6296	Sequence 6296, Ap	771	6	1.2	367	4	US-08-048-916B-4	Sequence 4, Appl
699	6	1.2	356	3	US-08-430-286A-2	Sequence 2, Appl	772	6	1.2	367	4	US-08-405-271A-23	Sequence 23, Appl
700	6	1.2	356	3	US-08-430-286A-5	Sequence 5, Appl	773	6	1.2	367	4	US-09-743-871B-15	Sequence 15, Appl
701	6	1.2	356	4	US-09-107-532A-6286	Sequence 6286, Ap	774	6	1.2	367	4	US-08-986-209A-2	Sequence 2, Appl
702	6	1.2	357	4	US-09-710-279-1360	Sequence 1360, Ap	775	6	1.2	367	5	PCT-US94-10358-17	Sequence 17, Appl
703	6	1.2	357	4	US-09-693-746-4	Sequence 4, Appl	776	6	1.2	368	3	US-08-709-838-2	Sequence 2, Appl
704	6	1.2	357	4	US-09-693-746-8	Sequence 8, Appl	777	6	1.2	368	3	US-08-829-839-2	Sequence 2, Appl
705	6	1.2	357	5	PCT-US91-00899-14	Sequence 14, Appl	778	6	1.2	368	4	US-09-595-549-2	Sequence 2, Appl
706	6	1.2	358	1	US-08-153-848-19	Sequence 19, Appl	779	6	1.2	368	4	US-09-595-549-4	Sequence 2, Appl
707	6	1.2	358	2	US-08-465-971B-4	Sequence 4, Appl	780	6	1.2	368	4	US-09-170-496D-20	Sequence 20, Appl
708	6	1.2	358	3	US-09-299-843A-19	Sequence 19, Appl	781	6	1.2	368	4	US-09-170-496D-174	Sequence 174, App
709	6	1.2	358	3	US-09-088-337B-19	Sequence 19, Appl	782	6	1.2	368	4	US-09-624-594-2	Sequence 2, Appl
710	6	1.2	358	4	US-09-198-452A-743	Sequence 743, App	783	6	1.2	368	4	US-09-583-110-3256	Sequence 3256, Ap
711	6	1.2	358	4	US-09-248-796A-20070	Sequence 20070, A	784	6	1.2	368	4	US-09-538-092-1226	Sequence 1226, Ap
712	6	1.2	358	5	PCT-US93-11153-19	Sequence 19, Appl	785	6	1.2	368	4	US-09-107-433-4257	Sequence 4257, Ap
713	6	1.2	359	1	US-08-153-848-24	Sequence 24, Appl	786	6	1.2	368	4	US-09-607-156-2	Sequence 2, Appl
714	6	1.2	359	3	US-09-299-843A-24	Sequence 24, Appl	787	6	1.2	369	4	US-09-489-039A-9526	Sequence 9526, Ap
715	6	1.2	359	3	US-09-088-337B-24	Sequence 24, Appl	788	6	1.2	370	3	US-08-369-822C-2	Sequence 2, Appl
716	6	1.2	359	4	US-09-761-962A-18	Sequence 18, Appl	789	6	1.2	370	3	US-08-582-776C-2	Sequence 2, Appl
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ALIGNMENTS

RESULT 1
 US-08-876-874-2
 ; Sequence 2, Application US/08876874
 ; Patent No. 5942405
 ; GENERAL INFORMATION:
 ; APPLICANT: Ames, Robert
 ; APPLICANT: Bergsma, Derek
 ; APPLICANT: Foley, James
 ; APPLICANT: Kumar, Chandrika
 ; APPLICANT: Sarau, Henry
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING
 ; METHODS USING C3A RECEPTOR AND C3A
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RATNER & PRESTIA
 ; STREET: P.O. BOX 980
 ; CITY: VALLEY FORGE
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
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 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 482 amino acids
 ; TYPE: amino acid

; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-876-874-2

Query Match 79.0%; Score 381; DB 2; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Qy 121 CLVVFKPIWQNHNVGMACISGCIWVAVFVVCIPVYVREIFTTNDHNRGKFGGLSS 180
 Db 121 CLVVFKPIWQNHNVGMACISGCIWVAVFVVCIPVYVREIFTTNDHNRGKFGGLSS 180
 Qy 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTNDDHPWTVPVTFQPTQRPESAD 240
 Db 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRLDPSSFQTNDDHPWTVPVTFQPTQRPESAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGPIEDHETSPDLNDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGPIEDHETSPDLNDAFLSTHLKLPESA 300
 Qy 301 SSNSFYSELPPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPVIMIACTYFIV 360
 Db 301 SSNSFYSELPPQGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPVIMIACTYFIV 360
 Qy 361 FRMQRGRFAKSQSKTRFVAVVWVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTRFVAVVWVAVFLVCMTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFSEELTRSTHCPSSNNVIERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGLEAFSEELTRSTHCPSSNNVIERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 2
 US-09-117-440-2
 ; Sequence 2, Application US/09117440
 ; Patent No. 6521418
 ; GENERAL INFORMATION:
 ; APPLICANT: Ye, Richard D
 ; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
 ; FILE REFERENCE: SCR2041S
 ; CURRENT APPLICATION NUMBER: US/09/117,440
 ; CURRENT FILING DATE: 1998-07-28
 ; EARLIER APPLICATION NUMBER: PCT/US97/01736
 ; EARLIER FILING DATE: 1997-01-30
 ; EARLIER APPLICATION NUMBER: 60/010,808
 ; EARLIER FILING DATE: 1996-01-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-117-440-2

Query Match 79.0%; Score 381; DB 4; Length 482;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MASPSAETNSTDLSSQNPBPVILSMVILSLTFLGPGNGLVWAGLKMORTVNTI 60
Db 1 MASPSAETNSTDLSSQNPBPVILSMVILSLTFLGPGNGLVWAGLKMORTVNTI 60
Qy 61 FLHUTLADLCLSLPFLSLAHALQOGWPYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
Db 61 FLHUTLADLCLSLPFLSLAHALQOGWPYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
Qy 121 CLVVFKPIWCONHRNVGMACSIICGCIWVAFVVCIPVYVREIPTTNDHRCGKFGSL 180
Db 121 CLVVFKPIWCONHRNVGMACSIICGCIWVAFVVCIPVYVREIPTTNDHRCGKFGSL 180
Qy 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRLDPSSFOTNDHPWTVTVFQPTQFORSAD 240
Db 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRLDPSSFOTNDHPWTVTVFQPTQFORSAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Qy 301 SSNSFYSESELPOGFDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
Db 301 SSNSFYSESELPOGFDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
Qy 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAFSBELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAFSBELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

```

```

RESULT 3
US-09-826-509-465
; Sequence 465, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brunema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 465
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-465

```

```

Query Match 58.1%; Score 280; DB 4; Length 482;
Best Local Similarity 99.6%; Pred. No. 2.5e-270;
Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MASPSAETNSTDLSSQNPBPVILSMVILSLTFLGPGNGLVWAGLKMORTVNTI 60
Db 1 MASPSAETNSTDLSSQNPBPVILSMVILSLTFLGPGNGLVWAGLKMORTVNTI 60
Qy 61 FLHUTLADLCLSLPFLSLAHALQOGWPYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120
Db 61 FLHUTLADLCLSLPFLSLAHALQOGWPYGRFLCKLIPSIIVLNMFASVFLTAISLDR 120

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Qy 121 CLVVFKPIWCONHRNVGMACSIICGCIWVAFVVCIPVYVREIPTTNDHRCGKFGSL 180
Db 121 CLVVFKPIWCONHRNVGMACSIICGCIWVAFVVCIPVYVREIPTTNDHRCGKFGSL 180
Qy 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRLDPSSFOTNDHPWTVTVFQPTQFORSAD 240
Db 181 SLDPYDFYGDPLENRSLENIIVQPGEMNDRLDPSSFOTNDHPWTVTVFQPTQFORSAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPPIEDHETSPLDNSDAFLSTHLKLPFSA 300
Qy 301 SSNSFYSESELPOGFDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
Db 301 SSNSFYSESELPOGFDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
Qy 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FRMQRGRFAKSQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAFSBELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAAFSBELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

```

```

RESULT 4
US-09-693-242-2
; Sequence 2, Application US/09693242
; Patent No. 6692936
; GENERAL INFORMATION:
; APPLICANT: Lee Harland
; TITLE OF INVENTION: No. 6692936el Polypeptide
; FILE REFERENCE: PCS10365ADAM
; CURRENT APPLICATION NUMBER: US/09/693,242
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 9924951.8
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-693-242-2

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```

Query Match 2.1%; Score 10; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 67 ADLLCCLSLP 76
Db 79 ADLLCCLSLP 88

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RESULT 5
US-09-786-442B-2
; Sequence 2, Application US/09786442B
; Patent No. 677204
; GENERAL INFORMATION:
; APPLICANT: TAKAHASHI, TSUNEO
; APPLICANT: ONO, MITSU HARU
; APPLICANT: ISHIMARU, HIROSHI
; APPLICANT: KANNO, KIMIYOSHI
; APPLICANT: TAKAHASHI, CHIAKI
; TITLE OF INVENTION: NOVEL RECEPTOR PROTEIN AND METHOD FOR THE DIAGNOSIS OF AN
; FILE REFERENCE: 8054-1005
; CURRENT APPLICATION NUMBER: US/09/786,442B

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;; CURRENT FILING DATE: 2001-03-05
;; PRIOR APPLICATION NUMBER: JP 10-249752
;; FILING DATE: 1998-09-03
;; PRIOR APPLICATION NUMBER: JP 11-070800
;; PRIOR FILING DATE: 1999-03-16
;; PRIOR APPLICATION NUMBER: PCT/JP99/04801
;; PRIOR FILING DATE: 1999-09-03
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 2
;; LENGTH: 337
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-786-442B-2

Query Match 2.1%; Score 10; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ADLCLSLP 76
Db 79 ADLCLSLP 88
|||||

RESULT 6
US-08-118-270-35
; Sequence 35, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-35

Query Match 1.9%; Score 9; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 VFKEPWQCN 132
Db 102 VFKEPWQCN 110
|||||

RESULT 7
PCT-US93-08528-35
; Sequence 35, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-35

Query Match 1.9%; Score 9; DB 5; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 VFKEPWQCN 132
Db 102 VFKEPWQCN 110
|||||

RESULT 8
US-09-576-160B-4
; Sequence 4, Application US/09576160B
; Patent No. 6469150
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; APPLICANT: Zhao, Jiuqiao
; APPLICANT: Swanson, Robert
; APPLICANT: Webb, Maria
; APPLICANT: Strohl, Barbara
; TITLE OF INVENTION: Cloning and Characterization of Genes Encoding
; TITLE OF INVENTION: Bradykinin B1 Receptor Homologues From Five Mammalian
; FILE REFERENCE: 1073.058
; CURRENT APPLICATION NUMBER: US/09/576,160B
; CURRENT FILING DATE: 2000-05-22


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; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-576-160B-4

Query Match      1.9%; Score 9; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      386 FLVCWTPYH 394
Db      256 FLVCWTPYH 264

RESULT 9
US-08-458-970A-9
; Sequence 9, Application US/08458970A
; Patent No. 5861272
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Csa Receptor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-970A-9

Query Match      1.9%; Score 9; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      124 VFKEPIWQCN 132
Db      138 VFKEPIWQCN 146

RESULT 10
US-09-576-160B-5
; Sequence 5, Application US/09576160B
```

```
; Patent No. 6469150
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; APPLICANT: Zhao, Jiuqiao
; APPLICANT: Swanson, Robert
; APPLICANT: Webb, Maria
; APPLICANT: Strohl, Barbara
; TITLE OF INVENTION: Cloning and Characterization of Genes Encoding
; TITLE OF INVENTION: Bradykinin B1 Receptor Homologues From Five Mammalian
; FILE REFERENCE: 1073.058
; CURRENT APPLICATION NUMBER: US/09/576,160B
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chimeric
; OTHER INFORMATION: molecule consisting of amino acids 1-315 of dog
; OTHER INFORMATION: bradykinin B1 receptor (BKR) and amino acids
; OTHER INFORMATION: 319-353 of human BKR
US-09-576-160B-5

Query Match      1.9%; Score 9; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      386 FLVCWTPYH 394
Db      256 FLVCWTPYH 264

RESULT 11
US-09-826-509-467
; Sequence 467, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 467
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-467

Query Match      1.9%; Score 9; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      124 VFKEPIWQCN 132
Db      138 VFKEPIWQCN 146

RESULT 12
US-09-674-973A-316
; Sequence 316, Application US/09674973A
; Patent No. 6759046
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;; GENERAL INFORMATION:
;; APPLICANT: NO. 6759046sk Hydro ASA
;; TITLE OF INVENTION: Peptides
;; FILE REFERENCE: 26625-296
;; CURRENT APPLICATION NUMBER: US/09/674,973A
;; CURRENT FILING DATE: 2001-06-04
;; NUMBER OF SEQ ID NOS: 459
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 316
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-674-973A-316

Query Match 1.7%; Score 8; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 LNMFAVSF 111
Db 1 LNMFAVSF 8

RESULT 13
US-09-674-973A-317
; Sequence 317, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: NO. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-317

Query Match 1.7%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 LNMFAVSF 111
Db 1 LNMFAVSF 8

RESULT 14
US-08-079-051-2
; Sequence 2, Application US/08079051
; Patent No. 5480974
; GENERAL INFORMATION:
; APPLICANT: MORGAN, EDWARD L.
; APPLICANT: EMBER, JULIA A.
; APPLICANT: HUGLI, TONY E.
; TITLE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/079,051
;; FILING DATE: 18-JUN-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wetherell, Jr., Ph.D., John W.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: PD-2790
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: C5aR(133-148)
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..16
US-08-079-051-2

Query Match 1.7%; Score 8; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 125 FKPIWQCN 132
Db 7 FKPIWQCN 14

RESULT 15
PCT-US94-06994-2
; Sequence 2, Application PC/TUS9406994
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06994
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tumarkin, Lisa A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD-2790
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: C5aR(133-148)
; FEATURE:

NAME/KEY: Peptide
 LOCATION: 1..16
 PCT-US94-06994-2

Query Match 1.7%; Score 8; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 FKPIWQCN 132
 |||||
 Db 7 FKPIWQCN 14

Search completed: April 13, 2005, 10:07:18
 Job time : 54 secs

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88	8	1.7	358	16	US-10-782-596-34	Sequence 34, Appl	161	7	1.5	116	9	US-09-764-893-73	Sequence 73, Appl
89	8	1.7	363	9	US-09-864-761-42849	Sequence 42849, A	162	7	1.5	116	9	US-09-764-886-60	Sequence 60, Appl
90	8	1.7	389	10	US-09-791-932-116	Sequence 116, App	163	7	1.5	116	9	US-09-764-853-482	Sequence 482, App
91	8	1.7	389	14	US-10-225-567A-442	Sequence 442, App	164	7	1.5	116	10	US-09-989-442-85	Sequence 85, Appl
92	8	1.7	389	14	US-10-130-845-2	Sequence 2, Appl	165	7	1.5	116	10	US-09-764-886-60	Sequence 60, Appl
93	8	1.7	389	15	US-10-221-555-2	Sequence 2, Appl	166	7	1.5	116	11	US-09-764-875-641	Sequence 641, App
94	8	1.7	395	14	US-10-266-886-2	Sequence 2, Appl	167	7	1.5	116	11	US-10-073-865-73	Sequence 73, Appl
95	8	1.7	395	14	US-10-266-886-8	Sequence 8, Appl	168	7	1.5	116	14	US-10-103-313-310	Sequence 310, App
96	8	1.7	395	14	US-10-225-567A-486	Sequence 486, App	169	7	1.5	116	14	US-10-073-885-87	Sequence 87, Appl
97	8	1.7	395	15	US-10-170-385-419	Sequence 419, App	170	7	1.5	117	15	US-10-424-599-245620	Sequence 245620, A
98	8	1.7	409	15	US-10-458-201-12	Sequence 12, Appl	171	7	1.5	117	15	US-10-425-114-42798	Sequence 42798, A
99	8	1.7	466	10	US-09-992-238-20	Sequence 20, Appl	172	7	1.5	118	15	US-10-424-599-204506	Sequence 204506, A
100	8	1.7	466	14	US-10-238-129-11	Sequence 11, Appl	173	7	1.5	121	15	US-10-147-603-41	Sequence 41, Appl
101	8	1.7	466	14	US-10-238-129-11	Sequence 11, Appl	174	7	1.5	124	15	US-10-264-237-1753	Sequence 1753, Ap
102	8	1.7	466	15	US-10-436-715-51	Sequence 51, Appl	175	7	1.5	124	16	US-10-437-963-121545	Sequence 121545, A
103	8	1.7	467	9	US-09-805-628-4	Sequence 4, Appl	176	7	1.5	129	15	US-10-264-237-2379	Sequence 2379, App
104	8	1.7	472	9	US-09-805-628-2	Sequence 2, Appl	177	7	1.5	131	9	US-09-864-761-37308	Sequence 37308, A
105	8	1.7	502	15	US-10-425-114-70825	Sequence 70825, A	178	7	1.5	132	15	US-10-147-603-42	Sequence 42, Appl
106	8	1.7	587	9	US-09-815-242-5694	Sequence 5694, Ap	179	7	1.5	134	16	US-10-437-963-192157	Sequence 192157, A
107	8	1.7	603	9	US-09-815-242-12667	Sequence 12667, A	180	7	1.5	141	16	US-10-767-701-55965	Sequence 55965, A
108	8	1.7	662	13	US-10-036-328A-8	Sequence 13667, A	181	7	1.5	143	16	US-10-437-963-167377	Sequence 167377, A
109	8	1.7	714	9	US-09-818-264-2	Sequence 8, Appl	182	7	1.5	153	16	US-10-437-963-123890	Sequence 123890, A
110	8	1.7	714	16	US-10-473-339-2	Sequence 2, Appl	183	7	1.5	154	16	US-10-767-701-61178	Sequence 61178, A
111	8	1.7	733	13	US-10-036-328A-4	Sequence 4, Appl	184	7	1.5	156	16	US-10-437-963-141299	Sequence 141299, A
112	8	1.7	1138	13	US-10-036-328A-6	Sequence 6, Appl	185	7	1.5	157	16	US-10-437-963-107021	Sequence 107021, A
113	8	1.7	1210	13	US-10-036-328A-2	Sequence 2, Appl	186	7	1.5	165	15	US-10-424-599-252214	Sequence 252214, A
114	7	1.5	30	17	US-10-783-519-7	Sequence 7, Appl	187	7	1.5	178	13	US-10-015-179-2	Sequence 2, Appl
115	7	1.5	37	11	US-09-833-245-662	Sequence 662, App	188	7	1.5	178	15	US-10-188-840-2	Sequence 2, Appl
116	7	1.5	37	11	US-09-833-245-663	Sequence 663, App	189	7	1.5	178	15	US-10-336-603A-32	Sequence 32, Appl
117	7	1.5	44	15	US-10-424-599-182793	Sequence 182793, A	190	7	1.5	180	9	US-09-867-550-1156	Sequence 1156, Ap
118	7	1.5	48	15	US-10-424-599-262396	Sequence 262396, A	191	7	1.5	181	15	US-10-424-599-152369	Sequence 152369, A
119	7	1.5	55	15	US-10-424-599-177311	Sequence 177311, A	192	7	1.5	187	16	US-10-437-963-179693	Sequence 179693, A
120	7	1.5	57	9	US-09-864-761-42932	Sequence 42932, A	193	7	1.5	187	16	US-10-424-599-257083	Sequence 257083, A
121	7	1.5	60	15	US-10-424-599-212201	Sequence 212201, A	194	7	1.5	193	16	US-10-767-701-55377	Sequence 55377, A
122	7	1.5	61	9	US-09-864-761-46220	Sequence 46220, A	195	7	1.5	199	13	US-10-104-019-34	Sequence 34, Appl
123	7	1.5	62	16	US-10-437-963-121501	Sequence 121501, A	196	7	1.5	199	14	US-10-104-019-34	Sequence 34, Appl
124	7	1.5	66	16	US-10-767-701-43908	Sequence 43908, A	197	7	1.5	199	16	US-10-437-963-139062	Sequence 139062, A
125	7	1.5	68	15	US-10-424-599-229296	Sequence 229296, A	198	7	1.5	200	14	US-10-428-826-34	Sequence 34, Appl
126	7	1.5	70	15	US-10-424-599-274334	Sequence 274334, A	199	7	1.5	200	15	US-10-108-260A-3363	Sequence 3363, Ap
127	7	1.5	71	9	US-09-864-761-37078	Sequence 37078, A	200	7	1.5	201	16	US-10-437-963-147244	Sequence 147244, A
128	7	1.5	71	15	US-10-424-599-273505	Sequence 273505, A	201	7	1.5	205	14	US-10-091-458-38	Sequence 38, Appl
129	7	1.5	72	14	US-10-097-111-372	Sequence 372, App	202	7	1.5	205	15	US-10-411-120-89	Sequence 89, Appl
130	7	1.5	72	15	US-10-424-599-229529	Sequence 229529, A	203	7	1.5	205	15	US-10-191-254-38	Sequence 38, Appl
131	7	1.5	73	14	US-10-326-102-7	Sequence 7, Appl	204	7	1.5	211	15	US-09-791-932-97	Sequence 97, Appl
132	7	1.5	73	15	US-10-407-079-7	Sequence 7, Appl	205	7	1.5	211	15	US-10-369-493-20515	Sequence 20515, A
133	7	1.5	75	9	US-09-796-632-2479	Sequence 2479, Ap	206	7	1.5	217	15	US-10-112-944-878	Sequence 878, App
134	7	1.5	75	14	US-10-040-862-2479	Sequence 2479, Ap	207	7	1.5	219	16	US-10-437-963-160216	Sequence 160216, A
135	7	1.5	75	15	US-10-057-475B-2479	Sequence 2479, Ap	208	7	1.5	222	15	US-10-425-114-57142	Sequence 57142, A
136	7	1.5	75	15	US-10-154-884B-2479	Sequence 2479, Ap	209	7	1.5	222	16	US-10-767-701-39399	Sequence 39399, A
137	7	1.5	75	16	US-10-764-324-2479	Sequence 2479, Ap	210	7	1.5	226	14	US-10-245-753-112	Sequence 112, App
138	7	1.5	76	10	US-09-404-132-22	Sequence 22, Appl	211	7	1.5	226	14	US-10-245-859-112	Sequence 112, App
139	7	1.5	81	16	US-10-437-963-180427	Sequence 180427, A	212	7	1.5	226	14	US-10-245-103-112	Sequence 112, App
140	7	1.5	88	10	US-09-929-752-11	Sequence 11, Appl	213	7	1.5	226	14	US-10-245-107-112	Sequence 112, App
141	7	1.5	88	14	US-10-184-426-11	Sequence 11, Appl	214	7	1.5	226	14	US-10-245-107-112	Sequence 112, App
142	7	1.5	88	15	US-10-424-599-273809	Sequence 273809, A	215	7	1.5	226	14	US-10-245-143-112	Sequence 112, App
143	7	1.5	90	16	US-10-437-963-123857	Sequence 123857, A	216	7	1.5	226	14	US-10-245-771-112	Sequence 112, App
144	7	1.5	92	14	US-10-156-761-11722	Sequence 11722, A	217	7	1.5	226	14	US-10-245-851-112	Sequence 112, App
145	7	1.5	93	15	US-10-424-599-217597	Sequence 217597, A	218	7	1.5	226	14	US-10-245-883-112	Sequence 112, App
146	7	1.5	93	16	US-10-437-963-158487	Sequence 158487, A	219	7	1.5	226	14	US-10-237-535-112	Sequence 112, App
147	7	1.5	93	16	US-10-437-963-158487	Sequence 158487, A	220	7	1.5	226	14	US-10-238-183-112	Sequence 112, App
148	7	1.5	94	11	US-09-833-245-1552	Sequence 1552, Ap	221	7	1.5	226	14	US-10-238-283-112	Sequence 112, App
149	7	1.5	98	15	US-10-424-599-194988	Sequence 194988, A	222	7	1.5	226	14	US-10-245-055-112	Sequence 112, App
150	7	1.5	98	16	US-10-437-963-118366	Sequence 118366, A	223	7	1.5	226	14	US-10-245-147-112	Sequence 112, App
151	7	1.5	99	15	US-10-424-599-151343	Sequence 151343, A	224	7	1.5	226	14	US-10-245-730-112	Sequence 112, App
152	7	1.5	100	15	US-10-424-599-250280	Sequence 250280, A	225	7	1.5	226	14	US-10-245-739-112	Sequence 112, App
153	7	1.5	101	16	US-10-437-963-125327	Sequence 125327, A	226	7	1.5	226	14	US-10-246-210-112	Sequence 112, App
154	7	1.5	101	16	US-10-437-963-125327	Sequence 125327, A	227	7	1.5	226	14	US-10-239-196-112	Sequence 112, App
155	7	1.5	102	16	US-10-767-701-44405	Sequence 44405, A	228	7	1.5	226	14	US-10-243-024-112	Sequence 112, App
156	7	1.5	102	16	US-10-767-701-60795	Sequence 60795, A	229	7	1.5	226	14	US-10-243-409-112	Sequence 112, App
157	7	1.5	103	15	US-10-424-599-218374	Sequence 218374, A	230	7	1.5	226	14	US-10-245-621-112	Sequence 112, App
158	7	1.5	105	15	US-10-147-603-43	Sequence 43, Appl	231	7	1.5	226	14	US-10-245-880-112	Sequence 112, App
159	7	1.5	106	15	US-10-424-599-192688	Sequence 192688, A	232	7	1.5	226	14	US-10-245-033-112	Sequence 112, App

233	7	1.5	226	14	US-10-243-095-112	Sequence 112, App	306	7	1.5	226	14	US-10-242-074-112	Sequence 112, App
234	7	1.5	226	14	US-10-245-185-112	Sequence 112, App	307	7	1.5	226	14	US-10-242-505-112	Sequence 112, App
235	7	1.5	226	14	US-10-245-427-112	Sequence 112, App	308	7	1.5	226	14	US-10-242-574-112	Sequence 112, App
236	7	1.5	226	14	US-10-245-473-112	Sequence 112, App	309	7	1.5	226	14	US-10-243-261-112	Sequence 112, App
237	7	1.5	226	14	US-10-245-770-112	Sequence 112, App	310	7	1.5	226	14	US-10-243-282-112	Sequence 112, App
238	7	1.5	226	14	US-10-245-877-112	Sequence 112, App	311	7	1.5	226	14	US-10-243-402-112	Sequence 112, App
239	7	1.5	226	14	US-10-246-976-112	Sequence 112, App	312	7	1.5	226	14	US-10-243-431-112	Sequence 112, App
240	7	1.5	226	14	US-10-243-320-112	Sequence 112, App	313	7	1.5	226	14	US-10-245-164-112	Sequence 112, App
241	7	1.5	226	14	US-10-242-743-112	Sequence 112, App	314	7	1.5	226	14	US-10-244-972-112	Sequence 112, App
242	7	1.5	226	14	US-10-242-845-112	Sequence 112, App	315	7	1.5	226	14	US-10-197-942-112	Sequence 112, App
243	7	1.5	226	14	US-10-237-636-112	Sequence 112, App	316	7	1.5	226	14	US-10-238-196-112	Sequence 112, App
244	7	1.5	226	14	US-10-238-325-112	Sequence 112, App	317	7	1.5	226	14	US-10-245-013-112	Sequence 112, App
245	7	1.5	226	14	US-10-238-346-112	Sequence 112, App	318	7	1.5	241	15	US-10-425-114-43006	Sequence 43006, A
246	7	1.5	226	14	US-10-238-411-112	Sequence 112, App	319	7	1.5	241	15	US-10-424-599-149784	Sequence 149784, A
247	7	1.5	226	14	US-10-243-124-112	Sequence 112, App	320	7	1.5	245	15	US-10-425-114-53349	Sequence 53349, A
248	7	1.5	226	14	US-10-243-425-112	Sequence 112, App	321	7	1.5	245	15	US-10-425-114-53369	Sequence 53369, A
249	7	1.5	226	14	US-10-243-446-112	Sequence 112, App	322	7	1.5	249	15	US-10-425-114-53110	Sequence 53110, A
250	7	1.5	226	14	US-10-245-874-112	Sequence 112, App	323	7	1.5	252	15	US-10-424-599-183937	Sequence 183937, A
251	7	1.5	226	14	US-10-242-653-112	Sequence 112, App	324	7	1.5	254	15	US-10-425-114-40031	Sequence 40031, A
252	7	1.5	226	14	US-10-243-167-112	Sequence 112, App	325	7	1.5	260	15	US-10-188-186-58	Sequence 58, Appl
253	7	1.5	226	14	US-10-243-388-112	Sequence 112, App	326	7	1.5	262	13	US-10-108-605-289	Sequence 289, App
254	7	1.5	226	14	US-10-244-947-112	Sequence 112, App	327	7	1.5	266	15	US-10-094-749-2516	Sequence 2516, App
255	7	1.5	226	14	US-10-244-968-112	Sequence 112, App	328	7	1.5	266	16	US-10-408-765A-2502	Sequence 2502, App
256	7	1.5	226	14	US-10-244-990-112	Sequence 112, App	329	7	1.5	274	14	US-10-099-553-3	Sequence 3, Appli
257	7	1.5	226	14	US-10-245-079-112	Sequence 112, App	330	7	1.5	274	14	US-10-099-553-4	Sequence 4, Appli
258	7	1.5	226	14	US-10-245-127-112	Sequence 112, App	331	7	1.5	274	15	US-10-425-114-37297	Sequence 37297, A
259	7	1.5	226	14	US-10-245-207-112	Sequence 112, App	332	7	1.5	277	15	US-10-108-260A-4456	Sequence 4456, App
260	7	1.5	226	14	US-10-245-646-112	Sequence 112, App	333	7	1.5	284	15	US-10-407-960-4	Sequence 4, Appli
261	7	1.5	226	14	US-10-245-695-112	Sequence 112, App	334	7	1.5	286	15	US-10-425-114-36687	Sequence 36687, A
262	7	1.5	226	14	US-10-245-699-112	Sequence 112, App	335	7	1.5	289	14	US-10-407-960-2	Sequence 2, Appli
263	7	1.5	226	14	US-10-245-737-112	Sequence 112, App	336	7	1.5	289	15	US-10-369-493-3627	Sequence 3627, App
264	7	1.5	226	14	US-10-245-878-112	Sequence 112, App	337	7	1.5	299	15	US-10-108-260A-4207	Sequence 4207, App
265	7	1.5	226	14	US-10-245-890-112	Sequence 112, App	338	7	1.5	299	15	US-10-282-122A-72817	Sequence 72817, A
266	7	1.5	226	14	US-10-245-899-112	Sequence 112, App	339	7	1.5	299	15	US-10-282-122A-75962	Sequence 75962, A
267	7	1.5	226	14	US-10-245-900-112	Sequence 112, App	340	7	1.5	300	15	US-10-424-599-240165	Sequence 240165, A
268	7	1.5	226	14	US-10-247-058-112	Sequence 112, App	341	7	1.5	301	16	US-10-437-963-145626	Sequence 145626, A
269	7	1.5	226	14	US-10-245-454-112	Sequence 112, App	342	7	1.5	301	16	US-10-437-963-167378	Sequence 167378, A
270	7	1.5	226	14	US-10-237-471-112	Sequence 112, App	343	7	1.5	304	15	US-10-108-260A-4875	Sequence 4875, App
271	7	1.5	226	14	US-10-238-261-112	Sequence 112, App	344	7	1.5	306	14	US-10-186-886-15	Sequence 15, Appl
272	7	1.5	226	14	US-10-238-324-112	Sequence 112, App	345	7	1.5	313	16	US-10-437-963-204461	Sequence 204461, A
273	7	1.5	226	14	US-10-241-860-112	Sequence 112, App	346	7	1.5	318	15	US-10-425-114-65623	Sequence 65623, A
274	7	1.5	226	14	US-10-242-172-112	Sequence 112, App	347	7	1.5	320	11	US-09-833-245-1580	Sequence 1580, App
275	7	1.5	226	14	US-10-242-652-112	Sequence 112, App	348	7	1.5	323	9	US-09-816-087-4	Sequence 4, Appli
276	7	1.5	226	14	US-10-242-990-112	Sequence 112, App	349	7	1.5	323	10	US-09-791-932-119	Sequence 119, App
277	7	1.5	226	14	US-10-243-023-112	Sequence 112, App	350	7	1.5	323	14	US-10-266-643-4	Sequence 4, Appli
278	7	1.5	226	14	US-10-243-103-112	Sequence 112, App	351	7	1.5	323	14	US-10-017-161-746	Sequence 746, App
279	7	1.5	226	14	US-10-243-376-112	Sequence 112, App	352	7	1.5	323	15	US-10-424-599-196294	Sequence 196294, A
280	7	1.5	226	14	US-10-243-326-112	Sequence 112, App	353	7	1.5	323	15	US-10-332-156-1	Sequence 1, Appli
281	7	1.5	226	14	US-10-243-364-112	Sequence 112, App	354	7	1.5	326	15	US-10-425-114-66137	Sequence 66137, A
282	7	1.5	226	14	US-10-243-494-112	Sequence 112, App	355	7	1.5	327	14	US-10-237-467-6	Sequence 6, Appli
283	7	1.5	226	14	US-10-244-995-112	Sequence 112, App	356	7	1.5	327	15	US-10-398-026-2	Sequence 2, Appli
284	7	1.5	226	14	US-10-245-230-112	Sequence 112, App	357	7	1.5	330	9	US-09-853-161-104	Sequence 104, App
285	7	1.5	226	14	US-10-245-253-112	Sequence 112, App	358	7	1.5	330	9	US-09-852-797-104	Sequence 104, App
286	7	1.5	226	14	US-10-245-479-112	Sequence 112, App	359	7	1.5	330	9	US-10-251-385-258	Sequence 258, App
287	7	1.5	226	14	US-10-245-499-112	Sequence 112, App	360	7	1.5	330	14	US-10-251-385-276	Sequence 276, App
288	7	1.5	226	14	US-10-245-772-112	Sequence 112, App	361	7	1.5	330	14	US-10-225-567A-467	Sequence 467, App
289	7	1.5	226	14	US-10-245-811-112	Sequence 112, App	362	7	1.5	330	14	US-10-348-190-2	Sequence 2, Appli
290	7	1.5	226	14	US-10-245-812-112	Sequence 112, App	363	7	1.5	330	14	US-10-348-190-4	Sequence 4, Appli
291	7	1.5	226	14	US-10-245-852-112	Sequence 112, App	364	7	1.5	330	14	US-10-337-992-2	Sequence 2, Appli
292	7	1.5	226	14	US-10-245-875-112	Sequence 112, App	365	7	1.5	330	14	US-10-029-386-34068	Sequence 34068, A
293	7	1.5	226	14	US-10-245-881-112	Sequence 112, App	366	7	1.5	330	15	US-10-058-993-104	Sequence 104, App
294	7	1.5	226	14	US-10-245-911-112	Sequence 112, App	367	7	1.5	330	16	US-10-789-241-28	Sequence 28, Appl
295	7	1.5	226	14	US-10-245-913-112	Sequence 112, App	368	7	1.5	341	14	US-10-270-587-3	Sequence 3, Appli
296	7	1.5	226	14	US-10-246-080-112	Sequence 112, App	369	7	1.5	342	14	US-10-226-102-4	Sequence 4, Appli
297	7	1.5	226	14	US-10-246-121-112	Sequence 112, App	370	7	1.5	342	15	US-10-407-079-4	Sequence 4, Appli
298	7	1.5	226	14	US-10-246-305-112	Sequence 112, App	371	7	1.5	343	9	US-09-985-694A-2	Sequence 2, Appli
299	7	1.5	226	14	US-10-246-329-112	Sequence 112, App	372	7	1.5	343	9	US-09-985-694A-9	Sequence 9, Appli
300	7	1.5	226	14	US-10-247-036-112	Sequence 112, App	373	7	1.5	343	10	US-09-929-752-2	Sequence 2, Appli
301	7	1.5	226	14	US-10-243-255-112	Sequence 112, App	374	7	1.5	343	10	US-09-929-752-9	Sequence 9, Appli
302	7	1.5	226	14	US-10-245-810-112	Sequence 112, App	375	7	1.5	343	13	US-10-176-079-2	Sequence 2, Appli
303	7	1.5	226	14	US-10-245-910-112	Sequence 112, App	376	7	1.5	343	13	US-10-176-079-9	Sequence 9, Appli
304	7	1.5	226	14	US-10-246-098-112	Sequence 112, App	377	7	1.5	343	14	US-10-225-567A-482	Sequence 482, App
305	7	1.5	226	14	US-10-237-496-112	Sequence 112, App	378	7	1.5	343	14		

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380	7	1.5	343	14	US-10-184-426-9	Sequence 9, Appli	453	7	1.5	380	14	US-10-166-359-2	Sequence 2, Appli
381	7	1.5	343	14	US-10-184-426-14	Sequence 14, Appli	454	7	1.5	380	14	US-10-166-113-2	Sequence 2, Appli
382	7	1.5	343	14	US-10-305-555-14	Sequence 14, Appli	455	7	1.5	380	14	US-10-166-357-2	Sequence 2, Appli
383	7	1.5	345	14	US-09-394-1428-2	Sequence 2, Appli	456	7	1.5	380	14	US-10-166-372-2	Sequence 3, Appli
384	7	1.5	345	14	US-10-099-553-2	Sequence 12, Appli	457	7	1.5	380	14	US-10-184-722-3	Sequence 62, Appli
385	7	1.5	345	16	US-10-003-632E-12	Sequence 2, Appli	458	7	1.5	380	14	US-10-251-385-62	Sequence 198, App
386	7	1.5	347	9	US-09-823-114-24	Sequence 24, Appli	459	7	1.5	380	14	US-10-251-385-198	Sequence 233, App
387	7	1.5	347	14	US-10-290-748-24	Sequence 24, Appli	460	7	1.5	380	14	US-10-225-567A-233	Sequence 19, Appli
388	7	1.5	352	14	US-10-017-161-2156	Sequence 2156, Ap	461	7	1.5	380	16	US-10-239-061A-19	Sequence 2, Appli
389	7	1.5	352	15	US-10-292-798-1802	Sequence 1802, Ap	462	7	1.5	380	17	US-10-486-061A-2	Sequence 9289, Ap
390	7	1.5	352	15	US-10-424-599-252215	Sequence 252215,	463	7	1.5	381	14	US-10-156-761-92819	Sequence 103157,
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392	7	1.5	356	14	US-10-226-102-2	Sequence 2, Appli	465	7	1.5	391	9	US-09-966-871-82	Sequence 463, App
393	7	1.5	356	14	US-10-326-102-17	Sequence 17, Appli	466	7	1.5	391	10	US-09-826-509-463	Sequence 82, Appli
394	7	1.5	356	14	US-10-251-385-246	Sequence 246, App	467	7	1.5	391	13	US-10-039-645-82	Sequence 12, Appli
395	7	1.5	356	14	US-10-251-385-270	Sequence 270, App	468	7	1.5	391	14	US-10-005-956-12	Sequence 564, App
396	7	1.5	356	14	US-10-225-567A-484	Sequence 484, App	469	7	1.5	391	14	US-10-005-956-564	Sequence 566, App
397	7	1.5	356	15	US-10-407-079-2	Sequence 2, Appli	470	7	1.5	391	14	US-10-005-956-568	Sequence 568, App
398	7	1.5	356	15	US-10-407-079-17	Sequence 17, Appli	471	7	1.5	391	14	US-10-005-956-568	Sequence 845, App
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402	7	1.5	359	9	US-09-966-871-81	Sequence 81, Appli	475	7	1.5	391	15	US-10-458-860-82	Sequence 463, App
403	7	1.5	359	9	US-09-867-915-3	Sequence 3, Appli	476	7	1.5	391	17	US-10-925-095-463	Sequence 1014, Ap
404	7	1.5	359	10	US-09-876-252-66	Sequence 66, Appli	477	7	1.5	391	17	US-10-741-600-1014	Sequence 1015, Ap
405	7	1.5	359	10	US-09-876-252-90	Sequence 90, Appli	478	7	1.5	391	17	US-10-741-600-1015	Sequence 3019, Ap
406	7	1.5	359	10	US-09-876-252-94	Sequence 94, Appli	479	7	1.5	395	15	US-10-094-749-3019	Sequence 2509, Ap
407	7	1.5	359	10	US-09-876-252-100	Sequence 100, App	480	7	1.5	395	16	US-10-408-768A-2509	Sequence 38, Appli
408	7	1.5	359	13	US-10-039-645-81	Sequence 81, Appli	481	7	1.5	396	9	US-09-798-710-2	Sequence 2, Appli
409	7	1.5	359	14	US-10-218-574-9	Sequence 9, Appli	482	7	1.5	396	14	US-10-094-417-4	Sequence 4, Appli
410	7	1.5	359	14	US-10-054-616A-6	Sequence 6, Appli	483	7	1.5	396	14	US-10-094-417-22	Sequence 22, Appli
411	7	1.5	359	14	US-10-225-567A-328	Sequence 328, App	484	7	1.5	396	14	US-10-225-567A-585	Sequence 585, App
412	7	1.5	359	14	US-10-044-643-49	Sequence 49, Appli	485	7	1.5	396	14	US-10-029-436-2	Sequence 2, Appli
413	7	1.5	359	14	US-10-044-643-50	Sequence 50, Appli	486	7	1.5	396	14	US-10-343-850A-46	Sequence 46, Appli
414	7	1.5	359	14	US-10-044-643-51	Sequence 51, Appli	487	7	1.5	396	15	US-10-073-885A-60	Sequence 60, Appli
415	7	1.5	359	14	US-10-044-643-52	Sequence 52, Appli	488	7	1.5	404	14	US-10-073-885A-46	Sequence 45227, A
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419	7	1.5	359	15	US-10-417-820A-94	Sequence 94, Appli	492	7	1.5	444	15	US-10-424-599-157459	Sequence 5, Appli
420	7	1.5	359	15	US-10-417-820A-100	Sequence 100, App	493	7	1.5	448	9	US-10-818-264-5	Sequence 36659, A
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422	7	1.5	359	15	US-10-633-438-45	Sequence 45, Appli	495	7	1.5	463	15	US-10-425-114-36659	Sequence 149275, A
423	7	1.5	359	16	US-10-723-955-66	Sequence 66, Appli	496	7	1.5	464	14	US-10-091-333-7	Sequence 3467, Ap
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425	7	1.5	359	16	US-10-723-955-94	Sequence 94, Appli	498	7	1.5	475	15	US-10-282-122A-69690	Sequence 566, App
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428	7	1.5	360	15	US-10-417-820A-106	Sequence 106, App	501	7	1.5	477	14	US-10-156-761-9692	Sequence 70395, A
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431	7	1.5	361	14	US-10-010-568-9	Sequence 9, Appli	504	7	1.5	504	15	US-10-104-047-3467	Sequence 1328, App
432	7	1.5	361	14	US-10-268-332-15	Sequence 15, Appli	505	7	1.5	504	15	US-10-225-567A-571	Sequence 566, App
433	7	1.5	361	15	US-10-375-157-9	Sequence 9, Appli	506	7	1.5	512	14	US-10-295-027-1338	Sequence 226114,
434	7	1.5	361	15	US-10-072-012-521	Sequence 521, App	507	7	1.5	512	15	US-10-424-599-226114	Sequence 159034,
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437	7	1.5	365	14	US-10-325-567A-332	Sequence 332, App	510	7	1.5	524	16	US-10-282-122A-70395	Sequence 3467, Ap
438	7	1.5	365	15	US-10-366-288-42	Sequence 42, App	511	7	1.5	527	15	US-09-899-642-2	Sequence 1328, App
439	7	1.5	365	16	US-10-753-695-2	Sequence 2, Appli	512	7	1.5	531	15	US-10-389-566-461	Sequence 566, App
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441	7	1.5	371	14	US-10-156-761-8524	Sequence 8524, Ap	514	7	1.5	531	16	US-10-311-956-4	Sequence 4, Appli
442	7	1.5	371	15	US-10-087-684-65	Sequence 65, Appli	515	7	1.5	537	14	US-10-010-568-12	Sequence 12, Appli
443	7	1.5	371	15	US-10-218-779-65	Sequence 65, Appli	516	7	1.5	537	15	US-10-375-157-12	Sequence 52, Appli
444	7	1.5	372	16	US-10-437-963-145960	Sequence 145960,	517	7	1.5	537	15	US-10-055-569A-52	Sequence 517, App
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446	7	1.5	374	14	US-10-010-568-13	Sequence 13, Appli	519	7	1.5	541	15	US-09-966-422B-10	Sequence 3, Appli
447	7	1.5	374	15	US-10-375-157-13	Sequence 13, Appli	520	7	1.5	541	14	US-10-120-604-3	Sequence 10, Appli
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449	7	1.5	375	16	US-10-706-532-3	Sequence 3, Appli	522	7	1.5	541	15	US-10-398-454-2	Sequence 2, Appli
450	7	1.5	377	10	US-09-745-842-17	Sequence 17, Appli	523	7	1.5	541	15		
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528	7	1.5	607	16	US-10-437-963-144123	Sequence 144123, A	601	6	1.2	12	16	US-10-623-075-29	Sequence 29, Appl
529	7	1.5	614	14	US-10-145-012-2	Sequence 2, Appl	602	6	1.2	12	16	US-10-622-928-29	Sequence 29, Appl
530	7	1.5	614	14	US-10-145-012-13	Sequence 5, Appl	603	6	1.2	12	16	US-10-622-928-29	Sequence 29, Appl
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536	7	1.5	685	15	US-10-369-493-12820	Sequence 12820, A	609	6	1.2	21	10	US-09-992-238-102	Sequence 102, App
537	7	1.5	685	16	US-10-437-963-175135	Sequence 175135, A	610	6	1.2	21	17	US-10-873-332-32	Sequence 32, Appl
538	7	1.5	689	16	US-10-437-963-188971	Sequence 188971, A	611	6	1.2	23	15	US-10-436-715-318	Sequence 318, App
539	7	1.5	692	16	US-10-437-963-185295	Sequence 185295, A	612	6	1.2	23	15	US-10-436-715-358	Sequence 358, App
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555	7	1.5	1343	16	US-10-437-963-149678	Sequence 149678, A	628	6	1.2	33	9	US-09-205-658-98	Sequence 98, Appl
556	7	1.5	1617	15	US-10-451-207-5	Sequence 5, Appl	629	6	1.2	33	9	US-09-844-353A-65	Sequence 65, Appl
557	7	1.5	2030	15	US-10-282-122A-56336	Sequence 56336, A	630	6	1.2	33	9	US-09-844-353A-98	Sequence 98, Appl
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575	7	1.5	2787	9	US-09-893-238-15	Sequence 15, Appl	648	6	1.2	40	15	US-10-424-599-267436	Sequence 267436, A
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586	6	1.2	11	14	US-10-139-084-46	Sequence 46, Appl	659	6	1.2	46	14	US-10-125-540-336	Sequence 336, App
587	6	1.2	11	14	US-10-139-084-58	Sequence 58, Appl	660	6	1.2	46	15	US-10-424-599-146044	Sequence 146044, A
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589	6	1.2	11	15	US-10-458-860-58	Sequence 58, Appl	662	6	1.2	46	15	US-10-424-599-283797	Sequence 283797, A
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591	6	1.2	12	14	US-10-007-880A-215	Sequence 215, App	664	6	1.2	47	15	US-10-424-599-208033	Sequence 208033, A
592	6	1.2	12	15	US-10-133-715-29	Sequence 29, Appl	665	6	1.2	49	14	US-10-029-386-299377	Sequence 299377, A
593	6	1.2	12	15	US-10-302-356A-29	Sequence 29, Appl	666	6	1.2	49	15	US-10-424-599-174032	Sequence 174032, A
594	6	1.2	12	15	US-10-163-657A-29	Sequence 29, Appl	667	6	1.2	49	15	US-10-424-599-238858	Sequence 238858, A
595	6	1.2	12	15	US-10-422-287-29	Sequence 29, Appl	668	6	1.2	50	10	US-09-397-945-410	Sequence 410, App
596	6	1.2	12	16	US-10-622-932-29	Sequence 29, Appl	669	6	1.2	50	15	US-10-424-599-155281	Sequence 155281, A
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672	6	1.2	51	9	US-09-764-855-131	Sequence 131, App	745	6	1.2	66	17	US-10-536-773-102	Sequence 102, App
673	6	1.2	51	11	US-09-864-408A-6484	Sequence 6484, App	746	6	1.2	67	9	US-09-864-761-42134	Sequence 42134, A
674	6	1.2	51	14	US-10-072-349-131	Sequence 131, App	747	6	1.2	67	15	US-10-424-599-160852	Sequence 160852,
675	6	1.2	51	14	US-10-029-386-32904	Sequence 32904, A	748	6	1.2	67	15	US-10-424-599-203115	Sequence 203115,
676	6	1.2	51	15	US-10-424-599-179609	Sequence 179609, A	749	6	1.2	67	15	US-10-424-599-204387	Sequence 204387,
677	6	1.2	51	15	US-10-424-599-205397	Sequence 205397,	750	6	1.2	67	15	US-10-437-963-134820	Sequence 134820,
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679	6	1.2	52	11	US-09-864-408A-4036	Sequence 4036, App	752	6	1.2	68	15	US-10-424-515-1628	Sequence 1628, App
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681	6	1.2	52	11	US-09-833-245-258	Sequence 258, App	754	6	1.2	68	16	US-10-437-963-171519	Sequence 171519,
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699	6	1.2	57	15	US-10-424-599-219226	Sequence 219226,	772	6	1.2	73	15	US-10-424-599-146994	Sequence 146994,
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703	6	1.2	58	15	US-10-372-876-225	Sequence 225, App	776	6	1.2	74	16	US-10-437-963-104998	Sequence 104998,
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707	6	1.2	59	19	US-10-082-830-202	Sequence 202, App	780	6	1.2	75	16	US-10-437-963-174145	Sequence 174145,
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712	6	1.2	60	14	US-10-106-698-7322	Sequence 7322, App	785	6	1.2	76	15	US-10-424-599-248063	Sequence 248063,
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727	6	1.2	63	16	US-10-437-963-30734	Sequence 30734, A	800	6	1.2	78	15	US-10-424-599-188321	Sequence 188321,
728	6	1.2	63	16	US-10-631-550A-44	Sequence 44, Appl	801	6	1.2	78	15	US-10-424-599-233050	Sequence 233050,
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730	6	1.2	64	9	US-10-264-049-3267	Sequence 3267, App	803	6	1.2	79	14	US-10-101-464A-696	Sequence 696, App
731	6	1.2	64	15	US-10-242-515-1351	Sequence 1351, App	804	6	1.2	79	15	US-10-424-599-166901	Sequence 166901,
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736	6	1.2	65	16	US-10-424-599-223419	Sequence 223419,	809	6	1.2	80	14	US-10-155-886-6	Sequence 63, Appl
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741	6	1.2	66	14	US-10-160-162-102	Sequence 162, App	814	6	1.2	81	10	US-09-948-783-134	Sequence 134, App
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865	6	1.2	88	16	US-10-767-701-58551	Sequence 58551, A	938	6	1.2	101	16	US-10-437-963-175748	Sequence 175748,
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867	6	1.2	89	14	US-10-074-095-493	Sequence 493, App	940	6	1.2	102	15	US-10-424-599-249957	Sequence 249957,
868	6	1.2	89	15	US-10-212-872-493	Sequence 493, App	941	6	1.2	102	15	US-10-424-599-264567	Sequence 264567,
869	6	1.2	89	15	US-10-424-599-150060	Sequence 150060,	942	6	1.2	102	16	US-10-767-701-55305	Sequence 55305, A
870	6	1.2	89	15	US-10-424-599-238357	Sequence 238357,	943	6	1.2	103	14	US-10-032-2018-96	Sequence 96, App1
871	6	1.2	89	15	US-10-424-599-284488	Sequence 284488,	944	6	1.2	103	15	US-10-424-599-214290	Sequence 214290,
872	6	1.2	90	10	US-10-424-599-4055	Sequence 4055, App	945	6	1.2	103	15	US-10-424-599-239127	Sequence 239127,
873	6	1.2	90	10	US-09-820-649-164	Sequence 164, App	946	6	1.2	104	11	US-09-833-245-1442	Sequence 1442, Ap
874	6	1.2	90	14	US-10-160-162-164	Sequence 164, App	947	6	1.2	104	11	US-09-833-245-1442	Sequence 1443, Ap
875	6	1.2	90	14	US-10-424-599-29595	Sequence 29595, A	948	6	1.2	104	15	US-10-108-260A-2906	Sequence 2906, Ap
876	6	1.2	90	15	US-10-424-599-179629	Sequence 179629,	949	6	1.2	104	15	US-10-630-590-220	Sequence 220, App
877	6	1.2	90	15	US-10-424-599-209577	Sequence 209577,	950	6	1.2	104	15	US-10-424-599-147540	Sequence 147540,
878	6	1.2	90	16	US-10-437-963-177814	Sequence 177814,	951	6	1.2	104	15	US-10-424-599-237404	Sequence 237404,
879	6	1.2	90	16	US-10-767-701-57916	Sequence 57916, A	952	6	1.2	104	15	US-10-424-599-244826	Sequence 244826,
880	6	1.2	91	17	US-10-936-773-164	Sequence 164, App	953	6	1.2	104	15	US-10-424-599-247009	Sequence 247009,
881	6	1.2	91	15	US-10-424-599-213472	Sequence 213472,	954	6	1.2	104	15	US-10-424-599-276163	Sequence 276163,
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883	6	1.2	91	15	US-10-425-114-68554	Sequence 68554, A	956	6	1.2	104	16	US-10-437-963-131693	Sequence 131693,
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886	6	1.2	92	14	US-10-146-337-51	Sequence 51, App1	959	6	1.2	105	15	US-10-424-599-164578	Sequence 164578,
887	6	1.2	92	15	US-10-424-599-229844	Sequence 229844,	960	6	1.2	105	15	US-10-424-599-203338	Sequence 203338,
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889	6	1.2	92	16	US-10-767-701-37164	Sequence 37164, A	962	6	1.2	105	16	US-10-437-963-196208	Sequence 196208,

963 6 1.2 105 16 US-10-657-740-18 Sequence 18, Appl
 964 6 1.2 105 16 US-10-767-701-54832 Sequence 54832, A
 965 6 1.2 105 17 US-10-864-252-523 Sequence 523, App
 966 6 1.2 106 13 US-10-078-929-162 Sequence 162, App
 967 6 1.2 106 15 US-10-424-599-144664 Sequence 144664,
 968 6 1.2 106 16 US-10-437-963-137125 Sequence 137125,
 969 6 1.2 106 16 US-10-437-963-163091 Sequence 163091,
 970 6 1.2 107 9 US-09-738-626-6874 Sequence 6874, Ap
 971 6 1.2 107 15 US-10-424-599-231735 Sequence 231735,
 972 6 1.2 107 15 US-10-424-599-237442 Sequence 237442,
 973 6 1.2 107 16 US-10-437-963-152253 Sequence 152253,
 974 6 1.2 108 11 US-09-978-360A-441 Sequence 441, App
 975 6 1.2 108 15 US-10-315-664-109 Sequence 109, App
 976 6 1.2 108 15 US-10-424-599-245001 Sequence 245001,
 977 6 1.2 109 15 US-10-108-260A-3280 Sequence 3280, Ap
 978 6 1.2 109 15 US-10-424-599-167477 Sequence 167477,
 979 6 1.2 109 15 US-10-424-599-202020 Sequence 202020,
 980 6 1.2 109 15 US-10-424-599-203285 Sequence 203285,
 981 6 1.2 109 15 US-10-424-599-271737 Sequence 271737,
 982 6 1.2 109 16 US-10-437-963-163094 Sequence 163094,
 983 6 1.2 109 16 US-10-767-701-32120 Sequence 32120, A
 984 6 1.2 109 16 US-10-767-701-49102 Sequence 49102, A
 985 6 1.2 110 9 US-09-764-853-808 Sequence 808, App
 986 6 1.2 110 9 US-09-764-864-1196 Sequence 1196, Ap
 987 6 1.2 110 14 US-10-029-386-31048 Sequence 31048, A
 988 6 1.2 110 15 US-10-424-599-208239 Sequence 208239,
 989 6 1.2 110 15 US-10-425-114-50828 Sequence 50828, A
 990 6 1.2 110 16 US-10-437-963-180652 Sequence 180652,
 991 6 1.2 110 17 US-10-873-332-34 Sequence 34, Appl
 992 6 1.2 111 16 US-10-437-963-105003 Sequence 105003,
 993 6 1.2 112 10 US-09-974-879-188 Sequence 188, App
 994 6 1.2 112 15 US-10-424-599-202061 Sequence 202061,
 995 6 1.2 112 15 US-10-621-401-188 Sequence 188, App
 996 6 1.2 112 16 US-10-437-963-163092 Sequence 163092,
 997 6 1.2 113 9 US-09-864-761-34675 Sequence 34675, A
 998 6 1.2 113 10 US-09-305-736-188 Sequence 188, App
 999 6 1.2 113 10 US-09-818-683-188 Sequence 188, App
 1000 6 1.2 113 11 US-09-818-683-188 Sequence 188, App

ALIGNMENTS

RESULT 1
 US-09-870-759-98
 ; Sequence 98, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 98
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-870-759-98

Query Match 100.0%; Score 482; DB 9; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFSATNSTDLISQPNPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTI 60
 Db 1 MASFSATNSTDLISQPNPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTI 60
 Qy 61 FLHLLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120

Db 61 FLHLLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
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 Db 121 CLVVFKPIWQNHNVGMACSI CGCIWVAVFVVCIPVYVREIETTDHNRCCGKFGGLSS 180
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 Db 181 SLDPYDPYGPDPLENRSLNIVQPPGEMNDRLDPSSFOTNDHPWTVPVTFQPTQRPSPAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300
 Qy 301 SSNSFYSESELPOGPDYVNLGQFTDDDOVTPVLAITITRLVVGFLPLPSVIMIACTSYIV 360
 Db 301 SSNSFYSESELPOGPDYVNLGQFTDDDOVTPVLAITITRLVVGFLPLPSVIMIACTSYIV 360
 Qy 361 FRMQRGRFAKSQSKTFRVAVVAVFLVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FRMQRGRFAKSQSKTFRVAVVAVFLVVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSNPFYALLGKDFRKKARQSIQGIIEAFAFSEBELTRSTHCPSSNNVISERNST 480
 Db 421 IALASANSNPFYALLGKDFRKKARQSIQGIIEAFAFSEBELTRSTHCPSSNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482

RESULT 2
 US-09-751-708A-98
 ; Sequence 98, Application US/09751708A
 ; Publication No. US20030157113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09/751,708A
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; PRIOR FILING DATE: 1999-12-28
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 98
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-751-708A-98

Query Match 100.0%; Score 482; DB 10; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFSATNSTDLISQPNPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTI 60
 Db 1 MASFSATNSTDLISQPNPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTI 60
 Qy 61 FLHLLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
 Db 61 FLHLLADLLCCLSLPFLSLAHLALQGWPGYGRFLCKLIPSIIVLNMFPASVFLTAISLDR 120
 Qy 121 CLVVFKPIWQNHNVGMACSI CGCIWVAVFVVCIPVYVREIETTDHNRCCGKFGGLSS 180
 Db 121 CLVVFKPIWQNHNVGMACSI CGCIWVAVFVVCIPVYVREIETTDHNRCCGKFGGLSS 180
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 Db 181 SLDPYDPYGPDPLENRSLNIVQPPGEMNDRLDPSSFOTNDHPWTVPVTFQPTQRPSPAD 240
 Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPFIEDHETSPLDNSDAFLSTHLKLPESA 300

Db 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPDIEDHETSPDNDSDAFLSTHLKLPFA 300
Qy 301 SSNSFYSESELPGQFDYNYLNGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
Db 301 SSNSFYSESELPGQFDYNYLNGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
Qy 361 FMQGRGFAKSKQKTFRVAVVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMQGRGFAKSKQKTFRVAVVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFLYALLGKDFRKKAROSIQGILEAAAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFLYALLGKDFRKKAROSIQGILEAAAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 3

US-10-225-567A-78
; Sequence 78, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-78

Query Match 100.0%; Score 482; DB 14; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MASFAETNSTDLLSQPNNEPVLISWVLSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
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Db 61 FLHLTLADLLCCLSLPFSLAHALQGWPGYGRFLCKLIPSIIVLNMFAVFLITAIISLDR 120
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Qy 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPDIEDHETSPDNDSDAFLSTHLKLPFA 300
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Db 301 SSNSFYSESELPGQFDYNYLNGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
Qy 361 FMQGRGFAKSKQKTFRVAVVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
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Qy 421 IALASANSFNPFLYALLGKDFRKKAROSIQGILEAAAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFLYALLGKDFRKKAROSIQGILEAAAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 4

US-10-206-395B-2
; Sequence 2, Application US/10206395B
; Publication No. US20030157570A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences, Inc.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; APPLICANT: Morningside, Douglas A.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS RELATED TO G
; FILE REFERENCE: 1920-1-6
; CURRENT APPLICATION NUMBER: US/10/206,395B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/250,251
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,452
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/330,036
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-395B-2

Query Match 100.0%; Score 482; DB 14; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MASFAETNSTDLLSQPNNEPVLISWVLSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
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Qy 301 SSNSFYSESELPGQFDYNYLNGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
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Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAFSEELTRSTHCPSCNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 5
US-10-292-798-662
; Sequence 662, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 662
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-662

Query Match 100.0%; Score 482; DB 15; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MASFSAEATNSTDLSSQPNNEPPVILSMVILSLTFLGLPGNGLVWAGLKMQRVTNTIW 60

Qy 61 FLHUTLADLLCCLSLPFSLAHLAQGWPGYGRFLCKLIPSIIVLNMFASVFLLTALSLDR 120
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Qy 121 CLVVFKEPIWCQNHRNVGMACSIQCGIWWVAFVVCIPVYREIFTTDNHNRCGYKFGLS 180
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Db 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRDLPSSFQTNDRHPWTPTVFQPTQRPSPAD 240

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Qy 301 SSNSFYSESELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIAICYFIV 360
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Qy 361 FMORGGRPAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMORGGRPAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAFSEELTRSTHCPSCNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAFSEELTRSTHCPSCNNVISERNST 480

Qy 481 TV 482
Db 481 TV 482

RESULT 6
US-10-764-649-2
; Sequence 2, Application US/10764649
; Publication No. US20040157253A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; APPLICANT: Chen, Hong
; APPLICANT: Barnes, Glenn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
; TITLE OF INVENTION: INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: METABOLIC DISORDERS
; FILE REFERENCE: MEI2003-025PIRNM
; CURRENT APPLICATION NUMBER: US/10/764,649
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/446041
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: human
US-10-764-649-2

Query Match 100.0%; Score 482; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 CLVVFKEPIWCQNHRNVGMACSIQCGIWWVAFVVCIPVYREIFTTDNHNRCGYKFGLS 180
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Qy 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRDLPSSFQTNDRHPWTPTVFQPTQRPSPAD 240
Db 181 SLDYPDFYGDPLENRSLENIQPPGEMNDRDLPSSFQTNDRHPWTPTVFQPTQRPSPAD 240

Qy 241 SLPRGSARLTSONLYSNVFKPADVWSPKIPSGFPIEDHETSPDNDSPDAFLSTHLKLPESA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVWSPKIPSGFPIEDHETSPDNDSPDAFLSTHLKLPESA 300

Qy 301 SSNSFYSESELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIAICYFIV 360
Db 301 SSNSFYSESELPGQFDYNNLGQFTDDQVPTPLVAITITRLVVGFLLPSPVIMIAICYFIV 360

Qy 361 FMORGGRPAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FMORGGRPAKQSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAFSEELTRSTHCPSCNNVISERNST 480
Db 421 IALASANSFNPFYALLGKDFRKKARQSIQIGILEAFSEELTRSTHCPSCNNVISERNST 480

Qy 481 TV 482
Db 481 TV 482

RESULT 7
US-08-462-314-2
; Sequence 2, Application US/08462314
; Publication No. US20030027245A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human G-protein coupled Receptor
; NUMBER OF SEQUENCES: 8

```

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ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSER: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,314
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01992
FILING DATE: 17 FEB 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-314-2

Query Match 79.0%; Score 381; DB 8; Length 482;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPPVILSMVILSTLTLGLPGNGLVWVAGLWAGLKMQRVTWII 60
DB 1 MASFAETNSTDLLSQPNNEPPVILSMVILSTLTLGLPGNGLVWVAGLWAGLKMQRVTWII 60
QY 61 FLHLLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMPASVFLLLTAISLDR 120
DB 61 FLHLLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMPASVFLLLTAISLDR 120
QY 121 CLVVFKEPIWQNHNVGMACSIWVAVFVYREIFVYREIFVYREIFVYREIFVYREIFVYREIF 180
DB 121 CLVVFKEPIWQNHNVGMACSIWVAVFVYREIFVYREIFVYREIFVYREIFVYREIFVYREIF 180
QY 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPHTVPTVFPQTFORPSAD 240
DB 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPHTVPTVFPQTFORPSAD 240
QY 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPIEDHETSPLDNSDAFLSTHLKLPFSA 300
DB 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPIEDHETSPLDNSDAFLSTHLKLPFSA 300
QY 301 SSNSFYESELPGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
DB 301 SSNSFYESELPGFQDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSVIMACYSFIV 360
QY 361 FMQGRFRAKSKOTFRVAVVAVFVLCWTYPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
DB 361 FMQGRFRAKSKOTFRVAVVAVFVLCWTYPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
QY 421 IALANSFCNPFYVALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPNSNNVIERNST 480
DB 421 IALANSFCNPFYVALLGKDFRKKARQSIQGLEAFAFSEELTRSTHCPNSNNVIERNST 480
QY 481 TV 482

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Db 481 TV 482

RESULT 8

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US-10-259-521-2
Sequence 2, Application US/10259521
Publication No. US20030022310A1
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/259,521
FILING DATE: 30-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/462,314
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US95/01992
FILING DATE: 17 FEB 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-382 (PF159)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-259-521-2

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Query Match 79.0%; Score 381; DB 14; Length 482;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASFAETNSTDLLSQPNNEPPVILSMVILSTLTLGLPGNGLVWVAGLWAGLKMQRVTWII 60
DB 1 MASFAETNSTDLLSQPNNEPPVILSMVILSTLTLGLPGNGLVWVAGLWAGLKMQRVTWII 60
QY 61 FLHLLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMPASVFLLLTAISLDR 120
DB 61 FLHLLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMPASVFLLLTAISLDR 120
QY 121 CLVVFKEPIWQNHNVGMACSIWVAVFVYREIFVYREIFVYREIFVYREIFVYREIFVYREIF 180
DB 121 CLVVFKEPIWQNHNVGMACSIWVAVFVYREIFVYREIFVYREIFVYREIFVYREIFVYREIF 180
QY 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPHTVPTVFPQTFORPSAD 240
DB 181 SLDPYDFYGDPLENRSLENIQPPGEMNDRLDPSSFQNDHPHTVPTVFPQTFORPSAD 240
QY 241 SLPRGSARLTSONLYSNVFKPADVVSFKIPSGFPIEDHETSPLDNSDAFLSTHLKLPFSA 300

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Db 241 SLPRGSARLTSONLYSNVFKPADVVPVKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
Qy 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMACYSFIV 360
Db 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMACYSFIV 360
Qy 361 FRMQRGFAKSKQKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Db 361 FRMQRGFAKSKQKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFLYALGKDFRKKAROSIQGILEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFLYALGKDFRKKAROSIQGILEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 9
US-10-367-035-2
; Sequence 2, Application US/10367035
; Publication No. US20030187244A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; FILE REFERENCE: TSRI 511.1D1
; CURRENT APPLICATION NUMBER: US/10/367,035
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/117,440
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: PCT/US97/01736
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 60/010,808
; PRIOR FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Human
US-10-367-035-2

Query Match 79.0%; Score 381; DB 14; Length 482;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVLWVAGLKMQRVTNTIW 60
Db 1 MASPSAETNSTDLLSQPNNEPPVILSMVILSLTFLGLPGNGLVLWVAGLKMQRVTNTIW 60
Qy 61 FLHUTLADLLCCLSLPSLAHALOGQMPYGRFLCKLIPSIIVLNMEASVFLITAIISLDR 120
Db 61 FLHUTLADLLCCLSLPSLAHALOGQMPYGRFLCKLIPSIIVLNMEASVFLITAIISLDR 120
Qy 121 CLVVFKPIWCONHRNVGMACISCCIIWVAVFVVCIPVYREIFTTNDNRCGKFGLS 180
Db 121 CLVVFKPIWCONHRNVGMACISCCIIWVAVFVVCIPVYREIFTTNDNRCGKFGLS 180
Qy 181 SLDPDPYDGPDLNRSLENIIVQPGEMNDRLDPSFQTNHDPWTVPTVFQPTQRPSPAD 240
Db 181 SLDPDPYDGPDLNRSLENIIVQPGEMNDRLDPSFQTNHDPWTVPTVFQPTQRPSPAD 240
Qy 241 SLPRGSARLTSONLYSNVFKPADVVPVKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
Db 241 SLPRGSARLTSONLYSNVFKPADVVPVKIPSGFPDIEDHETSPLDNSDAFLSTHLKLPSPA 300
Qy 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMACYSFIV 360
Db 301 SSNSFYSELPGQFDYNNLGQFTDDQVPTPLVAITITRLVWGFLPSVIMACYSFIV 360
Qy 361 FRMQRGFAKSKQKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Db 361 FRMQRGFAKSKQKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
Qy 421 IALASANSFNPFLYALGKDFRKKAROSIQGILEAFAFSEELTRSTHCPSPNNVISERNST 480
Db 421 IALASANSFNPFLYALGKDFRKKAROSIQGILEAFAFSEELTRSTHCPSPNNVISERNST 480
Qy 481 TV 482
Db 481 TV 482

RESULT 10
US-09-925-302-657
; Sequence 657, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 657
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-657

Query Match 68.7%; Score 331; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.3e-309; Mismatches 0; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 VMCIPFVYREIFTTNDNRCGKFGLSLDYDFYDGPDLNRSLENIIVQPGEMNDRL 211
Db 155 VMCIPFVYREIFTTNDNRCGKFGLSLDYDFYDGPDLNRSLENIIVQPGEMNDRL 214
Qy 212 DPSSFQTNHDPWTVPTVFQPTQRPSPADSILPRGSARLTSONLYSNVFKPADVVPKIPS 271
Db 215 DPSSFQTNHDPWTVPTVFQPTQRPSPADSILPRGSARLTSONLYSNVFKPADVVPKIPS 274
Qy 272 GPFIEDHETSPLDNSDAFLSTHLKLPFSASSNSFYSELPGQFDYNNLGQFTDDQVPT 331
Db 275 GPFIEDHETSPLDNSDAFLSTHLKLPFSASSNSFYSELPGQFDYNNLGQFTDDQVPT 334
Qy 332 PLVAITITRLVWGFLPSVIMACYSFIVFRMQRGFAKSKQKTFRVAVVAVFLVCWT 391
Db 335 PLVAITITRLVWGFLPSVIMACYSFIVFRMQRGFAKSKQKTFRVAVVAVFLVCWT 394
Qy 392 PYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFLYALGKDFRKKAROSIQ 451
Db 395 PYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFLYALGKDFRKKAROSIQ 454
Qy 452 GILEAFAFSEELTRSTHCPSPNNVISERNSTTV 482
Db 455 GILEAFAFSEELTRSTHCPSPNNVISERNSTTV 485

RESULT 11
US-09-925-302-657
; Sequence 657, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA104

;; CURRENT APPLICATION NUMBER: US/09/925.302

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05918

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 896

;; SOFTWARE: Patent in Ver. 2.0

;; SEQ ID NO 657

;; LENGTH: 485

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: SITE

;; LOCATION: (145)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-657

Query Match 68.7%; Score 331; DB 10; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.3e-309;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 VMCIPVYVRIETTDNHNRCGYKGLSSLDYDPDYGDPLENSLENIQPPGEMDRL 211

Db 155 VMCIPVYVRIETTDNHNRCGYKGLSSLDYDPDYGDPLENSLENIQPPGEMDRL 214

Qy 212 DPSSFQTNHDPWTVPTVFPQTFQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPS 271

Db 215 DPSSFQTNHDPWTVPTVFPQTFQPSADSLPRGSARLTSONLYSNVFKPADVVPKIPS 274

Qy 272 GPPIEDHETSPLDNSDAFLSTHLKLPFASNSFYSELPGQPDYNNLGQFTDDQVPT 331

Db 275 GPPIEDHETSPLDNSDAFLSTHLKLPFASNSFYSELPGQPDYNNLGQFTDDQVPT 334

Qy 332 PLVAITITRLVVGFLPSPVIMACYSFIVFMQRGRPAKSKTFRVAVVAVFLVCWT 391

Db 335 PLVAITITRLVVGFLPSPVIMACYSFIVFMQRGRPAKSKTFRVAVVAVFLVCWT 394

Qy 392 PYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFYALLGKDFRKKARQSIQ 451

Db 395 PYHIFGVLSLLTDPETPLGKTLMSWDHVCIALASANSFNPFYALLGKDFRKKARQSIQ 454

Qy 452 GILEAASFSEELTRSTHCPSPNNVISERNSTTV 482

Db 455 GILEAASFSEELTRSTHCPSPNNVISERNSTTV 485

RESULT 12

US-09-826-509-465

;; Sequence 465, Application US/09826509

;; Publication No. US20030204073A1

;; GENERAL INFORMATION:

;; APPLICANT: Lehmann-Bruinsma, Karin

;; APPLICANT: Liaw, Chen W.

;; APPLICANT: Lin, I-Lin

;; TITLE OF INVENTION: NO. US20030204073A1-Endogenous, Constitutively Activated Known G

;; FILE REFERENCE: AREN-207

;; CURRENT APPLICATION NUMBER: US/09/826.509

;; CURRENT FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 60/195,747

;; PRIOR FILING DATE: 2000-04-07

;; PRIOR APPLICATION NUMBER: 09/170,496

;; PRIOR FILING DATE: 1998-10-13

;; NUMBER OF SEQ ID NOS: 589

;; SOFTWARE: Patent in Version 2.1

;; SEQ ID NO 465

;; LENGTH: 482

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-826-509-465

Query Match

Best Local Similarity 99.6%; Pred. No. 1.6e-260;

Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 58.1%; Score 280; DB 10; Length 482;

Best Local Similarity 99.6%; Pred. No. 1.6e-260;

Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MASPSAETNSTDLISQPNWEPVILSMVILSLTLLGLPGNGLVWVAGLKMQRVTNTIW 60

Db 1 MASPSAETNSTDLISQPNWEPVILSMVILSLTLLGLPGNGLVWVAGLKMQRVTNTIW 60

Qy 61 FLHLTLADLLCCLSLPFLSLAHLALQGOQWPGYGRFLCKLIPSIIVLNMFAFVLLTAISLDR 120

Db 61 FLHLTLADLLCCLSLPFLSLAHLALQGOQWPGYGRFLCKLIPSIIVLNMFAFVLLTAISLDR 120

Qy 121 CLVVPKDIWCONHRNVGMACSIICCIWVAFWVCIPVYVREIETTDNHNRCGYKGLSS 180

Db 121 CLVVPKDIWCONHRNVGMACSIICCIWVAFWVCIPVYVREIETTDNHNRCGYKGLSS 180

Qy 181 SLDPYDFYGPDPLENSLENIQPPGEMNDRLDPSSFQTNHDPWTVPTVFPQTFQPSAD 240

Db 181 SLDPYDFYGPDPLENSLENIQPPGEMNDRLDPSSFQTNHDPWTVPTVFPQTFQPSAD 240

Qy 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSPGPFIEHETSPLDNSDAFLSTHLKLPSPA 300

Db 241 SLPRGSARLTSONLYSNVFKPADVVPKIPSPGPFIEHETSPLDNSDAFLSTHLKLPSPA 300

Qy 301 SSNSFYSELPGQPDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMACYSFIV 360

Db 301 SSNSFYSELPGQPDYNNLGQFTDDQVPTPLVAITITRLVVGFLPSPVIMACYSFIV 360

Qy 361 FMQRGRPAKSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Db 361 FMQRGRPAKSKTFRVAVVAVFLVCWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420

Qy 421 IALASANSFNPFYALLGKDFRKKARQSIQGLEAASFSEELTRSTHCPSPNNVISERNST 480

Db 421 IALASANSFNPFYALLGKDFRKKARQSIQGLEAASFSEELTRSTHCPSPNNVISERNST 480

Qy 481 TV 482

Db 481 TV 482

RESULT 13

US-10-925-095-465

;; Sequence 465, Application US/10925095

;; Publication No. US20050019840A1

;; GENERAL INFORMATION:

;; APPLICANT: Lehmann-Bruinsma, Karin

;; APPLICANT: Liaw, Chen W.

;; APPLICANT: Lin, I-Lin

;; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G

;; FILE REFERENCE: AREN-207

;; CURRENT APPLICATION NUMBER: US/10/925.095

;; CURRENT FILING DATE: 2004-08-24

;; PRIOR APPLICATION NUMBER: US/09/826,509

;; PRIOR FILING DATE: 2001-04-05

;; PRIOR APPLICATION NUMBER: 60/195,747

;; PRIOR FILING DATE: 2000-04-07

;; PRIOR APPLICATION NUMBER: 09/170,496

;; PRIOR FILING DATE: 1998-10-13

;; NUMBER OF SEQ ID NOS: 589

;; SOFTWARE: Patent in Version 2.1

;; SEQ ID NO 465

;; LENGTH: 482

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-925-095-465

Query Match

Best Local Similarity 99.6%; Pred. No. 1.6e-260;

Matches 480; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MASFAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
 Db 1 MASFAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Qy 121 CLVVFKEPIWCQHNHNVGMACSIICGCIWVAFVFCIPVYVREIFTTDNHNRCGYKFGLS 180
 Db 121 CLVVFKEPIWCQHNHNVGMACSIICGCIWVAFVFCIPVYVREIFTTDNHNRCGYKFGLS 180
 Qy 181 SLDYDFDYGDPLENRSLENIQVPGEMNDRLDPSFQTNDEHPWTPTVFQQTQRPESAD 240
 Db 181 SLDYDFDYGDPLENRSLENIQVPGEMNDRLDPSFQTNDEHPWTPTVFQQTQRPESAD 240
 Qy 241 SLPGSARLTSONLYSNVFKADVVSPKIPSGFPIEDHETSPDLSNDAFLSTHLKLPPSA 300
 Db 241 SLPGSARLTSONLYSNVFKADVVSPKIPSGFPIEDHETSPDLSNDAFLSTHLKLPPSA 300
 Qy 301 SSNSFYSELPGQDYNNLQGTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
 Db 301 SSNSFYSELPGQDYNNLQGTDDQVPTPLVAITITRLVVGFLPSPVIMIACTYFIV 360
 Qy 361 FMQGRFAKQSKTFRVAVVAVFLVCWTPPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Db 361 FMQGRFAKQSKTKRVAWVAVFLVCWTPPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSNNVISERNST 480
 Db 421 IALASANSFNPFLYALLGKDFRKKARQSIQGIIEAFAFSEELTRSTHCPSNNVISERNST 480
 Qy 481 TV 482
 Db 481 TV 482
 RESULT 14
 US-10-017-161-760
 ; Sequence 760, Application US/10017161
 ; Publication No. US20030143668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUWA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/0152
 ; CURRENT APPLICATION NUMBER: US/10/017,161
 ; CURRENT FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2430
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 760
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-017-161-760

Query Match 43.4%; Score 209; DB 14; Length 390;
 Best Local Similarity 100.0%; Pred. No. 2.9e-192;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MASFAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
 Db 1 MASFAETNSTDLQSQWNEPPVILSMVILSLTFLGLPGNGLVWVAGLKMORTVNTIW 60
 Qy 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Db 61 FLHUTLADLLCCLSLPFLSLAHLAQGWPGYGRFLCKLIPSIIVLNMFAVFLTAISLDR 120
 Qy 121 CLVVFKEPIWCQHNHNVGMACSIICGCIWVAFVFCIPVYVREIFTTDNHNRCGYKFGLS 180

Db 121 CLVVFKEPIWCQHNHNVGMACSIICGCIWVAFVFCIPVYVREIFTTDNHNRCGYKFGLS 180
 Qy 181 SLDYDFDYGDPLENRSLENIQVPGEMND 209
 Db 181 SLDYDFDYGDPLENRSLENIQVPGEMND 209
 RESULT 15
 US-09-892-206-2
 ; Sequence 2, Application US/09892206
 ; Patent No. US20020127712A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brennan, Thomas J.
 ; APPLICANT: Matthews, William
 ; APPLICANT: Moore, Mark
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING ANAPHYLATOXIN
 ; FILE REFERENCE: R-171
 ; CURRENT APPLICATION NUMBER: US/09/892,206
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/215,467
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 60/244,083
 ; PRIOR FILING DATE: 2000-10-26
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 477
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-892-206-2

Query Match 6.2%; Score 30; DB 9; Length 477;
 Best Local Similarity 100.0%; Pred. No. 7.4e-20;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 421 IALASANSFNPFLYALLGKDFRKKARQSI 450
 Db 414 IALASANSFNPFLYALLGKDFRKKARQSI 443

Search completed: April 13, 2005, 10:18:27
 Job time : 148 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 09:56:23 ; Search time 46 Seconds
(without alignments)
1008.184 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 482

Sequence: 1 MASFSAEETNSTDLLSQPWE.....TRSTHCPNNVIERNSTTV 482

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_79.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	79.0	482	2	S67566
2	29	6.0	473	2	JC5835
3	9	1.9	224	2	S56431
4	9	1.9	224	2	H31276
5	9	1.9	224	2	H86117
6	9	1.9	350	1	A37963
7	8	1.7	222	1	S25244
8	8	1.7	223	1	B48640
9	8	1.7	223	2	A42354
10	8	1.7	280	2	D84968
11	8	1.7	351	1	A46525
12	8	1.7	355	2	A55733
13	8	1.7	389	2	JC7356
14	8	1.7	413	2	G70439
15	8	1.7	466	2	A35375
16	8	1.7	518	2	T01318
17	8	1.7	1280	2	A39117
18	8	1.7	1292	2	T09229
19	8	1.7	84	2	G37721
20	7	1.5	111	2	S43115
21	7	1.5	148	2	T02352
22	7	1.5	150	2	G45714
23	7	1.5	156	2	B64036
24	7	1.5	167	2	S07473
25	7	1.5	172	2	PH1372
26	7	1.5	192	2	B84407
27	7	1.5	201	2	C36885
28	7	1.5	212	2	E89145
29	7	1.5	229	2	T29310

30	7	1.5	230	2	D84215	hypothetical prote
31	7	1.5	234	2	S35020	nmw protein - Rhi
32	7	1.5	241	2	T46390	hypothetical prote
33	7	1.5	243	2	A28993	auxin-induced prot
34	7	1.5	246	2	H27332	hypothetical prote
35	7	1.5	249	2	T38000	hypothetical prote
36	7	1.5	263	2	G85619	probable transport
37	7	1.5	263	2	A90756	probable transport
38	7	1.5	265	2	AC0441	probable aliphatic
39	7	1.5	266	2	AD3238	hypothetical prote
40	7	1.5	270	2	E72543	probable ABC trans
41	7	1.5	272	2	T07182	hypothetical prote
42	7	1.5	276	2	T30640	hypothetical prote
43	7	1.5	278	1	E64833	nitrate transport
44	7	1.5	284	2	A75422	acetyl-CoA carboxy
45	7	1.5	291	2	A22000	hypothetical prote
46	7	1.5	294	2	A35266	hypothetical prote
47	7	1.5	299	2	AB0609	probable membrane
48	7	1.5	299	2	D85599	probable surface p
49	7	1.5	299	2	H90748	hypothetical prote
50	7	1.5	306	2	AE1156	hypothetical prote
51	7	1.5	314	2	JH0389	pectin lyase (EC 4
52	7	1.5	317	2	AC0464	cell division regu
53	7	1.5	318	2	AB1792	transcription regu
54	7	1.5	318	2	C83383	probable transmemb
55	7	1.5	325	2	D75279	conserved hypothet
56	7	1.5	328	2	S65023	glucan endo-1,3-be
57	7	1.5	330	2	JC5717	G protein-coupled
58	7	1.5	330	2	F71146	hypothetical prote
59	7	1.5	333	2	T22227	hypothetical prote
60	7	1.5	337	2	S65022	glucan endo-1,3-be
61	7	1.5	343	2	A35639	G protein-coupled
62	7	1.5	344	2	R84376	Na+/Ca2+-exchangin
63	7	1.5	344	2	S09883	hypothetical prote
64	7	1.5	345	2	C55741	thymopoietin gamma
65	7	1.5	345	2	AH1514	hypothetical prote
66	7	1.5	352	2	T23664	hypothetical prote
67	7	1.5	359	2	S15403	angiotensin II rec
68	7	1.5	359	2	I51372	angiotensin II rec
69	7	1.5	359	2	I39418	angiotensin II rec
70	7	1.5	359	2	JC1104	angiotensin II rec
71	7	1.5	359	2	S44425	angiotensin II rec
72	7	1.5	359	2	A48857	angiotensin II rec
73	7	1.5	359	2	JH0621	angiotensin II rec
74	7	1.5	359	2	JC1194	angiotensin II rec
75	7	1.5	359	2	A42656	angiotensin II rec
76	7	1.5	359	2	JC2134	angiotensin II rec
77	7	1.5	361	2	T30033	hypothetical prote
78	7	1.5	363	2	A82567	GumF protein XF236
79	7	1.5	363	2	S43318	glucan endo-1,3-be
80	7	1.5	364	2	JQ1488	bradykinin B2 rece
81	7	1.5	365	2	S68679	G protein-coupled
82	7	1.5	367	2	JR0349	interferon-inducib
83	7	1.5	371	1	TVXL71	transforming prote
84	7	1.5	373	2	A47556	ATP receptor P2u -
85	7	1.5	375	2	A54946	p-2U nucleotide re
86	7	1.5	379	2	E72768	hypothetical prote
87	7	1.5	380	2	I38435	angiotensin recept
88	7	1.5	386	2	AE1996	D4 dopamine recept
89	7	1.5	387	2	I49246	hypothetical prote
90	7	1.5	389	2	T38455	hypothetical prote
91	7	1.5	389	2	T29488	chromate transport
92	7	1.5	397	2	F83721	antibiotic resista
93	7	1.5	399	2	D70072	hypothetical prote
94	7	1.5	413	2	H86825	multidrug-efflux t
95	7	1.5	413	2	B84085	conserved hypothet
96	7	1.5	421	2	F87040	hypothetical prote
97	7	1.5	421	2	H70607	probable membrane
98	7	1.5	427	2	E87669	conserved hypothet
99	7	1.5	427	2	S42160	MSSSI protein - ye
100	7	1.5	436	2	S42160	prophage pil prote
101	7	1.5	437	2	H86683	probable transcript
102	7	1.5	449	2	B97387	

103	7	1.5	454	1	A45340	nucleocapsid prote	176	6	1.2	38	2	PS0118	H-2 class I histoc
104	7	1.5	454	1	A45396	nucleocapsid prote	177	6	1.2	38	2	158994	MHC H2-L transmem
105	7	1.5	454	1	B45340	nucleocapsid prote	178	6	1.2	39	2	A32934	H-2 class I-like h
106	7	1.5	454	1	C45340	nucleocapsid prote	179	6	1.2	39	2	B95063	hypothetical prote
107	7	1.5	454	1	B5741	thymopoietin beta	180	6	1.2	45	2	I48726	QSk protein - mous
108	7	1.5	455	1	D45340	nucleocapsid prote	181	6	1.2	49	2	A99674	hypothetical prote
109	7	1.5	455	1	VH1HJ	nucleocapsid prote	182	6	1.2	52	2	S63601	glutathione S-tran
110	7	1.5	458	2	D97799	NADH2 dehydrogenas	183	6	1.2	55	2	S66333	protein kinase AK2
111	7	1.5	462	2	AC2605	transcription regu	184	6	1.2	59	2	G91095	hypothetical prote
112	7	1.5	504	2	S72699	serotonin receptor	185	6	1.2	59	2	C85941	hypothetical prote
113	7	1.5	506	2	E84670	hypothetical prote	186	6	1.2	60	2	S27152	GPI-anchored epidi
114	7	1.5	512	2	E36024	conserved hypotHet	187	6	1.2	61	2	S18766	GPI-anchored epidi
115	7	1.5	518	2	A12426	hypothetical prote	188	6	1.2	65	2	AG2966	hypothetical prote
116	7	1.5	519	2	E84811	hypothetical prote	189	6	1.2	65	2	D98316	conserved hypotHet
117	7	1.5	527	2	G99999	conserved hypotHet	190	6	1.2	67	2	A89894	serotonin receptor
118	7	1.5	531	2	T14640	cytochrome P450 Cy	191	6	1.2	68	2	S66489	hypothetical prote
119	7	1.5	539	2	S53529	monophenol monooxy	192	6	1.2	69	2	A84047	T-cell receptor al
120	7	1.5	540	2	S70403	zona pellucida gly	193	6	1.2	82	2	S35770	hypothetical prote
121	7	1.5	542	2	S73749	transport system p	194	6	1.2	87	2	AG0253	hypothetical prote
122	7	1.5	548	2	D32175	probable trypsin V	195	6	1.2	88	2	D83434	probable transloc
123	7	1.5	553	2	T06499	Rieske [2Fe-2S] ir	196	6	1.2	89	2	T03072	probable zinc fing
124	7	1.5	555	2	D96598	hypothetical prote	197	6	1.2	90	2	A60396	antigen 7H8/5 - ma
125	7	1.5	567	2	A31167	RNA-directed RNA p	198	6	1.2	91	2	A87622	Bola protein [impo
126	7	1.5	567	2	A20210	sulfate permease l	199	6	1.2	92	2	T49763	probable magnapori
127	7	1.5	576	2	E70539	probable membranep	200	6	1.2	92	2	G83144	hypothetical prote
128	7	1.5	598	1	RDEBFV	fumarate reductase	201	6	1.2	93	2	C87361	conserved hypotHet
129	7	1.5	599	2	S46630	hypothetical prote	202	6	1.2	93	2	T48522	hypothetical prote
130	7	1.5	613	2	D86147	hypothetical prote	203	6	1.2	95	2	AC1903	hypothetical prote
131	7	1.5	633	2	S87144	matng type A prot	204	6	1.2	97	2	S59888	C4 protein - tomat
132	7	1.5	642	2	E89144	probable formate C	205	6	1.2	97	2	C64022	hypothetical prote
133	7	1.5	655	2	E75206	alpha-amylase (or	206	6	1.2	98	2	C64011	hypothetical prote
134	7	1.5	657	2	H90523	excinuclease ABC s	207	6	1.2	98	2	D82859	hypothetical prote
135	7	1.5	694	2	E69143	hypothetical prote	208	6	1.2	99	2	S47084	lipid transfer lik
136	7	1.5	696	2	B86726	hypothetical prote	209	6	1.2	100	2	AD2566	hypothetical prote
137	7	1.5	700	2	T23629	hypothetical prote	210	6	1.2	100	2	I39666	rolA protein - Agr
138	7	1.5	720	2	T25883	hypothetical prote	211	6	1.2	102	2	A02196	MHC class I histoc
139	7	1.5	724	2	C83706	hypothetical prote	212	6	1.2	102	2	T40142	probable protein t
140	7	1.5	758	2	S62432	antibiotic merseac	213	6	1.2	102	2	F70534	hypothetical prote
141	7	1.5	781	2	S65169	major facilitator	214	6	1.2	103	2	D71047	hypothetical prote
142	7	1.5	781	2	T51433	probable cation tr	215	6	1.2	104	1	B37192	thioredoxin - Baci
143	7	1.5	788	2	I64045	recombination prot	216	6	1.2	104	2	T03778	probable ubiquitin
144	7	1.5	791	2	A99514	hypothetical prote	217	6	1.2	104	2	AC0044	probable chaperrone
145	7	1.5	796	2	G84570	biotin sulfoxide r	218	6	1.2	104	2	E71048	hypothetical prote
146	7	1.5	824	2	T09467	DNA-directed RNA p	219	6	1.2	105	2	A64166	hypothetical prote
147	7	1.5	860	2	T49910	hypothetical prote	220	6	1.2	105	2	I64170	hypothetical prote
148	7	1.5	909	2	S64038	probable membrane	221	6	1.2	108	2	T26880	hypothetical prote
149	7	1.5	925	2	T33732	probable exinucle	222	6	1.2	109	2	S14346	glutathione transf
150	7	1.5	958	2	S45466	probable DNA repai	223	6	1.2	111	2	A02197	MHC class I histoc
151	7	1.5	985	2	S67235	REVI protein - yea	224	6	1.2	111	2	FC2396	hypothetical 111 K
152	7	1.5	1086	2	T40354	hypothetical prote	225	6	1.2	114	2	C90820	hypothetical prote
153	7	1.5	1115	2	F86280	protein T5E21.11 f	226	6	1.2	114	2	G90851	hypothetical prote
154	7	1.5	1122	2	T14180	exit protein - Myc	227	6	1.2	114	2	C90874	hypothetical prote
155	7	1.5	1189	2	A54817	ATPase ScII. chrom	228	6	1.2	114	2	C90902	hypothetical prote
156	7	1.5	1199	2	T20319	Lian-Aal retrotran	229	6	1.2	114	2	D90911	hypothetical prote
157	7	1.5	1222	2	G72614	beta transducin-li	230	6	1.2	114	2	F90971	hypothetical prote
158	7	1.5	1249	2	T14150	probable reverse g	231	6	1.2	114	2	H91065	hypothetical prote
159	7	1.5	1384	2	S78132	vesicle associated	232	6	1.2	114	2	D85679	hypothetical prote
160	7	1.5	1401	2	T48079	DNA-directed RNA p	233	6	1.2	115	2	F85819	unknown protein en
161	7	1.5	1558	2	AB2457	hypothetical prote	234	6	1.2	115	2	H85627	hypothetical prote
162	7	1.5	1597	2	S55144	two-component hybr	235	6	1.2	116	2	B75456	hypothetical prote
163	7	1.5	1691	1	GH068	RIR1 protein - yea	236	6	1.2	116	2	A88450	hypothetical prote
164	7	1.5	1706	2	T19305	collagen alpha 6(I	237	6	1.2	117	2	S32508	protein F21H1.1 f
165	7	1.5	1816	2	F83901	protein kinase - f	238	6	1.2	118	2	S2673	ubiquitin-protein
166	7	1.5	2310	2	T38457	hypothetical prote	239	6	1.2	118	2	JT0273	homeotic protein H
167	7	1.5	2554	2	AB3528	extracellular aeri	240	6	1.2	120	2	B95297	hypothetical prote
168	7	1.5	2657	2	T18497	hypothetical prote	241	6	1.2	121	2	T28128	hypothetical prote
169	7	1.5	3412	1	GNWVB	genome polyprotein	242	6	1.2	121	2	AD2492	hypothetical prote
170	7	1.5	20	2	S63602	glutathione S-tran	243	6	1.2	122	2	B82271	hypothetical prote
171	6	1.2	23	2	A33948	glutathione transf	244	6	1.2	123	2	H27479	probable translati
172	6	1.2	32	2	A42037	GTPase-activating	245	6	1.2	123	2	F85744	unknown protein en
173	6	1.2	38	2	PS0115	H-2 class I histoc	246	6	1.2	124	2	AG2339	hypothetical prote
174	6	1.2	38	2	PS0115	H-2 class I histoc	247	6	1.2	124	2	E70008	conserved hypotHet
175	6	1.2	38	2	PS0114	H-2 class I histoc	248	6	1.2	124	2	G72693	hypothetical prote

249	6	1.2	125	2	A72490	hypothetical prote	322	1.2	160	2	T04346	glycine-rich RNA-b
250	6	1.2	126	2	T04682	high mobility grou	323	1.2	160	2	A97738	hypothetical prote
251	6	1.2	126	2	H95080	hypothetical prote	324	1.2	163	2	T48609	hypothetical prote
252	6	1.2	128	2	S76824	transposase sli158	325	1.2	164	2	I58201	MHC class I antige
253	6	1.2	128	2	C84074	hypothetical prote	326	1.2	164	2	F65031	hypothetical prote
254	6	1.2	129	2	T02012	probable cathepsin	327	1.2	165	2	T03583	glycine-rich RNA-b
255	6	1.2	129	2	T14451	ubiquitin conjugat	328	1.2	165	2	S37679	hypothetical prote
256	6	1.2	129	2	B71081	hypothetical prote	329	1.2	165	2	T38202	hypothetical serin
257	6	1.2	129	2	T49498	hypothetical prote	330	1.2	166	2	S37738	hypothetical 18.6K
258	6	1.2	129	2	E69188	hypothetical prote	331	1.2	167	2	E95875	hypothetical prote
259	6	1.2	129	2	A72753	hypothetical prote	332	1.2	168	2	T13326	hypothetical prote
260	6	1.2	130	2	C82616	hypothetical prote	333	1.2	168	2	T13631	hypothetical prote
261	6	1.2	131	2	T29743	hypothetical prote	334	1.2	168	2	S71562	drought-induced pr
262	6	1.2	131	2	B84598	hypothetical prote	335	1.2	168	2	AC3212	hypothetical prote
263	6	1.2	132	2	B70091	hypothetical prote	336	1.2	168	2	H75289	hypothetical prote
264	6	1.2	134	1	ERAD78	early E3B 14.9K pr	337	1.2	169	2	H72611	hypothetical prote
265	6	1.2	134	2	B35119	4-carboxymuonolac	338	1.2	170	2	S77192	general secretion
266	6	1.2	134	2	F72541	hypothetical prote	339	1.2	170	2	F84768	hypothetical prote
267	6	1.2	134	2	C82986	nucleoside diphosp	340	1.2	172	2	T04990	pathogenesis-relat
268	6	1.2	136	2	E70182	hypothetical prote	341	1.2	173	1	CYBOA	alpha-crystallin c
269	6	1.2	137	1	ERAD75	early E1B 15K prot	342	1.2	173	1	CYBMAA	alpha-crystallin c
270	6	1.2	137	2	A44031	probable membrane	343	1.2	173	1	CYGFMA	alpha-crystallin c
271	6	1.2	138	2	F70373	hypothetical prote	344	1.2	173	1	CYHOAA	alpha-crystallin c
272	6	1.2	138	2	S76592	hypothetical prote	345	1.2	173	1	CYHPAA	alpha-crystallin c
273	6	1.2	138	2	AC1486	hypothetical prote	346	1.2	173	1	CYRNAA	alpha-crystallin c
274	6	1.2	140	2	AC1284	hypothetical prote	347	1.2	173	2	B84348	hypothetical prote
275	6	1.2	141	2	S54700	PilB protein - Pse	348	1.2	173	2	A72620	probable NADH dehy
276	6	1.2	141	2	T17760	hypothetical prote	349	1.2	174	2	C59154	NADH2 dehydrogenas
277	6	1.2	141	2	T22730	hypothetical prote	350	1.2	174	2	T11517	NADH2 dehydrogenas
278	6	1.2	142	2	B81213	conserved hypotet	351	1.2	174	2	T14027	NADH2 dehydrogenas
279	6	1.2	142	2	S82958	spe-17 protein - C	352	1.2	175	2	D90090	mRNA cap binding p
280	6	1.2	143	2	AE3460	hypothetical cytos	353	1.2	175	2	T46022	hypothetical prote
281	6	1.2	144	2	H70971	hypothetical prote	354	1.2	176	2	H84065	molymdenum transpo
282	6	1.2	145	2	F81790	conserved hypotet	355	1.2	176	2	AE0526	2'-5' RNA ligase (
283	6	1.2	145	2	S73871	type I restriction	356	1.2	176	2	D72299	acetyltransferase,
284	6	1.2	146	2	D96666	protein F22C12.2 [357	1.2	177	1	W2VZA9	20K HindIII-C prot
285	6	1.2	147	2	H90116	ubiquitin conjugat	358	1.2	177	2	T30770	hypothetical prote
286	6	1.2	147	2	F90118	ubiquitin conjugat	359	1.2	178	2	G83802	forespore sigma-k
287	6	1.2	147	2	D90102	ubiquitin conjugat	360	1.2	178	2	AD1391	H+-transporting AT
288	6	1.2	147	2	F90082	ubiquitin conjugat	361	1.2	179	2	S23710	interferon alpha-I
289	6	1.2	147	2	F90137	ubiquitin conjugat	362	1.2	179	2	G85498	hypothetical prote
290	6	1.2	147	2	T39300	ubiquitin-conjugat	363	1.2	179	2	G90647	hypothetical prote
291	6	1.2	147	2	AD3081	hypothetical prote	364	1.2	179	2	C64738	yadp protein - Esc
292	6	1.2	147	2	D98205	hypothetical prote	365	1.2	179	2	AF1766	H+-transporting AT
293	6	1.2	147	2	D96712	probable mult prot	366	1.2	180	2	AC0197	conserved hypotet
294	6	1.2	147	2	T35980	probable peptide t	367	1.2	180	2	T49198	hypothetical prote
295	6	1.2	148	2	S32672	ubiquitin-protein	368	1.2	180	2	B95966	hypothetical prote
296	6	1.2	148	2	S32674	ubiquitin-protein	369	1.2	181	2	D87680	outer membrane lip
297	6	1.2	148	2	F84543	probable ubiquitin	370	1.2	181	2	E72022	hypothetical prote
298	6	1.2	148	2	T14541	ribosomal protein	371	1.2	181	2	G86600	hypothetical prote
299	6	1.2	149	2	F95872	hypothetical prote	372	1.2	181	2	A40607	monofunctional cho
300	6	1.2	150	2	JH0249	guanine nucleotide	373	1.2	182	2	A83289	DNA-3-methylasen
301	6	1.2	150	2	C87517	DnaJ-related prote	374	1.2	183	2	A81821	DNA-3-methyladenin
302	6	1.2	151	2	S48958	hypothetical prote	375	1.2	183	2	C81057	DNA-3-methyladenin
303	6	1.2	152	2	H97405	hypothetical prote	376	1.2	184	2	F42503	C8L protein - vacc
304	6	1.2	153	2	T44364	hypothetical prote	377	1.2	184	2	S74741	hypothetical prote
305	6	1.2	155	2	T25845	hypothetical prote	378	1.2	184	2	F69273	cytochrome-c oxida
306	6	1.2	155	2	A31055	hypothetical prote	379	1.2	185	1	HLMS2	MHC class I histoc
307	6	1.2	155	2	G82230	conserved hypotet	380	1.2	186	2	E75173	stage II sporulati
308	6	1.2	155	2	D85899	hypothetical prote	381	1.2	187	2	I37105	5-HT2c receptor -
309	6	1.2	156	2	H97334	hypothetical prote	382	1.2	188	2	T22358	hypothetical prote
310	6	1.2	156	2	D95290	hypothetical prote	383	1.2	189	2	H96520	potassium-transpor
311	6	1.2	156	2	B83138	hypothetical prote	384	1.2	190	2	AF1785	potassium-transpor
312	6	1.2	157	2	F83242	hypothetical prote	385	1.2	190	2	H75162	anthranilate synth
313	6	1.2	157	2	H90008	lytic regulatory p	386	1.2	190	2	A83102	conserved hypotet
314	6	1.2	157	2	T51841	RING-H2 finger pro	387	1.2	191	1	H69472	iron-dependent rep
315	6	1.2	157	2	T13027	RING-H2 finger pro	388	1.2	191	2	AE0412	probable 2'-5' RNA
316	6	1.2	158	2	D71111	hypothetical prote	389	1.2	192	2	T08066	probable membrane
317	6	1.2	159	2	AB0413	2-amino-4-hydroxy-	390	1.2	193	2	H84958	phosphonoprote iso
318	6	1.2	159	2	G97723	hypothetical prote	391	1.2	193	2	A82435	conserved hypotet
319	6	1.2	159	2	T43833	hypothetical prote	392	1.2	193	2	AG2567	hypothetical prote
320	6	1.2	159	2	AC2761	hypothetical prote	393	1.2	194	2	T47200	H+-transporting tw
321	6	1.2	159	2	T48209	hypothetical prote	394	1.2	194	2	S31410	transforming prote

395	1	196	1	WXKPB7	I196L protein - Af	468	6	1.2	221	2	S60596	transcription regu
396	2	196	2	H69647	2-dehydro-3-deoxy-	469	6	1.2	221	2	B81781	beta-phosphogluc
397	2	196	2	S56961	probable membrane	470	6	1.2	221	2	G81203	beta-phosphogluc
398	2	196	2	T29343	hypothetical prote	471	6	1.2	221	2	F81780	beta-phosphogluc
399	2	197	2	T03442	glycine-rich prote	472	6	1.2	221	2	B86678	beta-phosphogluc
400	2	197	2	F96799	Similar to 'MADS b	473	6	1.2	221	2	B84672	hypothetical prote
401	2	197	2	E97930	conserved hypoteth	474	6	1.2	222	2	AG0164	arginine transport
402	2	198	2	B83598	conserved hypoteth	475	6	1.2	222	2	B84410	hypothetical prote
403	2	198	2	S45530	sodium-translocati	476	6	1.2	222	2	F86758	DNA replication pr
404	2	198	2	T15128	hypothetical prote	477	6	1.2	222	2	H72662	hypothetical prote
405	2	198	2	A97404	hypothetical prote	478	6	1.2	222	2	E95294	conserved hypoteth
406	2	198	2	A12621	conserved hypoteth	479	6	1.2	224	2	G82199	conserved hypoteth
407	2	199	2	H70756	hypothetical prote	480	6	1.2	224	2	T32606	hypothetical prote
408	2	199	2	T26157	hypothetical prote	481	6	1.2	225	1	A48640	global nitrogen re
409	2	200	2	E96912	adenylsulfate ki	482	6	1.2	225	2	B45582	probable 1-acygly
410	2	200	2	A83323	hypothetical prote	483	6	1.2	226	2	H84132	beta-phosphogluc
411	2	200	2	T30223	hypothetical prote	484	6	1.2	228	1	S20448	cutinase (EC 3.1.-
412	2	201	2	C96565	hypothetical prote	485	6	1.2	229	2	AD1021	probable exported
413	2	202	2	AF0581	alpha-ribazole-5' -	486	6	1.2	230	2	C84756	hypothetical prote
414	2	202	2	T24134	hypothetical prote	487	6	1.2	231	1	C69540	cobalamin (5' -phos
415	2	202	2	F72220	hypothetical prote	488	6	1.2	231	2	F90046	hypothetical prote
416	2	203	2	H85563	phosphohistidine p	489	6	1.2	231	2	A86901	hypothetical prote
417	2	203	2	D90713	phosphoglycerate m	490	6	1.2	231	2	AF3037	transcription regu
418	2	203	2	D64798	hypothetical prote	491	6	1.2	232	2	C81688	transcription regu
419	2	203	2	C95120	hypothetical prote	492	6	1.2	232	2	H75422	ribonuclease III r
420	2	203	2	G97989	hypothetical prote	493	6	1.2	232	2	B89790	probable polysacch
421	2	204	2	C72365	hypothetical prote	494	6	1.2	233	2	F97382	holin-like protein
422	2	204	2	S73533	hypothetical prote	495	6	1.2	233	2	H82995	probable transport
423	2	205	2	H95861	conserved hypoteth	496	6	1.2	234	2	A55367	conserved hypoteth
424	2	205	2	S26854	microfilarial sheat	497	6	1.2	234	2	D84207	phosphatase cobb -
425	2	205	2	A40525	proline-rich sheat	498	6	1.2	234	2	G83698	hypothetical prote
426	2	206	2	G90567	hypothetical prote	499	6	1.2	235	1	WMBEXC	hypothetical prote
427	2	206	2	H84776	hypothetical prote	500	6	1.2	235	2	E70530	U156 protein - hum
428	2	207	2	J00397	noGS protein - Azo	501	6	1.2	236	2	G75311	hypothetical prote
429	2	207	2	E89917	hypothetical prote	502	6	1.2	236	2	T36849	branched-chain ami
430	2	208	2	T15783	hypothetical prote	503	6	1.2	236	2	B44805	probable transcript
431	2	209	2	A69864	conserved hypoteth	504	6	1.2	237	2	H90492	hypothetical prote
432	2	210	2	S51568	glutathione transf	505	6	1.2	237	2	C97948	ABC transporter, A
433	2	210	2	A42687	neutrophin-4 pre	506	6	1.2	237	2	C81291	hypothetical prote
434	2	210	2	A64702	hypothetical prote	507	6	1.2	238	2	AH0918	probable integral
435	2	210	2	D71819	hypothetical prote	508	6	1.2	238	2	F91221	conserved hypoteth
436	2	210	2	D44805	hypothetical prote	509	6	1.2	238	2	A86068	probable phosphata
437	2	211	2	T36101	hypothetical prote	510	6	1.2	238	2	D37841	probable phosphata
438	2	212	2	T35187	hypothetical prote	511	6	1.2	238	2	AB0468	hypothetical 27.1K
439	2	212	2	B83936	hypothetical prote	512	6	1.2	239	2	E84470	probable haloacid
440	2	213	2	A26423	serine proteinase	513	6	1.2	240	2	S44358	hypothetical prote
441	2	214	2	S59149	H+ transporting tw	514	6	1.2	240	2	S71878	glutathione transf
442	2	214	2	T08922	hypothetical prote	515	6	1.2	240	2	S27161	glutathione transf
443	2	214	2	S74854	hypothetical prote	516	6	1.2	241	2	S44438	hypothetical prote
444	2	215	2	S24717	pyroglutamyl-pepti	517	6	1.2	242	2	G90104	putative tetrameri
445	2	215	2	I52523	nucleoporin p62 ho	518	6	1.2	243	2	JG0186	vesicle-associated
446	2	215	2	H86774	hypothetical prote	519	6	1.2	244	2	S71879	glutathione transf
447	2	215	2	A83023	probable transcript	520	6	1.2	244	2	JC2425	glutathione transf
448	2	216	2	G81666	conserved hypoteth	521	6	1.2	245	2	D70882	probable dapB prot
449	2	216	2	F81737	hypothetical prote	522	6	1.2	245	2	D49898	cellulose phospho
450	2	216	2	A72345	conserved hypoteth	523	6	1.2	245	2	S20460	1-acylglycerol-3-p
451	2	216	2	D83457	probable transcript	524	6	1.2	245	2	AE0888	1-acyl-glycerol-3-
452	2	216	2	S73818	hypothetical prote	525	6	1.2	245	2	F85961	1-acyl-sn-glycerol
453	2	217	2	H86514	ABC amino acid tra	526	6	1.2	245	2	F91116	1-acyl-sn-glycerol
454	2	217	2	G72108	amino acid ABC tra	527	6	1.2	246	2	A82600	hypothetical prote
455	2	217	2	S36955	low Ca2+ response	528	6	1.2	246	2	R81349	probable ferredoxi
456	2	217	2	T48169	hypothetical prote	529	6	1.2	246	2	A84396	hypothetical prote
457	2	217	2	T27933	hypothetical prote	530	6	1.2	246	2	T35934	probable NAD(P)H o
458	2	217	2	AG1277	hypothetical prote	531	6	1.2	247	2	B42856	ubiquitin carrier
459	2	217	2	AG1640	hypothetical prote	532	6	1.2	247	2	I48149	serotonin receptor
460	2	219	2	E72866	AcOrf-132 protein	533	6	1.2	247	2	T17677	hypothetical prote
461	2	219	2	G90602	chromate transport	534	6	1.2	247	2	T49375	hypothetical prote
462	2	220	2	C83292	probable glutathio	535	6	1.2	248	2	AG3275	hexaprenylidhydrox
463	2	220	2	F64332	hypothetical prote	536	6	1.2	248	2	D90986	hypothetical prote
464	2	221	1	H69511	DNA repair protein	537	6	1.2	248	2	A70328	hypothetical prote
465	2	221	1	S39609	ERD2 protein - mal	538	6	1.2	248	2	G85831	hypothetical prote
466	2	221	2	AC3132	hypothetical prote	539	6	1.2	248	2	F64371	hypothetical prote
467	2	221	2	A98156	probable permease	540	6	1.2	249	2	T31061	hypothetical prote

541 1.2 249 2 B86273 hypothetical prote
542 1.2 249 2 AH2152 hypothetical prote
543 1.2 249 2 E98248 hypothetical prote
544 1.2 250 2 D98833 ABC transporter, A
545 1.2 250 2 C87353 conserved hypotet
546 1.2 251 2 H87692 ydfG protein - Hae
547 1.2 252 2 H84122 ABC transporter, p
548 1.2 252 2 F87575 biosynthesis of te
549 1.2 252 2 C86796 probable cyH - My
550 1.2 252 2 A69728 conserved hypotet
551 1.2 254 2 C70682 guanylate kinase
552 1.2 255 2 B81693 conserved hypotet
553 1.2 255 2 A63435 conserved hypotet
554 1.2 255 2 C75527 probable flagellin
555 1.2 255 2 C71169 spa29 protein - Sh
556 1.2 256 2 I49846 hypothetical prote
557 1.2 256 2 T06649 daunorubicin resis
558 1.2 257 2 D75108 hypothetical prote
559 1.2 257 2 H84597 hypothetical prote
560 1.2 257 2 G36810 hypothetical prote
561 1.2 257 2 AD0257 hypothetical prote
562 1.2 257 2 F75476 probable uroporphyr
563 1.2 258 1 DHMS phosphate-binding
564 1.2 258 1 I64120 ABC transporter, m
565 1.2 259 2 AC3100 hypothetical prote
566 1.2 259 2 G98186 probable permease
567 1.2 260 2 E98219 hypothetical prote
568 1.2 260 2 A83067 hypothetical prote
569 1.2 260 2 H83844 glutathione transp
570 1.2 261 2 S59629 cobalt transport p
571 1.2 261 2 AH2298 formate dehydrogen
572 1.2 261 2 AH1397 formate dehydrogen
573 1.2 261 2 AC1773 hypothetical prote
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575 1.2 261 2 T02891 cobalamin synthase
576 1.2 261 2 H83848 hypothetical prote
577 1.2 261 2 A81471 hypothetical serin
578 1.2 262 2 T40941 transcription regu
579 1.2 262 2 AG3047 hypothetical prote
580 1.2 263 2 T16399 orf3', to hsd -
581 1.2 263 2 F45734 hypothetical prote
582 1.2 263 2 A12384 uncharacterised pe
583 1.2 264 2 H86975 hypothetical prote
584 1.2 265 2 B72279 2-oxo-hept-3-ene-1
585 1.2 267 2 H83129 hypothetical prote
586 1.2 267 2 E85786 phosphonate ABC tr
587 1.2 269 2 A12561 probable anaerobic
588 1.2 269 2 AG0822 site-specific DNA-
589 1.2 270 2 S47099 hypothetical prote
590 1.2 270 2 T05048 probable methyltra
591 1.2 271 2 T34968 water channel prot
592 1.2 271 2 JT0750 spermidine/putresc
593 1.2 271 2 H84337 hypothetical prote
594 1.2 271 2 G97791 homeotic protein m
595 1.2 273 2 S32881 photosystem II oxy
596 1.2 274 2 S01261 probable ATP-bindin
597 1.2 274 2 G83214 protein kinase MNK
598 1.2 274 2 S33178 mitochondrial impo
599 1.2 275 1 RGBY7K chemotactic methyl
600 1.2 275 2 T08095 oxytocin receptor
601 1.2 275 2 G00019 conserved hypotet
602 1.2 275 2 F90173 hypothetical prote
603 1.2 275 2 A70908 nosy protein [impo
604 1.2 275 2 T44663 conserved hypotet
605 1.2 275 2 C98558 alpha 2-adrenergic
606 1.2 276 2 I53161 conserved hypotet
607 1.2 276 2 B63283 probable shikimate
608 1.2 278 2 C86973 probable protein k
609 1.2 278 2 S36387 pyrroline-5-carbox
610 1.2 279 2 AG1610 probable uridylyate
611 1.2 279 2 A87108 D-amino acid amino
612 1.2 280 2 E96997 probable transport
613 1.2 280 2 C90865

614 1.2 280 2 F85753 probable transport
615 1.2 280 2 C64880 probable multiple
616 1.2 280 2 E85295 hypothetical prote
617 1.2 280 2 T05790 hypothetical prote
618 1.2 281 2 F72364 hypothetical prote
619 1.2 281 2 AF0164 probable membrane
620 1.2 282 2 G83080 nicotinate-nucleot
621 1.2 283 2 A60364 tropomyosin - migr
622 1.2 283 2 S51047 mauT protein - Far
623 1.2 283 2 T19411 hypothetical prote
624 1.2 284 2 S74168 tropomyosin - Amer
625 1.2 284 2 D81199 conserved hypotet
626 1.2 284 2 D81834 conserved hypotet
627 1.2 284 2 AD0987 probable phosphos
628 1.2 284 2 AE0314 conserved hypotet
629 1.2 284 2 B41224 homeotic protein p
630 1.2 285 2 E84766 probable AT-hook D
631 1.2 285 2 S59328 TIS11 protein - ye
632 1.2 286 2 H87292 enoyl-CoA hydratase
633 1.2 286 2 H69671 pantothenate synth
634 1.2 286 2 A86480 F14D7.8 protein -
635 1.2 287 1 H69414 conserved hypotet
636 1.2 287 2 S73529 MG439 homolog R09
637 1.2 289 2 AH2088 heat shock protein
638 1.2 289 2 C83257 acetyl-CoA carboxy
639 1.2 290 2 G70337 hypothetical prote
640 1.2 291 1 DHMS Ig delta chain C r
641 1.2 291 2 S22041 hypothetical prote
642 1.2 292 1 KFRB3 tissue factor prec
643 1.2 292 2 C70421 conserved hypotet
644 1.2 293 2 B32010 flagellin - Rosebu
645 1.2 293 2 S41007 hypothetical prote
646 1.2 293 2 AD3438 CDpalcylglycerol-
647 1.2 294 2 B83040 ribosomal protein
648 1.2 294 2 H84115 major ferric iron-
649 1.2 294 2 C64048 hypothetical prote
650 1.2 294 2 B83964 hypothetical prote
651 1.2 294 2 T43978 hypothetical prote
652 1.2 294 2 AE2457 succinyl-CoA synth
653 1.2 295 2 B83446 conserved hypotet
654 1.2 295 2 T39012 conserved hypotet
655 1.2 296 2 T24549 conserved hypotet
656 1.2 296 2 AC2352 hypothetical prote
657 1.2 296 2 S63700 probable ubiquinol
658 1.2 297 2 T33914 hypothetical prote
659 1.2 297 2 F69054 cobalamin biosynth
660 1.2 297 2 T09396 hypothetical prote
661 1.2 297 2 C70251 immediate-early pr
662 1.2 297 2 T093311 hypothetical prote
663 1.2 298 2 B90435 conserved hypotet
664 1.2 298 2 E83627 conserved hypotet
665 1.2 298 2 S76437 helix-turn-helix d
666 1.2 299 2 T29374 hypothetical prote
667 1.2 299 2 A89103 protein C18B10.7 l
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670 1.2 299 2 S98238 helix-turn-helix d
671 1.2 300 2 D83391 hypothetical prote
672 1.2 300 2 T46403 hypothetical prote
673 1.2 301 2 C84331 homoserine kinase
674 1.2 301 2 E96921 oligopeptide trans
675 1.2 301 2 H70505 hypothetical prote
676 1.2 301 2 G83181 pecM-related transcrip
677 1.2 302 2 E75414 proline dehydrogen
678 1.2 302 1 H69758 tropinesterase hom
679 1.2 303 2 S73051 fructose 1-phospha
680 1.2 303 2 A89627 probable integral
681 1.2 303 2 H81367 hypothetical prote
682 1.2 305 2 A72636 conserved hypotet
683 1.2 305 2 AC2623 conserved hypotet
684 1.2 305 2 C97405 hypothetical prote
685 1.2 306 2 JC4347 uroporphyrin-III C

687 308 2 A52833 D-alanine:D-alanine
688 309 2 H75286 hypothetical prote
689 310 2 F86393 protein T24P13.4 [lipoic acid synth
690 311 2 E36953 site-specific DNA-
691 312 2 A46660 conserved hypot
692 313 2 A00779 olfactory recept
693 314 2 H23701 hypothetical prote
694 315 2 F26337 hypothetical prote
695 316 2 T15674 probable membran
696 317 2 B64826 protein F23F12.1 [probable periplasm
697 318 2 G88485 glucan endo-1,3-be
698 319 2 B81428 ABC transporter, p
699 320 2 S46237 probable nucleotid
700 321 2 F81712 melanotropin recep
701 322 2 T39000 nrfD protein - Esc
702 323 2 S29204 formate-dependent
703 324 1 D57987 formate-dependent
704 325 2 G91260 conserved hypot
705 326 2 C86101 chitinase (EC 3.2.
706 327 2 A86638 probable methionyl
707 328 2 JG2252 hypothetical prote
708 329 2 G71284 gluc protein - Rho
709 330 2 S64149 hypothetical prote
710 331 2 S82224 probable membran
711 332 2 S29666 hypothetical prote
712 333 2 T41002 hypothetical prote
713 334 2 T42988 cobalamin biosynth
714 335 2 H96994 probable peroxid
715 336 2 T09164 chitinase (EC 3.2.
716 337 2 T03614 heptosyltransfer
717 338 2 G87379 thiamin biosynthes
718 339 2 T44256 GDP dissociation i
719 340 2 C56024 transforming prote
720 341 2 T11075 NADH2 dehydrogen
721 342 2 S11001 transforming prote
722 343 2 TVH085 NADH2 dehydrogen
723 344 2 T11193 NADH2 dehydrogen
724 345 2 T11180 melanocortin 5 rec
725 346 2 T11180 melanocortin 5 rec
726 347 2 JG5592 hypothetical prote
727 348 2 JN0764 conserved hypot
728 349 2 T39520 gonadotropin-relea
729 350 2 F69784 gonadotropin-relea
730 351 2 A44013 fatty acid/phospho
731 352 2 T44432 cytochrome c oxida
732 353 2 AC2120 MHC H-2K transplan
733 354 2 J54414 gonadotropin-relea
734 355 2 JG1353 G protein-coupled
735 356 2 T38973 gonadotropin-relea
736 357 2 JN0882 asparaginase (EC 3
737 358 2 H71225 probable quinone o
738 359 2 T40981 structural protein
739 360 2 T19872 probable nucleotid
740 361 2 S32582 hypothetical prote
741 362 2 T35486 hypothetical prote
742 363 2 F82338 hypothetical prote
743 364 2 T49644 probable membran
744 365 2 A10491 hypothetical prote
745 366 2 T32305 protein K08P9.5 [i
746 367 2 E88991 hypothetical prote
747 368 2 T01838 L-lactate dehydrog
748 369 2 D8MSUC L-lactate dehydrog
749 370 2 T84639 iron utilization p
750 371 2 T10886 probable transport
751 372 2 H85899 probable transport
752 373 2 D91055 probable sugar tra
753 374 2 A65032 probable ion-chann
754 375 2 A80808 hypothetical prote
755 376 2 G84920 G protein-coupled
756 377 2 T38974 peptide ABC transp
757 378 2 B75381 conserved hypot
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759 380 2 C97567

760 6 1.2 334 2 F97610 D-alanine:D-alanine
761 6 1.2 334 2 A24582 MHC class I histoc
762 6 1.2 334 2 A39172 Ancho-RFamide neur
763 6 1.2 335 2 C89279 heat shock protein
764 6 1.2 335 2 C97053 mreB [imported] -
765 6 1.2 335 2 S73392 type I restriction
766 6 1.2 335 2 T28774 hypothetical prote
767 6 1.2 336 2 F90220 3-isopropylmalate
768 6 1.2 336 2 T38902 probable cinnamoyl
769 6 1.2 336 2 D69074 polyferredoxin 4x2
770 6 1.2 337 2 H97947 hypothetical prote
771 6 1.2 338 1 A65021 ethanalamine utili
772 6 1.2 338 2 H91043 ethanalamine utili
773 6 1.2 338 2 C85888 ethanalamine utili
774 6 1.2 338 2 E86311 hypothetical prote
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776 6 1.2 339 2 T35919 probable transmem
777 6 1.2 340 2 A45883 MHC class I histoc
778 6 1.2 340 2 S76294 hypothetical prote
779 6 1.2 341 2 F72215 oligopeptide ABC t
780 6 1.2 341 2 D70233 hypothetical prote
781 6 1.2 341 2 H90267 arginine deiminase
782 6 1.2 342 2 T52150 hypothetical prote
783 6 1.2 343 2 F87523 hypothetical prote
784 6 1.2 343 2 S66173 mating factor MAT-
785 6 1.2 344 2 A82050 glycerol-3-phospha
786 6 1.2 344 2 F72406 hypothetical prote
787 6 1.2 344 2 E71291 flagellar motor sw
788 6 1.2 344 2 S44364 1,3-beta-glucanase
789 6 1.2 344 2 T33264 hypothetical prote
790 6 1.2 344 2 T25567 NADH2 dehydrogen
791 6 1.2 345 2 T12368 hypothetical prote
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793 6 1.2 345 2 G83148 DNA polymerase III
794 6 1.2 345 2 G84509 hypothetical prote
795 6 1.2 346 2 E87600 alcohol dehydrogen
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797 6 1.2 346 2 C75139 bifunctional short
798 6 1.2 346 2 S12402 glucan endo-1,3-be
799 6 1.2 346 2 D82710 ribonucleoside-dip
800 6 1.2 346 2 D90450 conserved hypot
801 6 1.2 347 2 E95949 probable fructose-
802 6 1.2 347 2 A60747 MHC class I histoc
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804 6 1.2 348 2 AB2876 alpha-1-microglobu
805 6 1.2 349 2 S21089 MHC class I histoc
806 6 1.2 349 2 S20046 flagellar motor sw
807 6 1.2 349 2 H82116 polyferredoxin 4x2
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812 6 1.2 350 2 T25366 hypothetical prote
813 6 1.2 351 2 B42009 FIMP-related recep
814 6 1.2 351 2 T23423 complement C5a ana
815 6 1.2 352 1 S27357 N-foxylyl peptide r
816 6 1.2 352 2 A46520 probable transport
817 6 1.2 352 2 D85826 membrane protein y
818 6 1.2 352 2 D64966 probable transport
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820 6 1.2 352 2 T22019 MHC class I histoc
821 6 1.2 353 2 A45859 FIMP-related recep
822 6 1.2 353 2 C42009 fructose-1,6-bisph
823 6 1.2 354 2 C83575 G protein-coupled
824 6 1.2 354 2 B55733 dipeptide ABC tran
825 6 1.2 354 2 G69470 hypothetical prote
826 6 1.2 354 2 T21404 coat protein VP2 -
827 6 1.2 356 1 VVP2L cytochrome-c oxida
828 6 1.2 356 2 A14396 H-2 class I histoc
829 6 1.2 356 2 A21198 H-2 class I histoc
830 6 1.2 357 1 HLMS37 MHC class I histoc
831 6 1.2 357 2 B81396 probable aminotran
832 6 1.2 357 2 JC7319 probable allatosta

833	6	1.2	357	2	B90404	hypothetical prote	906	1.2	373	2	AI3491	acyltransferase (E
834	6	1.2	357	2	D2589	hypothetical prote	907	1.2	374	1	A42046	surfactant protein
835	6	1.2	358	2	H81618	arginine kinase-re	908	1.2	374	2	A59273	proteinase inhibit
836	6	1.2	358	2	B86578	arginine kinase [i	909	1.2	374	2	T44696	hypothetical prote
837	6	1.2	358	2	H83554	hypothetical prote	910	1.2	375	2	S25262	pectate lyase (EC
838	6	1.2	358	2	E72045	arginine kinase -	911	1.2	375	2	B98001	glycerate kinase [
839	6	1.2	359	2	T02011	probable cathepsin	912	1.2	375	2	C82642	hypothetical prote
840	6	1.2	359	2	S76332	hypothetical prote	913	1.2	375	2	A46390	cAMP receptor subt
841	6	1.2	359	2	J01516	angiotensin II rec	914	1.2	375	2	D87427	conserved hypothet
842	6	1.2	359	2	T18667	hypothetical prote	915	1.2	376	2	S34335	opsin - Sphodroman
843	6	1.2	359	2	T48001	hypothetical prote	916	1.2	376	2	AB0599	probable inner mem
844	6	1.2	359	2	T37880	probable protein d	917	1.2	377	2	G90737	hypothetical prote
845	6	1.2	359	2	S40746	hypothetical prote	918	1.2	377	2	C69758	amino acid transpo
846	6	1.2	360	2	A84944	hypothetical prote	919	1.2	377	2	H8587	hypothetical prote
847	6	1.2	360	2	T45956	hypothetical prote	920	1.2	377	2	A64816	ybhs protein - Esc
848	6	1.2	360	2	C72356	hypothetical prote	921	1.2	378	2	S38962	serpin - pig
849	6	1.2	360	2	AE3175	hypothetical prote	922	1.2	378	2	A45680	G protein-coupled
850	6	1.2	361	2	A95188	PTS system, IIC co	923	1.2	378	2	B55735	lymphocyte-specifi
851	6	1.2	361	2	AC1028	probable membrane	924	1.2	378	2	A55735	G protein-coupled
852	6	1.2	362	1	HLMSDB	MHC class I histoc	925	1.2	378	2	A55735	hypothetical prote
853	6	1.2	362	1	HLMSLD	MHC class I histoc	926	1.2	378	2	G70435	elastase inhibitor
854	6	1.2	362	2	C60854	MHC class I histoc	927	1.2	379	2	S27383	hypothetical prote
855	6	1.2	362	2	B60854	MHC class I histoc	928	1.2	379	2	T49866	hypothetical prote
856	6	1.2	362	2	B45876	class I histocompa	929	1.2	379	2	T32778	ubiquinol-cytochro
857	6	1.2	362	2	I71998	MHC H-2D-k protein	930	1.2	380	2	T11113	ubiquinol-cytochro
858	6	1.2	362	2	A45876	class I histocompa	931	1.2	380	2	JC2338	kappa opioid recep
859	6	1.2	362	2	A39714	G protein-coupled	932	1.2	380	2	A48227	kappa opioid recep
860	6	1.2	362	2	A30341	G protein-coupled	933	1.2	380	2	JC2434	kappa opioid recep
861	6	1.2	362	2	AH3144	conserved hypothet	934	1.2	380	2	S36143	kappa opioid recep
862	6	1.2	363	2	S72209	3-isopropylmalate	935	1.2	380	2	A55259	kappa opioid recep
863	6	1.2	363	2	JC2543	angiotensin II rec	936	1.2	380	2	H70590	hypothetical prote
864	6	1.2	363	2	I48261	angiotensin II rec	937	1.2	380	2	T18509	hypothetical prote
865	6	1.2	363	2	A49092	angiotensin II rec	938	1.2	380	2	T20269	hypothetical prote
866	6	1.2	363	2	E75457	probable phosphata	939	1.2	381	2	S28115	gas-vesicle protei
867	6	1.2	365	2	I57814	MHC class I-alpha	940	1.2	381	2	B99986	hypothetical prote
868	6	1.2	365	2	S27268	activin receptor S	941	1.2	381	2	C90543	hypothetical prote
869	6	1.2	366	1	TMSM4	monocyte surface g	942	1.2	381	2	T21849	hypothetical prote
870	6	1.2	366	1	CORTB2	bradykinin recepto	943	1.2	382	2	A28067	lysosomal membrane
871	6	1.2	366	2	I49519	bradykinin B2 rece	944	1.2	382	2	E95391	probable membrane
872	6	1.2	366	2	T20011	hypothetical prote	945	1.2	383	2	T01593	glycosyltransferas
873	6	1.2	367	1	DJPS3P	DNA-directed DNA p	946	1.2	383	2	T26902	hypothetical prote
874	6	1.2	367	2	JC2421	opioid receptor ho	947	1.2	383	2	E71246	hypothetical prote
875	6	1.2	367	2	I49022	kappa opioid recep	948	1.2	384	2	D69411	probable acyl-CoA
876	6	1.2	367	2	I56520	G protein-coupled	949	1.2	384	2	T37111	probable transcript
877	6	1.2	367	2	E69998	hypothetical prote	950	1.2	384	2	H87019	probable glycosyl
878	6	1.2	367	2	B88969	protein T27B7.1 [i	951	1.2	385	2	H83766	aspartate aminotra
879	6	1.2	368	1	HLMSKD	MHC class I histoc	952	1.2	385	2	G87340	aminotransferase,
880	6	1.2	368	2	I49712	H-2K-s - mouse	953	1.2	385	2	H86731	conserved hypothet
881	6	1.2	368	2	I49713	H-2K-sm1 - mouse	954	1.2	385	2	E96669	protein FIN19.19 [
882	6	1.2	368	2	I55961	MHC class I histoc	955	1.2	386	1	S34043	oxytocin receptor
883	6	1.2	368	2	I68705	MHC H-2K-w28 prote	956	1.2	386	2	A4709	L-seryl-tRNAsec se
884	6	1.2	368	2	A60854	MHC class I histoc	957	1.2	387	2	S55550	5-HT4S receptor -
885	6	1.2	368	2	T36414	probable iron-side	958	1.2	387	2	T75064	hypothetical prote
886	6	1.2	368	2	S67387	hypothetical prote	959	1.2	388	2	A55597	oxytocin receptor
887	6	1.2	369	1	HLMSKB	MHC class I histoc	960	1.2	388	2	T43183	probable 26S prote
888	6	1.2	369	1	HLMSKK	MHC class I histoc	961	1.2	388	2	AI3520	replication protei
889	6	1.2	369	2	JH0493	alpha-1-antichymot	962	1.2	388	2	AG3307	oxalate/formate an
890	6	1.2	369	2	I56077	MHC class I antige	963	1.2	389	2	A55493	oxytocin receptor
891	6	1.2	369	2	A82326	periplasmic amino	964	1.2	389	2	S71336	mesotocin receptor
892	6	1.2	370	2	S43087	orphan opioid rece	965	1.2	389	2	C89958	acetoin utilizatio
893	6	1.2	370	2	A95528	probable structura	966	1.2	389	2	F72554	hypothetical prote
894	6	1.2	370	2	A72542	hypothetical prote	967	1.2	389	2	S73910	probable serine/ch
895	6	1.2	370	2	G70872	hypothetical glyci	968	1.2	390	1	Q0BET9	protein U133 - hum
896	6	1.2	371	2	JC5498	G protein-coupled	969	1.2	390	2	G69044	N-acetyloronithine
897	6	1.2	371	2	JC5796	probable chemoattr	970	1.2	390	2	S53487	porphobilinogen sy
898	6	1.2	371	2	AH0147	outer membrane, pro	971	1.2	390	2	F71811	l-seryl-tRNA(ser)
899	6	1.2	371	2	C95130	conserved hypothet	972	1.2	392	2	D64433	hypothetical prote
900	6	1.2	371	2	F81102	conserved hypothet	973	1.2	392	2	S65693	opioid receptor mu
901	6	1.2	371	2	D81838	hypothetical prote	974	1.2	392	2	S72753	hypothetical prote
902	6	1.2	372	2	AB0276	probable membrane	975	1.2	392	2	A41238	chemoattractant re
903	6	1.2	372	2	S20056	para-hydroxybenzoa	976	1.2	393	2	H75137	phosphoglycerate k
904	6	1.2	373	2	H84404	ferrichrome ABC tr	977	1.2	394	1	K1BSGM	microbial aspartic
905	6	1.2	373	2	T47488	hypothetical prote	978	1.2	394	2	S16971	

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-224 <BLAT>
A:Cross-references: GB:AE000492; GB:U00096; NID:G1790649; PIDN:AAC77163.1; PID:G1790651;
A:Experimental source: strain K-12, substrain MGL655

Query Match 1.9%; Score 9; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 LVVGFLLPS 349
Db 54 LVVGFLLPS 62

RESULT 4
H91276
hypothetical protein ECs184 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H91276
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gisawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <AV>
A:Cross-references: UNIPROT:Q8XC11; GB:BA000007; PIDN:BA38607.1; PID:G13364661; GSPDB:C
A:Experimental source: strain O157:H7, substrain RMD 0509952
A:Gene: ECs184

Query Match 1.9%; Score 9; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 LVVGFLLPS 349
Db 54 LVVGFLLPS 62

RESULT 5
H86117
hypothetical protein ytfB [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H86117
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86117
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <STO>
A:Cross-references: UNIPROT:Q8XC11; GB:AE005174; NID:G12519202; PIDN:AGS9404.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
A:Gene: ytfB

Query Match 1.9%; Score 9; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 LVVGFLLPS 349
Db 54 LVVGFLLPS 62

RESULT 6
A37963
complement C5a anaphylatoxin receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: A37963; S13646; I52417; S30518
R:Boulay, F.; Mery, L.; Tardif, M.; Bouchon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
A:Title: Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60
A:Reference number: A37963; MUID:91175748; PMID:2007135
A:Accession: A37963
A:Molecule type: mRNA
A:Residues: 1-350 <BOU>
A:Cross-references: UNIPROT:P21730; GB:J05327; NID:G179699; PIDN:AAAG2831.1; PID:G179700
R:Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
A:Title: The chemotactic receptor for human C5a anaphylatoxin.
A:Reference number: S13646; MUID:91156029; PMID:1847994
A:Accession: S13646
A:Molecule type: mRNA
A:Residues: 1-350 <GR>
A:Cross-references: EMBL:X58674; NID:G29568; PIDN:CAB37830.1; PID:G4467832
R:Gerard, N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A:Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of th
A:Reference number: 152417; MUID:93192225; PMID:8393526
A:Accession: 152417
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:S56556; GB:S56557; NID:G298577; NID:G298578
C:Genetics:
A:Gene: GDB:CSR1; C5A; C5AR
A:Cross-references: GDB:128856; OMIM:113995
A:Map position: 19q13.3-19q13.4
A:Introns: 1/3
A:Note: the list of introns may be incomplete
C:Function:
A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymor
F:1-37/Domain: extracellular #status predicted <EX1>
F:38-61/Domain: transmembrane #status predicted <TM1>
F:62-71/Domain: intracellular #status predicted <IN1>
F:72-94/Domain: transmembrane #status predicted <TM2>
F:95-110/Domain: extracellular #status predicted <EX2>
F:111-132/Domain: transmembrane #status predicted <TM3>
F:133-149/Domain: intracellular #status predicted <IN2>
F:150-174/Domain: transmembrane #status predicted <TM4>
F:175-206/Domain: extracellular #status predicted <EX3>
F:207-227/Domain: transmembrane #status predicted <TM5>
F:228-242/Domain: intracellular #status predicted <IN3>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:265-283/Domain: extracellular #status predicted <EX4>
F:284-307/Domain: transmembrane #status predicted <TM7>
F:308-350/Domain: intracellular #status predicted <IN4>
F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.9%; Score 9; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.95; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 VFKPIWCQN 132
Db 138 VFKPIWCQN 146

RESULT 7
S25244
regulatory protein ntcA - Synecchococcus sp. (strain PCC 7942)
C:Species: Synecchococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S25244
R;Vega-Palas, M.A.; Flores, E.; Herrero, A.
Mol. Microbiol. 6, 1853-1859, 1992
A;Title: Ntca, a global nitrogen regulator from the cyanobacterium *Synechococcus* that be
A;Reference number: S25244; MUID:92334161; PMID:1630321
A;Accession: S25244
A;Molecule type: DNA
A;Residues: 1-222 <VEG>
A;Cross-references: UNIPROT:P29283; EMBL:X60197; PIDN:CAA42755.1; PID:g47622
C;Genetics:
A;Gene: ntca
C;Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding d
C;Keywords: DNA binding; transcription regulation

Query Match 1.7%; Score 8; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 396 FGVLSLLT 403
|||||
DB 74 FGVLSLLT 81

RESULT 8
B48640
regulatory protein ntca - Anabaena sp. (strain PCC 7120)
N;Alternate names: regulatory protein bifa
C;Species: Anabaena sp.
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: B48640; A40653; S32665
R;Frietas, J.B.; Merida, A.; Herrero, A.; Martin-Nieto, J.; Flores, E.
J. Bacteriol. 175, 5710-5713, 1993
A;Title: General distribution of the nitrogen control gene ntca in cyanobacteria.
A;Reference number: A48640; MUID:93374871; PMID:8366058
A;Accession: B48640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <FRI>
A;Cross-references: UNIPROT:Q05061; EMBL:X71608; NID:G296875; PIDN:CAA50608.1; PID:G2968
R;Wei, T.F.; Ramasubramanian, T.S.; Pu, F.; Golden, J.W.
J. Bacteriol. 175, 4025-4035, 1993
A;Title: Anabaena sp. strain PCC 7120 bifa gene encoding a sequence-specific DNA-binding
A;Reference number: A40653; MUID:93308081; PMID:8391534
A;Accession: A40653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <WEI>
A;Cross-references: GB:L10036; NID:g142008; PIDN:AAD04183.1; PID:g142009
C;Genetics:
A;Gene: ntca; bifa
C;Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding d
C;Keywords: DNA binding; transcription regulation
F;176-195/Region: helix-turn-helix crp-type motif

Query Match 1.7%; Score 8; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 396 FGVLSLLT 403
|||||
DB 75 FGVLSLLT 82

RESULT 9
AH2354
nitrogen-responsive regulatory protein ntca [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
A;Accession: AH2354
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2354
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <KUR>
A;Cross-references: UNIPROT:Q05061; GB:BA000019; PIDN:BAB76091.1; PID:g17133528; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: ntca
C;Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding d
Query Match 1.7%; Score 8; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 396 FGVLSLLT 403
|||||
DB 75 FGVLSLLT 82

RESULT 10
D84968
hypothetical protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
A;Accession: D84968
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: D84968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: YJJT; BU328

Query Match 1.7%; Score 8; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 NLYSNVEK 260
|||||
DB 196 NLYSNVEK 203

RESULT 11
A46525
complement C5a anaphylatoxin receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: A46525
R;Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
J. Immunol. 149, 2600-2606, 1992
A;Title: Structural diversity in the extracellular faces of peptidergic G-protein-couple
A;Reference number: A46525; MUID:93017861; PMID:1401897
A;Accession: A46525
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-351 <GER>
A;Cross-references: GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
A;Experimental source: BALB/C
A;Note: sequence extracted from NCBI backbone (NCBI:P116075)
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F;1-37/Domain: extracellular #status predicted <EX1>
F;38-61/Domain: transmembrane #status predicted <TM1>

F:62-71/Domain: intracellular #status predicted <IN1>
 F:72-94/Domain: transmembrane #status predicted <TM2>
 F:95-110/Domain: extracellular #status predicted <EX2>
 F:111-132/Domain: transmembrane #status predicted <TM3>
 F:133-149/Domain: intracellular #status predicted <IN2>
 F:150-174/Domain: transmembrane #status predicted <TM4>
 F:175-207/Domain: extracellular #status predicted <EX3>
 F:208-228/Domain: transmembrane #status predicted <TM5>
 F:229-243/Domain: intracellular #status predicted <IN3>
 F:244-265/Domain: transmembrane #status predicted <TM6>
 F:266-284/Domain: extracellular #status predicted <EX4>
 F:285-308/Domain: transmembrane #status predicted <TM7>
 F:309-351/Domain: intracellular #status predicted <IN4>
 F:6/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 8; DB 1; Length 351;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 VFKPIWQ 131
 |||||

Db 138 VFKPIWQ 145
 |||||

RESULT 12

A:Species: G protein-coupled receptor GPR1 - human

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C:Accession: A55733

R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L

Genomics 23, 609-618, 1994

A:Title: Cloning of human genes encoding novel G protein-coupled receptors.

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

A:Reference number: A55733; MUID:95154831; PMID:7851889

A:Accession: A55733

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-355 <MAR>

A:Cross-references: UNIPROT:P46091; GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g577413

C:Genetics:

A:Gene: GDB:GPR1

A:Cross-references: GDB:371707; OMIM:600239

A:Map position: 15q25-15q26.1

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 1.7%; Score 8; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 LNMFAVP 111
 |||||

Db 119 LNMFAVP 126
 |||||

RESULT 13

JC7356

A:Species: leukotriene B4 receptor 2, BLTR2 - human

C:Species: Homo sapiens (man)

C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004

C:Accession: JC7356

R:Tryselius, Y.; Nilsson, N.E.; Kotarsky, K.; Olde, B.; Oman, C.

Biochem. Biophys. Res. Commun. 274, 377-382, 2000

A:Title: Cloning and characterization of cDNA encoding a novel human leukotriene B4 receptor

A:Reference number: JC7356

A:Accession: JC7356

A:Molecule type: mRNA

A:Residues: 1-389 <TRY>

A:Cross-references: UNIPROT:Q9NPC1; GB:AF277230

A:Experimental source: leukocyte

C:Comment: This receptor, belonging to the superfamily of seven-transmembrane/heptahelical

C:Genetics:

A:Gene: bltr2

A:Map position: 14
 C:Keywords: disulfide bond; leukocyte; receptor; transmembrane protein

Query Match 1.7%; Score 8; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 LLGLPGNG 42
 |||||

Db 63 LLGLPGNG 70
 |||||

RESULT 14

G70439

A:Title: hypothetical protein aq_1618 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: G70439

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: G70439

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-413 <AQF>

A:Cross-references: UNIPROT:O67545; GB:AB000748; NID:g2983960; PIDN:AAO07516.1; PID:g298

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_1618

Query Match 1.7%; Score 8; DB 2; Length 413;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 396 FGVLSLLT 403
 |||||

Db 330 FGVLSLLT 337
 |||||

RESULT 15

A35375

A:Title: alpha-1-adrenergic receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C:Accession: A35375

R:Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Fremieu Jr., R.T.; Yang-Feng,

J. Biol. Chem. 265, 8183-8189, 1990

A:Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rec

A:Reference number: A35375; MUID:90243698; PMID:1970822

A:Accession: A35375

A:Molecule type: mRNA

A:Residues: 1-466 <SCH>

A:Cross-references: UNIPROT:P18130; GB:J05426; NID:g162663; PIDN:AAA30374.1; PID:g162664

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 1.7%; Score 8; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 SLPRGSAR 248
 |||||

Db 402 SLPRGSAR 409
 |||||

Search completed: April 13, 2005, 10:06:40
 Job time : 69 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2005, 09:48:18 ; Search time 184 Seconds

(without alignment)
1341.425 Million cell updates/sec

Title: US-10-764-649-2

Perfect score: 482

Sequence: 1 MASFSATNSDLSQPWNE.....TRSTHCPNNVNSRNSTTV 482

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	100.0	482	1	C3AR_HUMAN
2	57	11.8	481	2	Q8TAC8
3	30	6.2	477	1	C3AR_MOUSE
4	30	6.2	477	2	Q8C6R2
5	29	6.0	473	1	C3AR_RAT
6	19	3.9	475	1	C3AR_CAVPO
7	11	2.3	346	2	Q8T3R0
8	11	2.3	350	2	Q8UNA4
9	10	2.1	309	1	CLT2_MOUSE
10	10	2.1	309	1	CLT2_RAT
11	10	2.1	309	2	Q8R528
12	10	2.1	337	1	CSL2_HUMAN
13	10	2.1	337	2	Q8NW08
14	10	2.1	337	2	Q8NQ99
15	10	2.1	337	2	Q8NWR0
16	10	2.1	345	1	CLT2_PIG
17	9	1.9	110	2	Q71TA6
18	9	1.9	193	2	Q83IK8
19	9	1.9	212	1	Y7FB_ECOLI
20	9	1.9	224	2	Q8FAH3
21	9	1.9	224	2	Q8XC11
22	9	1.9	320	2	Q8HZP0
23	9	1.9	340	1	CSAR_GORGO
24	9	1.9	340	1	CSAR_PANTR
25	9	1.9	350	1	CSAR_HUMAN
26	9	1.9	350	1	CSAR_RABIT
27	9	1.9	350	2	Q8BDQ5
28	9	1.9	353	2	Q8K087
29	9	1.9	554	2	Q8GJF7
30	9	1.9	739	2	Q6MKW0
31	9	1.9	856	2	Q82VX6

32	8	1.7	72	2	Q24862	Q24862	entamoeba h
33	8	1.7	102	2	Q8H671	Q8H671	oryza sativ
34	8	1.7	112	2	Q866H1	Q866H1	bos taurus
35	8	1.7	134	2	Q8L895	Q8L895	prochloroco
36	8	1.7	205	2	Q8KPE6	Q8KPE6	prochloroco
37	8	1.7	213	2	Q8L1A9	Q8L1A9	rattus norv
38	8	1.7	214	2	Q8E9W0	Q8E9W0	shewanella
39	8	1.7	220	2	Q8ESJ9	Q8ESJ9	rattus norv
40	8	1.7	222	1	NTCA_SYN7	NTCA_SYN7	synchococc
41	8	1.7	222	2	Q7TUN1	Q7TUN1	prochloroco
42	8	1.7	223	1	NTCA_ANASP	NTCA_ANASP	anabaena sp
43	8	1.7	223	2	Q6YNZ3	Q6YNZ3	nostoc punc
44	8	1.7	224	2	Q30778	Q30778	synchococc
45	8	1.7	237	2	Q7TTY5	Q7TTY5	synchococc
46	8	1.7	243	2	Q93UM0	Q93UM0	synchococc
47	8	1.7	244	2	Q7TUG3	Q7TUG3	prochloroco
48	8	1.7	244	2	Q7VDU1	Q7VDU1	prochloroco
49	8	1.7	268	2	Q8KY22	Q8KY22	rhizobium e
50	8	1.7	284	2	Q8MZS9	Q8MZS9	entamoeba h
51	8	1.7	284	2	Q8MZT0	Q8MZT0	entamoeba h
52	8	1.7	332	2	Q7TOX4	Q7TOX4	xenopus lae
53	8	1.7	338	1	RSMC_BUCAI	RSMC_BUCAI	buchnera ap
54	8	1.7	339	1	GP33_MOUSE	GP33_MOUSE	mus musculu
55	8	1.7	342	2	Q6ZM91	Q6ZM91	brachydanio
56	8	1.7	347	1	CSAR_MOUSE	CSAR_MOUSE	mus musculu
57	8	1.7	352	1	CSAR_RAT	CSAR_RAT	rattus norv
58	8	1.7	353	1	APJ_XENLA	APJ_XENLA	xenopus lae
59	8	1.7	354	1	OPSD_GAMAF	OPSD_GAMAF	gambusia af
60	8	1.7	355	1	GPRI_HUMAN	GPRI_HUMAN	homo sapien
61	8	1.7	355	1	GPRI_MACMU	GPRI_MACMU	macaca mula
62	8	1.7	355	2	Q6NVX4	Q6NVX4	homo sapien
63	8	1.7	355	2	Q95LH1	Q95LH1	macaca fasc
64	8	1.7	358	1	L4R2_RAT	L4R2_RAT	rattus norv
65	8	1.7	359	1	PYRD_CORST	PYRD_CORST	corynebacte
66	8	1.7	360	1	L4R2_MOUSE	L4R2_MOUSE	mus musculu
67	8	1.7	382	1	GP44_MOUSE	GP44_MOUSE	mus musculu
68	8	1.7	389	1	L4R2_HUMAN	L4R2_HUMAN	homo sapien
69	8	1.7	395	1	GP44_HUMAN	GP44_HUMAN	homo sapien
70	8	1.7	400	2	Q868G2	Q868G2	branchiost
71	8	1.7	403	2	Q6XKD3	Q6XKD3	rattus norv
72	8	1.7	407	2	Q9KJ93	Q9KJ93	streptomyce
73	8	1.7	408	2	Q9LCV6	Q9LCV6	streptomyce
74	8	1.7	413	1	YG18_AQUAE	YG18_AQUAE	aquifex aeo
75	8	1.7	449	2	Q65UT3	Q65UT3	mannheimia
76	8	1.7	466	1	ALAA_BOVIN	ALAA_BOVIN	bos taurus
77	8	1.7	518	2	Q81301	Q81301	arabidopsis
78	8	1.7	533	2	Q6NSY7	Q6NSY7	rhodospseudo
79	8	1.7	554	2	Q7NV37	Q7NV37	chromobacte
80	8	1.7	603	2	Q6GDN2	Q6GDN2	staphylococ
81	8	1.7	705	2	Q88HD0	Q88HD0	pseudomonas
82	8	1.7	810	2	Q7QUH4	Q7QUH4	giardia lam
83	8	1.7	1285	1	SLI7_ENTHI	SLI7_ENTHI	entamoeba h
84	8	1.7	1292	2	Q24835	Q24835	entamoeba h
85	8	1.7	2799	1	G112_HUMAN	G112_HUMAN	homo sapien
86	7	1.5	16	2	Q6LBM5	Q6LBM5	xenopus lae
87	7	1.5	48	2	Q88Q87	Q88Q87	pseudomonas
88	7	1.5	49	2	Q67RN3	Q67RN3	symbiobacte
89	7	1.5	53	2	Q6Z7G2	Q6Z7G2	oryza sativ
90	7	1.5	54	1	MRGG_HUMAN	MRGG_HUMAN	homo sapien
91	7	1.5	58	2	Q9K3A9	Q9K3A9	bacillus su
92	7	1.5	62	2	Q75GR9	Q75GR9	oryza sativ
93	7	1.5	62	2	Q7M585	Q7M585	tupaia aden
94	7	1.5	63	2	Q87UJ8	Q87UJ8	pseudomonas
95	7	1.5	65	2	Q89IG9	Q89IG9	bradyrhizob
96	7	1.5	65	2	Q8DMT8	Q8DMT8	synchococc
97	7	1.5	66	2	Q8KHU8	Q8KHU8	rickettsia
98	7	1.5	66	2	Q8KTB5	Q8KTB5	rickettsia
99	7	1.5	66	2	Q8KTC0	Q8KTC0	rickettsia
100	7	1.5	66	2	Q7B6F4	Q7B6F4	rickettsia
101	7	1.5	74	2	Q7WWR6	Q7WWR6	canis famil
102	7	1.5	74	2	Q95162	Q95162	canis famil
103	7	1.5	79	2	Q8VAL9	Q8VAL9	white spot
104	7	1.5	84	2	Q92J92	Q92J92	rickettsia

105	7	1.5	90	2	QY2H3	Q7y2h3 stx2 conver	178	7	1.5	217	2	Q6D320	Q6d320 erwinia cal
106	7	1.5	90	2	Q7Y2Y6	Q7y2y6 stx1 conver	179	7	1.5	219	2	Q7MGA0	Q7mga0 vibrio vuln
107	7	1.5	92	2	Q82FR4	Q82fr4 streptomyc	180	7	1.5	221	2	Q6K5M2	Q6k5m2 oryza sativ
108	7	1.5	95	2	Q6ZL66	Q6zL66 oryza sativ	181	7	1.5	226	2	Q9BSN7	Q9bn7 homo sapien
109	7	1.5	97	2	Q9N0D1	Q9n0d1 macaca fasc	182	7	1.5	227	1	PYRH_AERPE	Q9y40 aeropyrum p
110	7	1.5	97	2	Q9PXZ6	Q9pxz6 human t-lym	183	7	1.5	229	2	Q8RW15	Q8rw15 aeropyrum p
111	7	1.5	101	2	Q6W393	Q6w393 uncultured	184	7	1.5	230	2	Q9HRS0	Q9hr0 halobacteri
112	7	1.5	102	2	Q6TMM7	Q6tmw7 streptomyc	185	7	1.5	233	1	AMP_ONYPE	Q7mt6 onion yello
113	7	1.5	104	2	Q7N4K0	Q7n4k0 photorhabdu	186	7	1.5	233	2	Q9AIR8	Q9air8 aster yello
114	7	1.5	107	2	Q9P1N8	Q9p1n8 homo sapien	187	7	1.5	233	2	Q6S189	Q6s189 african swi
115	7	1.5	110	2	Q8WQ91	Q8wq91 carcinus ma	188	7	1.5	233	2	Q6S189	Q6s189 african swi
116	7	1.5	110	2	Q683N4	Q683n4 carcinus ma	189	7	1.5	233	2	Q6S234	Q6s234 african swi
117	7	1.5	110	2	Q683N5	Q683n5 carcinus ma	190	7	1.5	234	1	NOLW_RHIFR	P53112 rhizobium f
118	7	1.5	110	2	Q683N6	Q683n6 carcinus ma	191	7	1.5	234	1	NOLW_RHISN	P55712 rhizobium f
119	7	1.5	110	2	Q683N7	Q683n7 carcinus ma	192	7	1.5	237	2	Q8T8Y1	Q8t8y1 drosophila
120	7	1.5	111	2	Q8JUX0	Q8jux0 feline papi	193	7	1.5	237	2	Q9VDX9	Q9vdx9 drosophila
121	7	1.5	111	2	Q8QSA0	Q8qsa0 felis domes	194	7	1.5	238	2	Q9NT39	Q9nt39 homo sapien
122	7	1.5	114	2	Q9UDC9	Q9udc9 homo sapien	195	7	1.5	241	2	Q9Q9K8	Q9q9k8 fowl adenov
123	7	1.5	116	2	Q85CW1	Q85cw1 opisthoproc	196	7	1.5	242	2	Q9Q9K8	Q9q9k8 fowl adenov
124	7	1.5	117	2	Q7SVE3	Q7sve3 human immun	197	7	1.5	243	1	AXZ8_SOYEN	P13089 glycine mar
125	7	1.5	119	2	Q8K4I8	Q8k4i8 streptomyc	198	7	1.5	243	2	Q8DI69	Q8di69 synchococc
126	7	1.5	125	2	Q8FC55	Q8fc55 escherichia	199	7	1.5	245	2	Q9XBQ5	Q9xbq5 rhodoplanes
127	7	1.5	126	2	Q8T449	Q8t449 drosophila	200	7	1.5	247	2	Q8N2X0	Q8n2x0 homo sapien
128	7	1.5	126	2	Q9WJ36	Q9wj36 tick-borne	201	7	1.5	247	1	YFGD_SCHPO	Q13952 schizosacch
129	7	1.5	135	1	P2Y4_MERUN	Q99pe4 meriones un	202	7	1.5	250	2	Q7NS34	Q7ns34 chromobacte
130	7	1.5	135	2	Q8XQT7	Q8xqt7 ralstonia s	203	7	1.5	250	2	Q8AWL5	Q8aw15 gymnocephal
131	7	1.5	137	2	Q63XAL	Q63xal burkholderi	204	7	1.5	253	2	Q8AWL5	Q8aw15 gymnocephal
132	7	1.5	140	2	Q785D2	Q785d2 neurospora	205	7	1.5	254	2	Q754D8	Q754d8 ashbya goss
133	7	1.5	141	2	Q88P08	Q88p08 pseudomonas	206	7	1.5	254	2	Q68FD8	Q68fd8 mus musculu
134	7	1.5	145	2	Q8EWS3	Q8ews3 mycoplasma	207	7	1.5	257	2	Q8U4R9	Q8u4r9 pyrococcus
135	7	1.5	148	2	Q80801	Q80801 arabidopsis	208	7	1.5	257	2	Q89KL8	Q89kl8 bradyrhizob
136	7	1.5	150	2	Q9PXZ7	Q9pxz7 human t-lym	209	7	1.5	259	2	Q6IT13	Q6it13 edwardsiell
137	7	1.5	152	2	Q653N9	Q653n9 oryza sativ	210	7	1.5	262	2	Q24050	Q24050 drosophila
138	7	1.5	153	2	Q6KA31	Q6ka31 oryza sativ	211	7	1.5	262	2	Q8E6T5	Q8e6t5 streptococc
139	7	1.5	156	1	YF60_HAEIN	P4253 haemophilus	212	7	1.5	263	1	SSUC_ECOLI	P75951 escherichia
140	7	1.5	156	2	Q9FTX5	Q9ftx5 oryza sativ	213	7	1.5	263	2	Q8XDE5	Q8xde5 escherichia
141	7	1.5	157	2	Q8H080	Q8h080 oryza sativ	214	7	1.5	264	2	Q8PHQ2	Q8phq2 xanthomonas
142	7	1.5	161	2	Q7T5L0	Q7t5l0 cryptophleb	215	7	1.5	264	2	Q8XZQ5	Q8xzq5 ralestonia s
143	7	1.5	165	2	Q8TJ13	Q8tj13 methanosarc	216	7	1.5	264	2	Q8FJ94	Q8fj94 escherichia
144	7	1.5	167	1	ELI6_HORVU	P14896 hordeum vul	217	7	1.5	265	2	Q6CYU3	Q6cyu3 erwinia car
145	7	1.5	167	2	Q6CKZ1	Q6ckz1 kluyveromyc	218	7	1.5	265	2	Q7PIQ6	Q7piq6 anopheles g
146	7	1.5	169	2	Q6ZDF8	Q6zdf8 oryza sativ	219	7	1.5	265	2	Q665B5	Q665b5 yersinia ps
147	7	1.5	170	2	Q8N2G2	Q8n2g2 homo sapien	220	7	1.5	265	2	Q8ZB03	Q8zb03 yersinia pe
148	7	1.5	170	2	Q9H7G5	Q9h7g5 homo sapien	221	7	1.5	266	2	Q96MV7	Q96mv7 homo sapien
149	7	1.5	176	2	Q9P0Q6	Q9p0q6 homo sapien	222	7	1.5	266	2	Q6EFFZ0	Q6effz0 acinetobact
150	7	1.5	176	2	Q75HP6	Q75hf6 oryza sativ	223	7	1.5	266	2	Q8U649	Q8u649 agrobacteri
151	7	1.5	177	1	AG2T_RAT	P34977 rattus norv	224	7	1.5	267	2	Q7V2M9	Q7v2m9 prochloroco
152	7	1.5	178	2	Q6O831	Q6o831 homo sapien	225	7	1.5	270	2	Q9YBG4	Q9ybg4 aeropyrum p
153	7	1.5	178	2	Q94YD3	Q94yd3 sorex ungui	226	7	1.5	270	2	Q8F485	Q8f485 leptospira
154	7	1.5	182	2	Q95313	Q95313 soriculus f	227	7	1.5	271	2	Q9AVC8	Q9avc8 varanus pil
155	7	1.5	182	2	Q6A9P3	Q6a9p3 propionibac	228	7	1.5	272	2	Q756T6	Q756t6 ashbya goss
156	7	1.5	182	2	Q9DK76	Q9dk76 human immun	229	7	1.5	273	2	Q43521	Q43521 lycopersico
157	7	1.5	183	2	Q6D932	Q6d932 erwinia car	230	7	1.5	273	2	Q6MMA7	Q6mma7 bdellovibri
158	7	1.5	188	2	Q72JV9	Q72jv9 thermus the	231	7	1.5	274	1	BAG1_HUMAN	Q99933 homo sapien
159	7	1.5	191	2	Q8RUQ0	Q8ruq0 oryza sativ	232	7	1.5	276	2	Q833V9	Q833v9 enterococcu
160	7	1.5	192	2	Q9HME6	Q9hme6 halobacteri	233	7	1.5	276	2	Q88206	Q88206 molluscum c
161	7	1.5	195	2	Q6GVN4	Q6gvn4 homo sapien	234	7	1.5	277	2	Q983R6	Q983r6 rhizobium l
162	7	1.5	196	2	Q8SSK4	Q8ssk4 encephalito	235	7	1.5	277	2	Q74F93	Q74f93 geobacter s
163	7	1.5	199	2	Q8D4P8	Q8d4p8 vibrio vuln	236	7	1.5	281	2	Q9YGN6	Q9ygn6 xenopus lae
164	7	1.5	200	2	Q84979	Q84979 porcine rep	237	7	1.5	284	2	Q9V4R9	Q9v4r9 drosophila
165	7	1.5	201	2	Q43890	Q43890 acetobacter	238	7	1.5	284	2	Q9RV15	Q9rv15 deinococcus
166	7	1.5	201	2	Q811B4	Q811e4 mus musculu	239	7	1.5	288	2	Q89FK1	Q89fk1 bradyrhizob
167	7	1.5	203	2	Q938Y4	Q938y4 uncultured	240	7	1.5	288	2	Q8QKY3	Q8qky3 ectocarpus
168	7	1.5	203	2	Q938Y5	Q938y5 uncultured	241	7	1.5	289	2	Q8WVU6	Q8wvu6 homo sapien
169	7	1.5	203	2	Q6N9H3	Q6n9h3 rhodopseudo	242	7	1.5	289	2	Q9NZ63	Q9nz63 homo sapien
170	7	1.5	207	2	Q21559	Q21559 oryzomys al	243	7	1.5	289	2	Q99JW3	Q99jw3 mus musculu
171	7	1.5	207	2	Q93HS3	Q93hs3 bradyrhizob	244	7	1.5	290	2	Q89QZ1	Q89qz1 bradyrhizob
172	7	1.5	211	2	Q80319	Q80319 brachydanio	245	7	1.5	290	2	Q640Y5	Q640y5 xenopus lae
173	7	1.5	212	2	Q26453	Q26453 methanobact	246	7	1.5	291	2	Q91CD1	Q91cd1 ochrobactru
174	7	1.5	212	2	Q6L596	Q6l596 oryza sativ	247	7	1.5	291	2	Q8YWP9	Q8ywp9 anabaena sp
175	7	1.5	215	2	Q7WT32	Q7wt32 streptomyc	248	7	1.5	292	2	Q7ZVU5	Q7zvu5 brachydanio
176	7	1.5	215	2	Q6P0G3	Q6p0g3 brachydanio	249	7	1.5	293	2	Q6Z1N2	Q6z1n2 oryza sativ
177	7	1.5	217	2	Q83RY2	Q83ry2 shigella fl	250	7	1.5	294	2	Q8CCX5	Q8ccx5 mus musculu

251	7	1.5	294	2	Q91B66	Q91b66 fowl adenov	324	7	1.5	349	2	Q6P852	Q6p852 xenopus tro
252	7	1.5	294	2	Q8B5H3	Q8b5h3 fowl adenov	325	7	1.5	351	2	Q986W6	Q986w6 rhizobium l
253	7	1.5	294	2	Q8B5H4	Q8b5h4 fowl adenov	326	7	1.5	352	2	O62311	O62311 caenorhabdi
254	7	1.5	297	2	Q84Q82	Q84q82 elaeis guin	327	7	1.5	354	2	O62KP4	O62kp4 oryza sativ
255	7	1.5	298	2	Q7SY08	Q7sy08 brachydanio	328	7	1.5	354	2	O7NSP6	O7nsf6 chromobacte
256	7	1.5	299	2	Q7PNV7	Q7pny7 anopheles g	329	7	1.5	355	2	O88DH5	O88dh5 pseudomonas
257	7	1.5	299	2	Q8Z828	Q8z828 salmonella	330	7	1.5	356	1	O7S388	O7s388 homo sapien
258	7	1.5	299	2	Q8ZQ87	Q8zq87 salmonella	331	7	1.5	356	2	O6NW55	O6nw55 homo sapien
259	7	1.5	299	2	Q8FJ99	Q8fj99 escherichia	332	7	1.5	357	2	O6TLJ0	O6tlj0 mustela put
260	7	1.5	299	2	Q8X6K8	Q8x6k8 escherichia	333	7	1.5	359	1	AG2R_BOVIN	AG2r0104 bos taurus
261	7	1.5	300	2	Q6RXC9	Q6rcx9 human cytom	334	7	1.5	359	1	AG2R_CANFA	AG2r240 canis famil
262	7	1.5	301	2	Q7RJ07	Q7rj07 plasmodium	335	7	1.5	359	1	AG2R_CAVPO	AG2r266 cavia porce
263	7	1.5	301	2	O6A1K7	O6aik7 lycopersico	336	7	1.5	359	1	AG2R_CHICK	AG2r785 gallus gall
264	7	1.5	302	2	O6EYQ1	O6eyq1 sulfolobus	337	7	1.5	359	1	AG2R_HUMAN	AG2r056 homo sapien
265	7	1.5	304	2	Q8N7J6	Q8n7j6 homo sapien	338	7	1.5	359	1	AG2R_MELGA	AG2r336 meleagris g
266	7	1.5	305	2	O7SZR2	O7szr2 brachydanio	339	7	1.5	359	1	AG2R_MERUN	AG2r210 meriones un
267	7	1.5	306	1	DDL_BUCAP	O51927 bruchynera ap	340	7	1.5	359	1	AG2R_MOUSE	AG2r754 mus musculu
268	7	1.5	306	2	Q8Y980	Q8y980 listeria mo	341	7	1.5	359	1	AG2R_PANTR	AG2r919 pan troglod
269	7	1.5	311	2	O7SFM7	O7sfm7 neurospora	342	7	1.5	359	1	AG2R_PIG	AG2r055 sus scrofa
270	7	1.5	312	2	Q8GV86	Q8gv86 solanum tub	343	7	1.5	359	1	AG2R_RABIT	AG2r976 oryctolagus
271	7	1.5	313	2	Q6SWJ4	Q6swj4 human cytom	344	7	1.5	359	1	AG2R_RAT	AG2r095 rattus norv
272	7	1.5	314	1	PLYD_ERWCA	P24112 erwinia car	345	7	1.5	359	1	AG2R_SHEEP	O77590 ovis aries
273	7	1.5	314	2	Q8PY28	Q8py28 human cytom	346	7	1.5	359	1	AG2S_HUMAN	AG2r3725 homo sapien
274	7	1.5	314	2	O68PF8	Q68pf8 xenopus lae	347	7	1.5	359	1	AG2S_MOUSE	AG2r755 mus musculu
275	7	1.5	317	2	Q94V44	Q94va4 varanus sca	348	7	1.5	359	1	AG2S_RAT	AG2r089 rattus norv
276	7	1.5	317	2	Q66FW2	Q66fw2 yersinia ps	349	7	1.5	359	2	O8TBK4	O8tbk4 homo sapien
277	7	1.5	317	2	Q8ZAJ0	Q8zaj0 yersinia pe	350	7	1.5	359	2	Q6NUP5	Q6nup5 homo sapien
278	7	1.5	318	2	Q94V90	Q94v90 varanus tri	351	7	1.5	359	2	O9N0U1	O9n0u1 ovis aries
279	7	1.5	318	2	Q94V93	Q94v93 varanus tim	352	7	1.5	359	2	O8BU69	Q8bu69 mus musculu
280	7	1.5	318	2	Q927A9	Q927a9 listeria in	353	7	1.5	359	2	O9EP93	O9ep93 cavia porce
281	7	1.5	318	2	O9I221	Q9i221 pseudomonas	354	7	1.5	359	2	O9EQ89	O9eqr9 meriones un
282	7	1.5	319	2	Q94VC5	Q94vc5 varanus pri	355	7	1.5	359	2	O7TGS2	O7tgs2 murine hepa
283	7	1.5	320	2	Q7SDX9	Q7sdx9 neurospora	356	7	1.5	361	1	P2Y4_MOUSE	Q9j187 mus musculu
284	7	1.5	320	2	Q94VH6	Q94vh6 varanus gla	357	7	1.5	361	1	P2Y4_RAT	O35811 rattus norv
285	7	1.5	320	2	Q9DGH4	Q9dgh4 salmo salar	358	7	1.5	361	2	O8ZW99	Q8zw99 pyrobaculum
286	7	1.5	321	2	Q94V87	Q94v87 varanus var	359	7	1.5	361	2	O19607	O19607 caenorhabdi
287	7	1.5	321	2	Q94V89	Q94ve9 varanus kom	360	7	1.5	363	1	E132_SOLTU	P52401 solanum tub
288	7	1.5	321	2	Q94V12	Q94vi2 varanus gig	361	7	1.5	363	2	O65360	O65360 solanum tub
289	7	1.5	321	2	Q6I7T5	Q6i7t5 varanus kom	362	7	1.5	363	2	O87BQ6	Q87bq6 xyella fas
290	7	1.5	322	2	Q6CZ09	Q6cz09 erwinia car	363	7	1.5	363	2	O8FHX9	O8fhx9 escherichia
291	7	1.5	325	2	Q9RR76	Q9rrt6 deinococcus	364	7	1.5	363	2	O9PAY0	Q9pay0 xyella fas
292	7	1.5	327	2	O751B9	O751e9 ashbya goss	365	7	1.5	364	2	O68DM8	Q68dm8 homo sapien
293	7	1.5	328	1	E133_SOLTU	P52402 solanum tub	366	7	1.5	365	1	P2Y4_HUMAN	P51582 homo sapien
294	7	1.5	328	2	Q8IXE2	Q8ixe2 homo sapien	367	7	1.5	367	1	CCR3_MOUSE	O88410 mus musculu
295	7	1.5	328	2	Q722P6	Q722p6 listeria mo	368	7	1.5	367	2	Q9RP77	Q9rp77 pasteurella
296	7	1.5	328	2	Q9EDG8	Q9edg8 human immun	369	7	1.5	367	2	O9JII9	Q9jii9 rattus norv
297	7	1.5	328	2	Q9EEI6	Q9eei6 human immun	370	7	1.5	367	2	O9QWN6	Q9qwn6 mus musculu
298	7	1.5	328	2	Q9EKU4	Q9eku4 human immun	371	7	1.5	371	1	WNT1_XENLA	P10108 xenopus lae
299	7	1.5	328	2	Q9ELF1	Q9elf1 human immun	372	7	1.5	371	2	O9GU63	Q9gu63 megoura vic
300	7	1.5	330	1	G843_HUMAN	O15552 homo sapien	373	7	1.5	371	2	O82PD8	Q82pd8 streptomyce
301	7	1.5	330	2	O58121	O58121 pyrococcus	374	7	1.5	373	1	P2Y2_MOUSE	P35383 mus musculu
302	7	1.5	330	2	Q9VCK6	Q9vck6 mus musculu	375	7	1.5	374	1	P2Y2_RAT	P41232 rattus norv
303	7	1.5	330	2	Q76E16	Q76e16 rattus norv	376	7	1.5	377	1	APJ_MOUSE	Q9wv08 mus musculu
304	7	1.5	331	2	O6K4Y0	O6k4y0 oryza sativ	377	7	1.5	377	1	APJ_RAT	Q9jhg3 rattus norv
305	7	1.5	332	2	Q7WND7	Q7wnd7 bordetella	378	7	1.5	377	1	P2Y2_HUMAN	P41231 homo sapien
306	7	1.5	333	2	Q20437	Q20437 caenorhabdi	379	7	1.5	377	2	O8BVF1	Q8bvf1 mus musculu
307	7	1.5	334	2	Q750K6	Q750k6 ashbya goss	380	7	1.5	379	2	O9YFW4	Q9yfw4 aeropyrum p
308	7	1.5	334	2	Q65DZ5	Q65dz5 bacillus li	381	7	1.5	379	2	O8N3D0	Q8n3d0 homo sapien
309	7	1.5	337	1	E131_SOLTU	P52400 solanum tub	382	7	1.5	380	1	APJ_HUMAN	P35414 homo sapien
310	7	1.5	340	2	Q8G7C9	Q8g7c9 bifidobacte	383	7	1.5	380	1	APJ_MACMU	O97666 macaca mula
311	7	1.5	343	1	MRGF_HUMAN	Q96am1 homo sapien	384	7	1.5	381	2	O82MB0	Q82mb0 streptomyce
312	7	1.5	343	1	MRGF_MOUSE	Q8vcj6 mus musculu	385	7	1.5	386	2	Q4YNS7	Q4yws7 anabaena sp
313	7	1.5	343	2	O6L5G1	P23749 rattus norv	386	7	1.5	387	1	D4DR_MOUSE	P51436 mus musculu
314	7	1.5	343	2	Q7TU90	Q7tu90 oryza sativ	387	7	1.5	387	2	O8BXS4	Q8bxs4 mus musculu
315	7	1.5	343	2	O7TU90	Q7tu90 prochloroco	388	7	1.5	388	2	O6P387	Q6p387 homo sapien
316	7	1.5	343	2	Q9QW32	Q9qw32 rattus sp.	389	7	1.5	388	2	O73PV0	O73pv0 treponema d
317	7	1.5	344	1	ULB6_HCMVA	P16833 human cytom	390	7	1.5	389	1	Y817_SCHPO	O14001 schizosacch
318	7	1.5	344	2	Q9HN44	Q9hn44 halobacteri	391	7	1.5	389	2	Q95018	Q95018 caenorhabdi
319	7	1.5	344	2	Q8BXK4	Q8bxk4 mus musculu	392	7	1.5	389	2	Q7TT80	Q7tt80 mus musculu
320	7	1.5	345	2	Q92E05	Q92e05 listeria in	393	7	1.5	391	1	BRB2_HUMAN	P30411 homo sapien
321	7	1.5	346	2	Q9GRY3	Q9gry3 caenorhabdi	394	7	1.5	392	2	Q9S3V9	Q9s3v9 bordetella
322	7	1.5	347	2	O72R14	Q72r14 leptospira	395	7	1.5	394	2	O8SRM9	Q8srm9 encephalico
323	7	1.5	348	2	Q9EMY0	Q9emy0 amsacta moo	396	7	1.5	394	2	Q7VCN7	Q7vcn7 prochloroco

543	7	1.5	620	1	KUP1_RHOPA	Q6n5f2 rhodopseudo	616	7	1.5	865	2	Q84W43	Q84w43 arabidopsis
544	7	1.5	620	2	Q8N91	Q8nj8 candida gla	617	7	1.5	867	2	Q8WN91	Q8wn91 bog taurus
545	7	1.5	620	2	Q6FWP2	Q6fwp2 candida gla	618	7	1.5	867	2	Q8W7C6	Q8w7c6 gallus gall
546	7	1.5	624	2	Q7MY79	Q7my79 photorhabdu	619	7	1.5	870	2	Q9PTB3	Q9ptb3 coturnix co
547	7	1.5	629	2	Q7NSV4	Q7nsy4 chromobacte	620	7	1.5	884	2	Q88213	Q88213 lactopacill
548	7	1.5	631	2	Q7NYD2	Q7nyd2 chromobacte	621	7	1.5	885	2	Q74AA7	Q74aa7 geobacter s
549	7	1.5	633	2	Q00355	Q00355 coprinus ci	622	7	1.5	892	2	Q8F846	Q8f846 leptospira
550	7	1.5	633	2	Q76Y18	Q76y18 bacterioph	623	7	1.5	894	2	Q8FXH7	Q8fxh7 candida gla
551	7	1.5	634	1	KUP2_RHOPA	Q6n5g6 rhodopseudo	624	7	1.5	898	2	Q8NI77	Q8ni77 homo sapien
552	7	1.5	634	2	Q8F706	Q8n596 rhodopseudo	625	7	1.5	898	2	Q86V85	Q86v85 homo sapien
553	7	1.5	636	1	DXS_COREF	Q8fp12 corynebacte	626	7	1.5	898	2	Q9H0F3	Q9h0f3 homo sapien
554	7	1.5	642	2	Q64B25	Q64b15 uncultured	627	7	1.5	905	2	Q8A284	Q8a284 bacteroides
555	7	1.5	642	2	Q26446	Q26446 methanobact	628	7	1.5	905	2	Q6IO23	Q6io23 mus musculu
556	7	1.5	642	2	Q72PD3	Q72pd3 leptospira	629	7	1.5	907	2	Q7U862	Q7u862 synechococc
557	7	1.5	650	2	Q8GS07	Q8gs07 arabidopsis	630	7	1.5	909	1	MTC2_YEAST	P53185 saccharomyc
558	7	1.5	653	2	Q7Q3B5	Q7q3b5 anopheles m	631	7	1.5	925	1	UVRA_ZYMO	O31151 zymomonas m
559	7	1.5	653	2	Q7QWY4	Q7qw44 giardia lam	632	7	1.5	929	2	Q6XG56	Q6xg56 trypanosoma
560	7	1.5	655	1	MYA_PYRAB	Q9v298 pyrococcus	633	7	1.5	929	2	Q75QN6	Q75qn6 arabidopsis
561	7	1.5	655	2	Q726K1	Q726k1 desulfovibr	634	7	1.5	929	2	Q6P9N3	Q6p9n3 mus musculu
562	7	1.5	656	2	Q99354	Q99354 tick-borne	635	7	1.5	946	2	Q9VJ04	Q9vj04 drosophila
563	7	1.5	657	1	UVRB_MYCPU	P58174 mycoplasma	636	7	1.5	946	2	Q9FFA8	Q9ffas arabidopsis
564	7	1.5	665	1	CVAI_RHIME	P19485 rhizobium m	637	7	1.5	951	2	Q6CL12	Q6cl12 kluyveromyc
565	7	1.5	668	2	Q7R8J8	Q7r8j8 plasmodium	638	7	1.5	958	1	YBS3_YEAST	P38086 saccharomyc
566	7	1.5	668	2	Q83CR8	Q83cr8 coxiella bu	639	7	1.5	962	2	Q8JXN5	Q8jxm5 fowl adenov
567	7	1.5	669	2	Q83C15	Q83ci5 coxiella bu	640	7	1.5	962	2	Q8QXY9	Q8qxy9 fowl adenov
568	7	1.5	677	2	Q8R251	Q8r251 mus musculu	641	7	1.5	968	2	Q63I12	Q63it2 burkholderi
569	7	1.5	685	2	Q8S0J3	Q8s0j3 oryza sativ	642	7	1.5	969	2	Q6ZU90	Q6zu90 homo sapien
570	7	1.5	687	2	Q6AX13	Q6axl3 brachydanio	643	7	1.5	970	2	Q6GZU9	Q6gzuz frog virus
571	7	1.5	687	2	Q74ZA2	Q74za2 ashbya goss	644	7	1.5	970	2	Q6YH66	Q6yh66 ambystoma t
572	7	1.5	689	2	Q9AWX9	Q9awx9 oryza sativ	645	7	1.5	985	1	REV1_YEAST	P12689 saccharomyc
573	7	1.5	691	2	Q87019	Q87019 cryptococcu	646	7	1.5	999	2	Q7RSF7	Q7rsa7 plasmodium
574	7	1.5	694	2	Q26439	Q26439 methanobact	647	7	1.5	1030	2	Q7S8D2	Q7s8d2 neurospora
575	7	1.5	696	2	Q7QCHC2	Q7qchc2 lactococcus	648	7	1.5	1044	2	Q6AVD8	Q6avd8 oryza sativ
576	7	1.5	697	2	Q74DM1	Q74dm1 geobacter s	649	7	1.5	1061	2	Q96998	Q96998 leishmania
577	7	1.5	700	2	O17951	O17951 caenorhabdi	650	7	1.5	1064	2	Q6NPT2	Q6npt2 arabidopsis
578	7	1.5	711	1	ETF2_MYXVL	Q9gk4 myxoma viru	651	7	1.5	1069	2	Q8CB37	Q8cb37 mus musculu
579	7	1.5	711	1	ETF2_SFVXA	Q9gk4 shope fibro	652	7	1.5	1086	2	Q43043	Q43043 schizosacch
580	7	1.5	719	2	Q8ET15	Q8et15 oceanobacil	653	7	1.5	1108	1	STV_ARATH	P33736 arabidopsis
581	7	1.5	719	2	Q8BS69	Q8bs69 mus musculu	654	7	1.5	1122	2	Q8S018	Q8s018 mycobacteri
582	7	1.5	720	2	O01605	O01605 caenorhabdi	655	7	1.5	1143	2	Q8CFE9	Q8cef9 mus musculu
583	7	1.5	724	2	Q72NE0	Q72ne0 leptospira	656	7	1.5	1165	2	Q6F3F9	Q6f3f9 mus musculu
584	7	1.5	724	2	Q9KFW8	Q9kfm8 bacillus ha	657	7	1.5	1178	2	Q7ZAL0	Q7zal0 streptococc
585	7	1.5	727	1	SAH_MOUSE	Q8bj11 mus musculu	658	7	1.5	1181	2	Q9UM06	Q9um06 homo sapien
586	7	1.5	758	1	YA93_SCHPO	Q9782 schizosacch	659	7	1.5	1189	1	SMC2_CHICK	Q90988 gallus gall
587	7	1.5	758	1	YF58_YEAST	Q99299 saccharomyc	660	7	1.5	1189	2	O18558	O18558 aedes aegypt
588	7	1.5	769	2	Q6BQM4	Q6bqm4 debaryomyc	661	7	1.5	1191	1	Y143_SYNY3	P74442 synechocyst
589	7	1.5	774	1	CUL1_DROME	Q24311 drosophila	662	7	1.5	1193	2	Q6F3F7	Q6f3f7 homo sapien
590	7	1.5	775	2	Q8LG30	Q8lga0 arabidopsis	663	7	1.5	1216	2	Q6ZMY3	Q6zmy3 homo sapien
591	7	1.5	775	2	Q9C5N5	Q9c5n5 arabidopsis	664	7	1.5	1220	2	Q7LCX9	Q7lcx9 homo sapien
592	7	1.5	775	2	Q9LUM3	Q9lum3 arabidopsis	665	7	1.5	1220	2	Q9UM05	Q9um05 homo sapien
593	7	1.5	781	1	POT8_ARATH	Q9m7j9 arabidopsis	666	7	1.5	1221	1	GL26_HUMAN	Q8esq4 homo sapien
594	7	1.5	788	1	REC2_HAETN	P44408 haemophilus	667	7	1.5	1221	2	Q6F3F8	Q6f3f8 homo sapien
595	7	1.5	791	2	Q8RI59	Q6ri99 rhizobium f	668	7	1.5	1222	1	RGY2_AERPE	Q9yc75 aeropyrum p
596	7	1.5	791	2	Q98RJ1	Q98rj1 mycoplasma	669	7	1.5	1222	2	Q8IXA4	Q8ixa4 homo sapien
597	7	1.5	795	2	Q9AYF1	Q9ayf1 oryza sativ	670	7	1.5	1222	2	Q6DHZ4	Q6dhz4 homo sapien
598	7	1.5	796	2	Q25163	Q25163 helicobacte	671	7	1.5	1222	2	Q6F3F5	Q6f3f5 homo sapien
599	7	1.5	805	2	Q8QGN7	Q8qgn7 murine hepa	672	7	1.5	1229	2	Q94979	Q94979 homo sapien
600	7	1.5	807	2	Q7SBL8	Q7sbl8 neurospora	673	7	1.5	1249	2	Q9Z2Q1	Q9z2q1 rattus norv
601	7	1.5	815	2	Q961J4	Q961j4 drosophila	674	7	1.5	1250	2	Q6F3F6	Q6f3f6 homo sapien
602	7	1.5	816	2	Q93YV3	Q93yv3 olea europ	675	7	1.5	1279	2	Q7PR24	Q7pr24 anopheles g
603	7	1.5	824	2	Q78798	Q78798 pylaella l	676	7	1.5	1299	2	Q9STE0	Q9ste0 brassica na
604	7	1.5	829	2	Q7S115	Q7s115 neurospora	677	7	1.5	1318	2	Q9XYE5	Q9xyp5 junonia coe
605	7	1.5	830	1	VFP3_HUMAN	Q13488 h vacuolar	678	7	1.5	1342	2	Q9VHH2	Q9vhh2 drosophila
606	7	1.5	830	2	Q8WVC5	Q8wvc5 homo sapien	679	7	1.5	1343	2	Q7XWN3	Q7xwn3 oryza sativ
607	7	1.5	834	2	Q3U7C0	Q9u7q0 eufolliculi	680	7	1.5	1368	2	O81809	O81809 arabidopsis
608	7	1.5	838	2	Q8PJM9	Q8pjm9 xanthomonas	681	7	1.5	1368	2	O81809	O81809 arabidopsis
609	7	1.5	851	2	Q8L6L3	Q8l6l3 arabidopsis	682	7	1.5	1384	2	O21238	O21238 arabidopsis
610	7	1.5	853	2	Q9J7C2	Q9j7c2 black queen	683	7	1.5	1401	2	Q9LZHE	Q9lzh6 arabidopsis
611	7	1.5	858	2	Q8EVL1	Q8evl1 mycoplasma	684	7	1.5	1449	2	Q8T675	Q8t675 dictyosteli
612	7	1.5	859	2	Q6GQ12	Q6gq12 xenopus lae	685	7	1.5	1449	2	Q8T680	Q8t680 dictyosteli
613	7	1.5	860	2	Q91XU3	Q91xu3 arabidopsis	686	7	1.5	1452	2	Q8CDM9	Q8cdm9 mus musculu
614	7	1.5	862	2	Q6GL61	Q6gl61 xenopus tro	687	7	1.5	1471	2	Q8CHG4	Q8chg4 mus musculu
615	7	1.5	862	2	Q6GP97	Q6gp97 xenopus lae	688	7	1.5	1481	2	Q8BSP0	Q8bsp0 debaryomyc

689	7	1.5	1558	2	Q8YL76	Q8YL76 anabaena sp	762	6	1.2	59	2	Q9DIS5	Q9dis5 hepatitis c
690	7	1.5	1597	1	RLR1 YEAST	P53552 saccharomyc	763	6	1.2	60	1	CD52_MACEFA	P32763 macaca faec
691	7	1.5	1600	1	Q9UEH6	Q9ueh6 homo sapien	764	6	1.2	60	1	Q83ZF3	Q83zf3 mycobacteri
692	7	1.5	1612	1	LAP4 MOUSE	Q8ou72 mus musculu	765	6	1.2	61	1	CD52_HUMAN	P31358 homo sapien
693	7	1.5	1630	1	LAP4_HUMAN	Q14160 homo sapien	766	6	1.2	61	2	Q85425	Q85425 mycobacteri
694	7	1.5	1691	1	CA64 MOUSE	Q14031 homo sapien	767	6	1.2	62	2	Q85425	Q85425 mycobacteri
695	7	1.5	1706	2	O42900	O42900 schizosacch	768	6	1.2	62	2	Q85425	Q85425 mycobacteri
696	7	1.5	1751	2	Q7PXF5	Q7pxf5 anopheles g	769	6	1.2	62	2	Q85425	Q85425 mycobacteri
697	7	1.5	1775	2	Q68FD6	Q68fd6 mus musculu	770	6	1.2	63	2	Q85425	Q85425 mycobacteri
698	7	1.5	1816	2	Q9KBB4	Q9kbb4 bacillus ha	771	6	1.2	63	2	Q85425	Q85425 mycobacteri
699	7	1.5	1922	2	Q8TTP1	Q8ttp1 methanosarc	772	6	1.2	63	2	Q85425	Q85425 mycobacteri
700	7	1.5	2205	2	Q6BJF0	Q6bjf0 debaryomyce	773	6	1.2	64	2	Q85425	Q85425 mycobacteri
701	7	1.5	2310	2	O14002	O14002 schizosacch	774	6	1.2	64	2	Q85425	Q85425 mycobacteri
702	7	1.5	2554	2	Q8YDM7	Q8ydm7 brucella me	775	6	1.2	64	2	Q85425	Q85425 mycobacteri
703	7	1.5	2597	2	Q6WRH9	Q6wrh9 rattus norv	776	6	1.2	65	2	Q85425	Q85425 mycobacteri
704	7	1.5	2870	2	Q77380	Q77380 plasmodium	777	6	1.2	65	2	Q85425	Q85425 mycobacteri
705	7	1.5	2874	2	Q9QDE1	Q9qde1 cryptonectr	778	6	1.2	66	2	Q85425	Q85425 mycobacteri
706	7	1.5	2874	2	Q9QDE2	Q9qde2 cryptonectr	779	6	1.2	66	2	Q85425	Q85425 mycobacteri
707	7	1.5	3412	1	POLG_TBVS	P07720 t genome po	780	6	1.2	66	2	Q85425	Q85425 mycobacteri
708	7	1.5	3414	2	Q8VBS4	Q8vbs4 tick-borne	781	6	1.2	66	2	Q85425	Q85425 mycobacteri
709	7	1.5	3414	2	Q8ORN9	Q8orn9 tick-borne	782	6	1.2	66	2	Q85425	Q85425 mycobacteri
710	7	1.5	3420	2	Q8FUS1	Q8fus1 brucella su	783	6	1.2	66	2	Q85425	Q85425 mycobacteri
711	6	1.2	15	1	OBP3_SOLTU	P81420 solanum tub	784	6	1.2	66	2	Q85425	Q85425 mycobacteri
712	6	1.2	18	2	Q7Y4G6	Q7y4g6 lactococcus	785	6	1.2	67	2	Q85425	Q85425 mycobacteri
713	6	1.2	20	2	Q9QV46	Q9qv46 rattus sp.	786	6	1.2	67	2	Q85425	Q85425 mycobacteri
714	6	1.2	31	2	Q9F215	Q9f215 roseateles	787	6	1.2	67	2	Q85425	Q85425 mycobacteri
715	6	1.2	35	2	Q31223	Q31223 mus musculu	788	6	1.2	67	2	Q85425	Q85425 mycobacteri
716	6	1.2	35	2	Q8DUY1	Q8duy1 streptococ	789	6	1.2	68	2	Q85425	Q85425 mycobacteri
717	6	1.2	38	2	O19473	O19473 mus musculu	790	6	1.2	68	2	Q85425	Q85425 mycobacteri
718	6	1.2	38	2	Q6LBR5	Q6lbr5 mus musculu	791	6	1.2	68	2	Q85425	Q85425 mycobacteri
719	6	1.2	38	2	Q333B1	Q333b1 bacillus ce	792	6	1.2	68	2	Q85425	Q85425 mycobacteri
720	6	1.2	39	2	Q31198	Q31198 mus musculu	793	6	1.2	68	2	Q85425	Q85425 mycobacteri
721	6	1.2	39	2	Q8MB67	Q8mb67 hildebrandt	794	6	1.2	69	2	Q85425	Q85425 mycobacteri
722	6	1.2	39	2	Q97S66	Q97s66 streptococ	795	6	1.2	69	2	Q85425	Q85425 mycobacteri
723	6	1.2	40	2	Q8QYNA	Q8qyna potato leaf	796	6	1.2	69	2	Q85425	Q85425 mycobacteri
724	6	1.2	40	2	Q8IME0	Q8ime0 drosophila	797	6	1.2	69	2	Q85425	Q85425 mycobacteri
725	6	1.2	41	1	LFW_VIBPA	P22100 vibrio para	798	6	1.2	69	2	Q85425	Q85425 mycobacteri
726	6	1.2	42	2	Q8RVK2	Q8rvk2 malus domes	799	6	1.2	69	2	Q85425	Q85425 mycobacteri
727	6	1.2	42	2	Q6ATY2	Q6aty2 oryza sativ	800	6	1.2	69	2	Q85425	Q85425 mycobacteri
728	6	1.2	42	2	Q877N6	Q877n6 vibrio para	801	6	1.2	69	2	Q85425	Q85425 mycobacteri
729	6	1.2	43	2	Q7SEH1	Q7seh1 neurospora	802	6	1.2	69	2	Q85425	Q85425 mycobacteri
730	6	1.2	43	2	Q28784	Q28784 propithecus	803	6	1.2	70	1	DI31_HUMAN	P59861 homo sapien
731	6	1.2	45	2	Q36B35	Q36b35 homo sapien	804	6	1.2	70	2	Q6EQO1	Q6eqo1 oryza sativ
732	6	1.2	45	2	Q7P176	Q7p176 anopheles g	805	6	1.2	70	2	Q7XDQ0	Q7xdq0 oryza sativ
733	6	1.2	45	2	Q62142	Q62142 mus musculu	806	6	1.2	70	2	Q9FRQ5	Q9frq5 oryza sativ
734	6	1.2	46	2	Q8KJW2	Q8kjw2 proteus vul	807	6	1.2	71	2	Q648L3	Q648l3 uncultured
735	6	1.2	46	2	Q8G199	Q8g199 brucella su	808	6	1.2	71	2	Q7PEL8	Q7pel8 anopheles g
736	6	1.2	47	2	Q856G2	Q856g2 mycobacteri	809	6	1.2	71	2	Q7NN24	Q7nn24 gloeobacter
737	6	1.2	48	2	Q80734	Q80734 mus musculu	810	6	1.2	72	2	Q7WZ18	Q7wz18 pseudomonas
738	6	1.2	48	2	Q57533	Q57533 xenopus lae	811	6	1.2	72	2	Q7UL44	Q7ul44 rhodopirell
739	6	1.2	49	2	Q8X370	Q8x370 escherichia	812	6	1.2	72	2	Q83CK5	Q83ck5 coxiella bu
740	6	1.2	49	2	Q81WM4	Q81wm4 bacillus an	813	6	1.2	72	2	Q8CR08	Q8cr08 staphylococ
741	6	1.2	50	2	Q9BSY8	Q9bsy8 homo sapien	814	6	1.2	73	2	Q8TTK5	Q8ttk5 methanosarc
742	6	1.2	50	2	Q7MZG6	Q7mzg6 photorhabdu	815	6	1.2	73	2	Q65219	Q65219 oryza sativ
743	6	1.2	50	2	Q8CL17	Q8cl17 yersinia pe	816	6	1.2	73	2	Q62192	Q62192 oryza sativ
744	6	1.2	52	2	Q95LC5	Q95lc5 sus scrofa	817	6	1.2	73	2	Q7T9D7	Q7t9d7 human cytom
745	6	1.2	52	2	Q6ERM9	Q6erm9 oryza sativ	818	6	1.2	74	2	Q8GAV0	Q8gav0 wolbachia e
746	6	1.2	52	2	Q7M0F0	Q7m0f0 mus musculu	819	6	1.2	74	2	Q6HEK5	Q6hek5 bacillus th
747	6	1.2	53	2	Q29334	Q29334 sus scrofa	820	6	1.2	75	2	Q21995	Q21995 streptococ
748	6	1.2	53	2	Q86962	Q86962 human papil	821	6	1.2	75	2	Q82275	Q82275 arabidopsis
749	6	1.2	54	2	Q8H9V1	Q8h9v1 pseudomonas	822	6	1.2	75	2	Q7P7D4	Q7p7d4 fusobacteri
750	6	1.2	55	2	Q38986	Q38986 arabidopsis	823	6	1.2	75	2	Q635W9	Q635w9 bacillus ce
751	6	1.2	55	2	Q91J98	Q91j98 hepatitis c	824	6	1.2	75	2	Q8VJL0	Q8vj10 mycobacteri
752	6	1.2	56	2	Q8WFO0	Q8wfo0 diadema set	825	6	1.2	75	2	Q732B0	Q732b0 bacillus ce
753	6	1.2	57	2	Q8VPL6	Q8vpl6 salmonella	826	6	1.2	75	2	Q81MS7	Q81ms7 bacillus an
754	6	1.2	58	2	Q8ZVS9	Q8zvs9 pyrobaculum	827	6	1.2	75	2	Q9RZX0	Q9rzx0 borrelia bu
755	6	1.2	58	2	Q6YS37	Q6ys37 oryza sativ	828	6	1.2	76	1	EX75_STAEP	Q8cp39 staphylococ
756	6	1.2	58	2	Q8VLJ9	Q8vlj9 bacillus su	829	6	1.2	76	2	Q8RIY1	Q8riy1 mus musculu
757	6	1.2	58	2	Q7ZE28	Q7ze28 desulfovibr	830	6	1.2	77	1	G101_MOUSE	Q80t62 mus musculu
758	6	1.2	59	1	Q8HR_MACMU	Q8pzi1 macaca mula	831	6	1.2	77	2	Q96WF2	Q96wf2 metarhizium
759	6	1.2	59	2	Q819L9	Q819l9 bacillus ce	832	6	1.2	78	2	Q9QY97	Q9qy97 rattus norv
760	6	1.2	59	2	Q8X6D2	Q8x6d2 escherichia	833	6	1.2	80	2	Q932J4	Q932j4 staphylococ
761	6	1.2	59	2	Q6TRU3	Q6tru3 sulfolobus	834	6	1.2	82	2	Q17276	Q17276 brugia paha

981 6 1.2 100 2 Q6J5E6
 982 6 1.2 100 2 Q8YK03
 983 6 1.2 100 2 Q8A025
 984 6 1.2 100 2 Q8EHU0
 985 6 1.2 100 2 Q8GGG7
 986 6 1.2 100 2 Q8YH4
 987 6 1.2 101 2 Q62721
 988 6 1.2 101 2 Q883B7
 989 6 1.2 101 2 Q99M68
 990 6 1.2 102 1 S61B_SCHPO
 991 6 1.2 102 2 P90600
 992 6 1.2 102 2 Q6IM10
 993 6 1.2 102 2 Q31193
 994 6 1.2 102 2 Q7X8E3
 995 6 1.2 102 2 Q6REF5
 996 6 1.2 102 2 Q8GIV5
 997 6 1.2 102 2 Q6G780
 998 6 1.2 102 2 Q6MRK2
 999 6 1.2 102 2 Q7UI18
 1000 6 1.2 103 1 THIO_BACSU

ALIGNMENTS

RESULT 1
 C3AR HUMAN STANDARD; PRT; 482 AA.
 ID Q16581; O43771; Q92868;
 AC Q16581; O43771; Q92868;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).
 GN Name=C3AR1; Synonym=AK3B, C3R1, HNFAG09;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96180983; PubMed=8605247; DOI=10.1016/0167-4781(95)00209-X;
 RA Roglic A., Prossnitz E.R., Cavanagh S.L., Fan Z., Zou A., Ye R.D.;
 RT "Cloning of a novel G protein-coupled receptor with a large
 RT extracellular loop structure."
 RL Biochim. Biophys. Acta 1305:39-43(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96350520; PubMed=8765043;
 RA Crass I., Raffetseder U., Martin U., Grove M., Klos A., Koehl J.,
 RA Bartsch W.;
 RT "Expression cloning of the human C3a anaphylatoxin receptor (C3AR)
 RT from differentiated U-937 cells."
 RL Eur. J. Immunol. 26:1944-1950(1996).
 RN [3]
 RP REVISIONS.
 RA Bartsch W.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96355342; PubMed=8702752; DOI=10.1074/jbc.271.34.20231;
 RA Ames R.S., Li Y., Sarau H.M., Nuhulaganti P., Foley J.J., Ellis C.,
 RA Zeng Z., Su K., Jurewicz A.J., Hertzberg R.P., Bergsma D.J., Kumar C.;
 RT "Molecular cloning and characterization of the human anaphylatoxin C3a
 RT receptor."
 RL J. Biol. Chem. 271:20231-20234(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-136.
 RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi Q., Nickerson D.A.;
 RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SULFATION.
 RX PubMed=12871936; DOI=10.1074/jbc.M306061200;
 RA Gao J., Choe H., Bota D., Wright P.L., Gerard C., Gerard N.P.;
 RT "Sulfation of tyrosine 174 in the human C3a receptor is essential for
 RT binding of C3a anaphylatoxin."
 RL J. Biol. Chem. 278:37902-37908(2003).
 CC -1- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 CC anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
 CC enzyme release and superoxide anion production.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed in several differentiated
 CC hematopoietic cell lines, in the lung, spleen, ovary, placenta,
 CC small intestine, throughout the brain, heart, and endothelial
 CC cells. Mostly expressed in lymphoid tissues.
 CC -1- PTM: Among the sulfation sites Tyr-174 is essential for binding of
 CC C3a anaphylatoxin.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC EMBL; Z73157; CAA97504.1; -;
 CC EMBL; U62027; AAC50657.1; -;
 CC EMBL; AB065870; BAC06088.1; -;
 CC EMBL; AY268431; AAP23198.1; -;
 CC EMBL; AY455929; AAR13862.1; -;
 CC EMBL; BC020742; AAH20742.1; -;
 CC PIR; S65766; S65766.
 CC Genew; HGNC:13119; C3AR1.
 CC H-InvDB; HIX0010402; -;

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DR MIM: 605246; -: C:integral to plasma membrane; TAS.
DR GO: GO:0005887; F:C3a anaphylatoxin receptor activity; TAS.
DR GO: GO:0004943; F:C3a anaphylatoxin receptor activity; TAS.
DR GO: GO:0004876; F:G-protein coupled receptor activity; TAS.
DR GO: GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO: GO:0004435; P:phosphoinositide phospholipase C activity; TAS.
DR GO: GO:0008015; P:circulation; TAS.
DR GO: GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR GO: GO:0006954; P:inflammatory response; TAS.
DR InterPro: IPR002234; C3aR receptor.
DR InterPro: IPR001644; C3aR receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01104; ANPHYLATXNR.
DR PRINTS: PR01060; C3ANPHYLTXNR.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Polymorphism;
KW Sulfation; Transmembrane.
FT DOMAIN 1 23 Extracellular (Potential).
FT TRANSMEM 24 46 1 (Potential).
FT DOMAIN 47 57 Cytoplasmic (Potential).
FT TRANSMEM 58 80 2 (Potential).
FT DOMAIN 81 96 Extracellular (Potential).
FT TRANSMEM 97 118 3 (Potential).
FT DOMAIN 119 139 Cytoplasmic (Potential).
FT TRANSMEM 140 160 4 (Potential).
FT DOMAIN 161 340 Extracellular (Potential).
FT TRANSMEM 341 360 5 (Potential).
FT DOMAIN 361 377 Cytoplasmic (Potential).
FT TRANSMEM 378 400 6 (Potential).
FT DOMAIN 401 417 Extracellular (Potential).
FT TRANSMEM 418 438 7 (Potential).
FT DOMAIN 439 482 Cytoplasmic (Potential).
FT MOD_RES 174 174 Sulfotyrosine.
FT MOD_RES 184 184 Sulfotyrosine.
FT MOD_RES 318 318 Sulfotyrosine.
FT CARBOHYD 9 9 N-linked (GlcNAc. .) (Potential).
FT DISULFID 95 172 N-linked (GlcNAc. .) (Potential).
FT VARIANT 136 136 By similarity.
FT CONFLICT 151 151 /FTD=VAR_019164.
FT CONFLICT 203 203 F -> C (in Ref. 4).
FT CONFLICT 203 203 P -> R (in Ref. 1).
SQ SEQUENCE 482 AA; 53864 MW; 287E219D98CED203 CRC64;

Query Match 100.0%; Score 482; DB 1; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASFSATNSTDLSSQPNNEPVLISVILSLTLLGLPGNLVWAGLKWQRTVNTI 60
DB 1 MASFSATNSTDLSSQPNNEPVLISVILSLTLLGLPGNLVWAGLKWQRTVNTI 60
QY 61 FLHLTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNNFASVFLTA 120
DB 61 FLHLTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNNFASVFLTA 120
QY 121 CLVFKPTWCQNRHNVGNACISGCIWVAFVFCIPVYREIFTTNDHNRGKFGLS 180
DB 121 CLVFKPTWCQNRHNVGNACISGCIWVAFVFCIPVYREIFTTNDHNRGKFGLS 180
QY 181 SLDPDFDGDPLENRSLENIQPCGMNDRLDPSFQNDHPWTPTVFQPTQFQPSAD 240
DB 181 SLDPDFDGDPLENRSLENIQPCGMNDRLDPSFQNDHPWTPTVFQPTQFQPSAD 240
QY 241 SLPRGSARLTQNLVSNVFKPADVSPKIPSGFFIEDHETSPDLSNDAFLSTHLKLP 300
DB 241 SLPRGSARLTQNLVSNVFKPADVSPKIPSGFFIEDHETSPDLSNDAFLSTHLKLP 300
QY 301 SSNSFYSELPGQFDYINLQFTDDDDQVTPPLVAITITRLVVGFLLPVIMACYSFIV 360

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DB 301 SSNSFYSELPGQFDYINLQFTDDDDQVTPPLVAITITRLVVGFLLPVIMACYSFIV 360
QY 361 FRMQRGRFAKSQSKTFPRVAVVAVFLVCTWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
DB 361 FRMQRGRFAKSQSKTFPRVAVVAVFLVCTWTPYHIFGVLSLLTDPETPLGKTLMSWDHVC 420
QY 421 IALASANSNCFNPLYALLGKDFRKRKARQSQIGILEAAAFSEELTRSTHCPSNNVISERNST 480
DB 421 IALASANSNCFNPLYALLGKDFRKRKARQSQIGILEAAAFSEELTRSTHCPSNNVISERNST 480
QY 481 TV 482
DB 481 TV 482

RESULT 2
Q6TAC8 PRELIMINARY; PRT; 481 AA.
AC Q6TAC8; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Anaphylatoxin C3a receptor.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Therien A.G.; Gervais F.G.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426336; AAR06214.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004943; F:C3a anaphylatoxin receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0006935; P:chemotaxis; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR002234; Anphylx_receptor.
DR InterPro: IPR001644; C3aR_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01104; ANPHYLATXNR.
DR PRINTS: PR01060; C3ANPHYLTXNR.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW Receptor.
SQ SEQUENCE 481 AA; 53577 MW; 4C64DCBAA006BA4F CRC64;

Query Match 11.8%; Score 57; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 5.6e-49;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 WFLHLTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNNFASVFLTA 116
DB 60 WFLHLTLADLLCLSLPFLSLAHALQGGWPYGRFLCKLIPSIIVLNNFASVFLTA 116

RESULT 3
C3AR_MOUSE STANDARD; PRT; 477 AA.
AC C3AR_MOUSE; 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C3a anaphylatoxin chemotactic receptor (C3a-R) (Complement
DE component 3a receptor 1).
GN Name=C3arl; Synonym=C3rl;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1] _SEQUENCE FROM N.A.
 RP STRAIN=129/SVJ; and C57BL/6; TISSUE=Brain;
 RC MEDLINE=97307604; PubMed=9164946;
 RA Tornetta M.A., Foley J.J., Sarau H.M., Ames R.S.;
 RT "The mouse anaphylatoxin C3a receptor: molecular cloning, genomic
 organization, and functional expression.";
 RL J. Immunol. 158:5277-5282(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98044205; PubMed=9382922; DOI=10.1007/s002510050327;
 RA Hsu M.H., Ember J.A., Wang M., Prossnitz E.R., Hugli T.E., Ye R.D.;
 RT "Cloning and functional characterization of the mouse C3a
 anaphylatoxin receptor gene.";
 RL Immunogenetics 47:64-72(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98357887; PubMed=9694514; DOI=10.1016/S0161-5890(98)00021-2;
 RA Hollmann T.J., Haviland D.L., Kildgaard J., Watts K., Wetsel R.A.;
 RT "Cloning, expression, sequence determination, and chromosome
 localization of the mouse complement C3a anaphylatoxin receptor
 gene.";
 RL Mol. Immunol. 35:137-148(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
 enzyme release and superoxide anion production.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Detected in varying levels in all tissues
 examined except the spleen. Especially abundant in heart and lung.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; U77461; AAC53204.1; -;
 DR EMBL; U77460; AAC53203.1; -;
 DR EMBL; AF053757; AAC40193.1; -;
 DR EMBL; BC003728; AAC03728.1; -;

DR MGD; MGI:1097680; C3arl.
 DR InterPro; IPR002234; Anaphylx_receptor.
 DR InterPro; IPR001644; C3Aantx_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01104; ANPHYLATOXNR.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
 KW Transmembrane.
 FT DOMAIN 1 23 Extracellular (Potential).
 FT TRANSMEM 24 46 1 (Potential).
 FT DOMAIN 47 57 Cytoplasmic (Potential).
 FT TRANSMEM 58 80 2 (Potential).
 FT DOMAIN 81 96 Extracellular (Potential).
 FT TRANSMEM 97 118 3 (Potential).
 FT DOMAIN 119 139 Cytoplasmic (Potential).
 FT TRANSMEM 140 160 4 (Potential).
 FT DOMAIN 161 333 Extracellular (Potential).
 FT TRANSMEM 334 353 5 (Potential).
 FT DOMAIN 354 370 Cytoplasmic (Potential).
 FT TRANSMEM 371 393 6 (Potential).
 FT DOMAIN 394 410 Extracellular (Potential).
 FT TRANSMEM 411 431 7 (Potential).
 FT DOMAIN 432 477 Cytoplasmic (Potential).
 FT MOD_RES 174 174 Sulfotyrosine (By similarity).
 FT MOD_RES 184 184 Sulfotyrosine (By similarity).
 FT MOD_RES 312 312 Sulfotyrosine (By similarity).
 FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
 FT DISULFID 95 172 By similarity.
 FT CONFLICT 173 173 R -> K (in Ref. 2).
 FT CONFLICT 195 195 E -> K (in Ref. 2).
 FT CONFLICT 243 243 D -> N (in Ref. 2).
 FT CONFLICT 276 276 D -> N (in Ref. 2).
 FT CONFLICT 380 382 FIC -> LS (in Ref. 2).
 FT CONFLICT 391 391 V -> I (in Ref. 2).
 FT CONFLICT 460 460 N -> S (in Ref. 2).
 SQ SEQUENCE 477 AA; 53575 MW; 9873F464A1520984 CRC64;
 Query Match 6.2%; Score 30; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 2.4e-21;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 421 IALASNSCFNPFLYALLGKDFRKARQSI 450
 Db 414 IALASNSCFNPFLYALLGKDFRKARQSI 443
 RESULT 4
 ID Q8C6R2 PRELIMINARY; PRT; 477 AA.
 AC Q8C6R2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-
 DE length enriched library, clone:E230012109 product:complement component
 DE 3a receptor 1, full insert sequence.
 GN Name=C3arl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;

QY	421	ILALNSCNFPFLYALLGKDFRKKARQSI	450
DB	414	ILALNSCNFPFLYALLGKDFRKKARQSI	443

RESULT 5	
C3AR_RAT	
ID	C3AR_RAT
AC	O55197;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).
OS	Names=C3arl;
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Wistar; TISSUE=Lung;
RX	MEDLINE=98125550; PubMed=9464274; DOI=10.1006/bbrc.1997.8034;
RA	Fukuoka Y., Ember J.A., Hugli T.E.;
RT	"Cloning and characterization of rat C3a receptor: differential
RT	expression of rat C3a and C5a receptors for LPS stimulation.";
RT	Biochem. Biophys. Res. Commun. 242:663-668(1998).
CC	-1- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC	anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
CC	enzyme release and superoxide anion production.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U86379; AAC40071.1; --
DR	PIR; JC5835; JC5835.
DR	RGD; 620537; C3arl.
DR	InterPro; IPR002234; Anphylx receptor.
DR	InterPro; IPR001644; C3aantx receptor.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm1.1; 1.
DR	PRINTS; PR01104; ANPHYLATOXNR.
DR	PRINTS; PR01060; C3ANPHYLTXNR.
DR	PRINTS; PR00237; GPCRHHODPSN.
DR	PROSITE; PS00237; G PROTEIN RECEP F1.1; 1.
DR	PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
KW	Chemotaxis; G-protein coupled receptor; Glycoprotein; Sulfation;
KW	Transmembrane.
FT	DOMAIN 1 23 Extracellular (Potential).
FT	TRANSMEM 24 46 1 (Potential).
FT	TRANSMEM 47 57 Cytoplasmic (Potential).
FT	TRANSMEM 58 80 2 (Potential). (Potential).
FT	DOMAIN 81 96 Extracellular (Potential).
FT	TRANSMEM 97 118 3 (Potential).
FT	DOMAIN 119 139 Cytoplasmic (Potential).
FT	TRANSMEM 140 160 4 (Potential).
FT	DOMAIN 161 329 Extracellular (Potential).
FT	TRANSMEM 330 349 5 (Potential).
FT	DOMAIN 350 366 Cytoplasmic (Potential).
FT	TRANSMEM 367 389 6 (Potential).
FT	DOMAIN 390 406 Extracellular (Potential).
FT	TRANSMEM 407 427 7 (Potential).
FT	DOMAIN 428 473 Cytoplasmic (Potential).
FT	DISULFID 95 172 By similarity. (By similarity).
FT	MOD_RES 174 184 Sulfotyrosine (By similarity).
FT	MOD_RES 184 184 Sulfotyrosine (By similarity).

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FT MOD RES 308 308 Sulfotyrosine (By similarity).
FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 473 AA; 52896 MW; 722F16F64B16451 CRC64;

Query Match 6.0%; Score 29; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.5e-20; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0;

QY 421 IALASANSFCNPFYALLGKPRKQARQS 449
DB 410 IALASANSFCNPFYALLGKPRKQARQS 438

RESULT 6
C3AR_CAVPO STANDARD; PRT; 475 AA.
ID C3AR_CAVPO
AC O88680; Q90W93;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR).
GN Name=C3AR;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98391014; PubMed=9725198;
RA Lienenklaus S., Ames R.S., Tornetta M.A., Sarau H.M., Foley J.J.,
RA Crass T., Sohns B., Raffetseder U., Grove M., Hoelzer A., Klos A.,
RA Koehl J., Bautsch W.;
RT "Human anaphylatoxin C3a is a potent agonist of the guinea pig but not
RL the human C3a receptor.";
RL J. Immunol. 161:2089-2093 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC STRAIN=Hartley; Tissue=Spleen;
RX MEDLINE=98414293; PubMed=9743361;
RA Fukuko Y., Ember J.A., Hugli T.E.;
RT "Molecular cloning of two isoforms of the guinea pig C3a anaphylatoxin
RL receptor: alternative splicing in the large extracellular loop.";
RL J. Immunol. 161:2977-2984 (1998).
CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC anaphylatoxin C3a. This receptor stimulates chemotaxis, granule
CC enzyme release and superoxide anion production.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=gpC3AR-L;
CC IsoId=O88680-1; Sequence=Displayed;
CC Name=2; Synonyms=gpC3AR-S;
CC IsoId=O88680-2; Sequence=VSP_010628;
CC -!- TISSUE SPECIFICITY: Expressed in the heart, kidney, lung, liver,
CC peritoneal macrophages and spleen.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC EMBL; AJ006402; CAA07002.1; -
CC EMBL; U86378; AAC36503.1; -
CC InterPro; IPR002234; Anphylx_receptor.
CC InterPro; IPR001644; C3Aantx_receptor.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR01104; ANPHYLATXNR.

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DR PRINTS; PR01060; C3ANPHYLTXNR.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW Alternative splicing; Chemotaxis; G-protein coupled receptor;
KW Glycoprotein; Sulfation; Transmembrane
FT DOMAIN 1 23 Extracellular (Potential).
FT TRANSMEM 24 46 1 (Potential).
FT DOMAIN 47 57 Cytoplasmic (Potential).
FT TRANSMEM 58 80 2 (Potential).
FT DOMAIN 81 96 Extracellular (Potential).
FT TRANSMEM 97 118 3 (Potential).
FT DOMAIN 119 139 Cytoplasmic (Potential).
FT TRANSMEM 140 160 4 (Potential).
FT DOMAIN 161 331 Extracellular (Potential).
FT TRANSMEM 332 351 5 (Potential).
FT DOMAIN 352 368 Cytoplasmic (Potential).
FT TRANSMEM 369 391 6 (Potential).
FT DOMAIN 392 408 Extracellular (Potential).
FT TRANSMEM 409 429 7 (Potential).
FT DOMAIN 430 475 Cytoplasmic (Potential).
FT DISULFID 95 172 By similarity.
FT MOD RES 174 174 Sulfotyrosine (By similarity).
FT MOD RES 183 183 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 273 273 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 254 288 Missing (in isoform 2).
FT CONFLICT 2 2 E -> D (in Ref. 2).
FT CONFLICT 357 357 V -> A (in Ref. 2).
SQ SEQUENCE 475 AA; 53570 MW; OD6FF5627A53330 CRC64;

Query Match 3.9%; Score 19; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 IALASANSFCNPFYALLG 439
DB 412 IALASANSFCNPFYALLG 430

RESULT 7
Q6T3R0
ID Q6T3R0 PRELIMINARY; PRT; 346 AA.
AC Q6T3R0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C3a receptor (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15034053;
RA Boshra H., Li J., Peters R., Hansen J., Matlapudi A., Sunyer J.O.;
RT "Cloning, expression, cellular distribution, and role in chemotaxis of
RT a c3a receptor in rainbow trout: the first identification of a c3a
RT receptor in a nonmammalian species.";
RL J. Immunol. 172:4381-4390 (2004).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC EMBL; AY438032; AAR97322.1; -
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0004982; F:N-formyl peptide receptor activity; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
CC InterPro; IPR000826; FRT/met_receptor.

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DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00526; FMETLEUPHER.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 346 346
SQ SEQUENCE 346 AA; 38845 MW; 33A597F1A24E0020 CRC64;

Query Match 2.3%; Score 11; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LADLLCLSLP 76
| | | | | | | | | |
Db 80 LADLLCLSLP 90

RESULT 8
Q6UNNA4 PRELIMINARY; PRT; 350 AA.
AC Q6UNNA4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Csa receptor.
GN Name=CsaR;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Head kidney;
RX PubMed=14628104;
RA Fujiki K., Liu L., Sundick R.S., Dixon B.;
RT "Molecular cloning and characterization of rainbow trout (Oncorhynchus mykiss) Csa anaphylatoxin receptor."
RL Immunogenetics 55:640-646(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AY366354; AAR12188.1; -.
DR EMBL: AY366353; AAR12187.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004982; F: N-oxyl peptide receptor activity; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000826; Ftm/met_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00526; FMETLEUPHER.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 39322 MW; 949F76B24CB597F1 CRC64;

Query Match 2.3%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LADLLCLSLP 76
| | | | | | | | | |
Db 80 LADLLCLSLP 90

RESULT 9
CLT2_MOUSE STANDARD; PRT; 309 AA.
ID CLT2_MOUSE
AC Q920A1;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyln leukotriene receptor 2 (CysLTR2).
GN Name=CysLTR2; Synonyms=CysLT2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Heart;
MEDLINE=21601669; PubMed=11591709; DOI=10.1074/jbc.M107556200;
Hui Y., Yang G., Galczinski H., Figueroa D.J., Austin C.P.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;
"The murine cysteinyl leukotriene 2 (CysLTR2) receptor. cDNA and genomic cloning, alternative splicing, and in vitro characterization."
J. Biol. Chem. 276:47489-47495 (2001).
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTC4 = LTD4 >> LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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-----
DR EMBL: AF331658; AAK97354.1; -.
DR MGD; MGI:191736; CysLTR2.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0001631; F: cysteinyl leukotriene receptor activity; IEA.
DR InterPro: IPR004071; Cysleuk_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01533; CysLTR2RECEPTOR.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26 Extracellular (Potential).
FT TRANSMEM 27 47 1 (Potential).
FT DOMAIN 48 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 98 Extracellular (Potential).
FT TRANSMEM 99 119 3 (Potential).
FT DOMAIN 120 138 Cytoplasmic (Potential).
FT TRANSMEM 139 159 4 (Potential).
FT DOMAIN 160 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 35227 MW; 327B14A6EDD2A02 CRC64;

Query Match 2.1%; Score 10; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 ANSCFNPLY 435

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Db 280 ANSCFNPFY 289
|||||

RESULT 10

CLT2_RAT STANDARD; PRT; 309 AA.
AC Q924T9;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyll leukotriene receptor 2 (CysLT2) (RSAPT32).
GN Name=CysLT2; Synonyms=Cyslt2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushima H., Furuichi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
receptors.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
mediated via a G-protein that activates a phosphatidylinositol-
calcium second messenger system (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB052661; BAB60816.1; -;
CC RGD; 619797; Cyslt2.
CC InterPro; IPR004071; Cysleuk receptor.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR01533; CysLTRECPTR.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26 Extracellular (Potential).
FT TRANSMEM 27 47 1 (Potential).
FT DOMAIN 48 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 98 Extracellular (Potential).
FT TRANSMEM 99 119 3 (Potential).
FT DOMAIN 120 137 Cytoplasmic (Potential).
FT TRANSMEM 138 158 4 (Potential).
FT DOMAIN 159 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 2.1%; Score 10; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 ANSCFNPFY 435
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Db 280 ANSCFNPFY 289

RESULT 11

Q8R528 PRELIMINARY; PRT; 309 AA.
AC Q8R528;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cysteinyll leukotriene 2 receptor.
GN Name=Cyslt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;
RA Gasawara H., Ishii S., Yokomizo T., Kakinuma T., Komine M.,
RA Tanaka K., Shimizu T., Izumi T.;
RT "Characterization of Mouse Cysteinyll Leukotriene Receptors mCysLT1 and
mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE
DISTRIBUTION.";
RL J. Biol. Chem. 277.18763-18768(2002).
DR EMBL; AB058930; BAB86881.1; -;
DR MGD; MGI:1917336; Cyslt2.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0001631; F: cysteinyl leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01533; CysLTRECPTR.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC6B8AF96974 CRC64;

Query Match 2.1%; Score 10; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 ANSCFNPFY 435
|||||
Db 280 ANSCFNPFY 289

RESULT 12

C5L2_HUMAN STANDARD; PRT; 337 AA.
AC Q9P256;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C5a anaphylatoxin chemotactic receptor C5L2.
GN Name=QPR77; Synonyms=C5L2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ohno M., Hirata T., Enomoto M., Araki T., Sato K., Ishimaru H.,
RA Takahashi T.A.;
RT "A putative chemoattractant receptor, C5L2 is expressed in granulocyte
and immature dendritic cells, but mature dendritic cells.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=11165367; DOI=10.1016/S0169-328X(00)00242-4;

RA Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
 RA Lynch K.R., O'Dowd B.F.;
 RT "Identification of four novel human G protein-coupled receptors
 RT expressed in the brain.";
 RL Brain Res. Mol. Brain Res. 86:13-22(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RN Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21850712; PubMed=11773063; DOI=10.1074/jbc.C100714200;
 RA Cain S.A., Monk P.N.;
 RT "The orphan receptor CSL2 has high affinity binding sites for
 RL J. Biol. Chem. 277:7165-7169(2002).
 CC -|- FUNCTION: Receptor for the chemotactic and inflammatory peptide
 CC anaphylatoxin C5a, C4a and C3a and their des argininated
 CC derivatives. Couples weakly to G α -mediated signaling pathways.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- TISSUE SPECIFICITY: Frontal cortex, hippocampus, hypothalamus,
 CC pons and liver.
 CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB038237; BAA95414.1; -;
 DR EMBL; AF317655; AAK12640.1; -;
 DR EMBL; AY268430; AAP23197.1; -;
 DR Genew; HGNC:4527; GPR77.
 DR GO; GO:0016526; P:G-protein coupled receptor activity, unknown. . .; NAS.
 DR InterPro; IPR001274; CSAantx receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00426; CSANPHYLTXNR.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP F1_1; FALSE_NEG.
 DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 38
 FT Extracellular (Potential).
 FT TRANSMEM 39 61
 FT Cytoplasmic (Potential).
 FT DOMAIN 62 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 114
 FT Extracellular (Potential).
 FT TRANSMEM 115 137
 FT DOMAIN 138 149
 FT Cytoplasmic (Potential).
 FT TRANSMEM 150 172
 FT DOMAIN 173 202
 FT Extracellular (Potential).
 FT TRANSMEM 203 225
 FT DOMAIN 226 237
 FT Cytoplasmic (Potential).
 FT TRANSMEM 238 260
 FT DOMAIN 261 274
 FT Extracellular (Potential).
 FT TRANSMEM 275 294
 FT DOMAIN 295 337
 FT Cytoplasmic (Potential).
 FT CARBOHYD 3 3
 FT N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 107 186
 FT By similarity.
 SQ SEQUENCE 337 AA; 36080 MW; 53AF41B129F8FE6 CRC64;

Query Match 2.1%; Score 10; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ADLLCCLSLP 76
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Db 79 ADLLCCLSLP 88
 RESULT 13
 Q6NWQ8
 ID Q6NWQ8 PRELIMINARY; PRT; 337 AA.
 AC Q6NWQ8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE G protein-coupled receptor CSL2.
 GN Name=GPR77;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067480; AAH67480.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004944; F:C5a anaphylatoxin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0006935; F:chemotaxis; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR001274; CSAantx receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00426; CSANPHYLTXNR.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 337 AA; 36068 MW; 548641B1250BFE6 CRC64;
 Query Match 2.1%; Score 10; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ADLLCCLSLP 76
 |||||

Db 79 ADLLCCLSLP 88
 RESULT 14
 Q6NWQ9
 ID Q6NWQ9 PRELIMINARY; PRT; 337 AA.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RR EMBL; BC067477; AAH67477.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004944; F:C5a anaphylatoxin receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0003584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR001274; CSAntx receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00426; C5ANPHYLTXNR.
DR PRINTS; PR00237; GPCRRHODOPSIN.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 337 AA; 36138 MW; B544A21A270A33EC CRC64;

Query Match 2.1%; Score 10; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 ADLLCCLSLP 76
|||
DB 79 ADLLCCLSLP 88

Search completed: April 13, 2005, 10:06:09
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